Computer-Assisted Language Comparison in Practice

Tutorials on Computational Approaches to the History and Diversity of Languages

Contributions from 2019

Edited by

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Contents

Introduction

By comparing the languages of the world, we gain invaluable insights into human prehistory, predating the appearance of written records by thousands of years. The traditional methods for language comparison are based on manual data inspection. With more and more data available, they reach their practical limits. Computer applications, however, are not capable of replacing experts' experience and intuition. In a situation where computers cannot replace experts and experts do not have enough time to analyse the massive amounts of data, a new framework, neither completely computer-driven, nor ignorant of the help computers provide, becomes urgent.

The weblog *Computer-Assisted Language Comparison in Practice*, published on the Hypotheses platform for scientific blogging, offers tutorials and discussion notes on computer-assisted approaches to the history and diversity of languages. A substantial part of its content is contributed as part of the ERC Starting Grant "Computer-Assisted Language Comparison" (CALC, 715618), funded by the European Research Council. But on the long run, we want to make this blog a platform for everybody willing to share ideas on small or big problems involving data preparation and analysis in computer-assisted or computer-based approaches to language comparison.

This document summarizes all contributions from 2019. If you want to cite them, please follow the instructions at the end of each contribution. I express my gratitude to all contributors, who helped to make this an interesting collection of tutorials, algorithms, and initial theories related to the fields of computer-assisted language comparison.

Johann-Mattis List (Jena, November 2020)

From Fieldwork to Trees III: CLDF recipes

Gereon A. Kaiping (21/01/2019)

Categories: Code

Tags: Austronesian Languages, CLDF recipes, cross-linguistic data formats, example, lexical data

In the previous two posts, I took you from a matrix of word lists from fieldwork to a LingPy-compatible CLDF Wordlist with cognate codes and alignments. We can now feed this dataset into existing tools and recipes for visualizing and analyzing CLDF Wordlists.

If we add geolocations to the languages in our dataset, we can use an existing CLDF recipe from the CLDF cookbook (Forkel et al. 2018) to plot the density of the data on a map. Some more metadata on the lects would be a good thing to have anyway, so let us add a table to the dataset. Dialects are described in another CSV or TSV table, like this:

ID	Name	Glottocode	Latitude	Longitude
dul	Dulolong	alor1247	8.2357	124.4444
alk	Alor Kecil	alor1247	8.2591	124.4092
alb	Alor Besar	alor1247	8.2224	124.4079

The metadata file then gets some additional entries (mostly the description of this new table, as well as a "Foreign Key" relationship linking the form table to this table) to make sure that this data is found and properly associated with the forms in the table, which I have added to `Alorese-Lects-metadata.json`. If we had descriptions of the concepts, eg. with links to Concepticon (List, Cysouw & Forkel 2016), they would also be associated using the metadata file.

Before we start using this enriched wordlist for other purposes, it may be useful to see whether the file is indeed valid CLDF. The Python `pycldf` package comes with a tool to validate and list statistics of datasets.

```
$ pip install pycldf...
$ cldf validate Alorese-Lects-metadata.json
$ cldf stats Alorese-Lects-metadata.json
<cldf:v1.0:Wordlist at .>
key                        value
special:publisher_url      http://www.universiteitleiden.nl/en/humanities/
    leiden-university-centre-for-linguistics
dc:license                 (C) 2018 Yunus Sulistyono
special:contact            g.a.kaiping@hum.leidenuniv.nl
dc:identifier              Alorese Dialects 0.1.0, abridged
dc:conformsTo              http://cldf.clld.org/v1.0/terms.rdf#Wordlist
dc:title                   Alorese Dialects, abridged
dc:publisher               Leiden University Centre for Linguistics
dc:isReferencedBy          https://calc.hypotheses.org/803
dc:creator                 ['Sulistyono, Yunus', '', 'Kaiping, Gereon
    Alexander']
dc:description             Lexical data of 13 Alorese [alor1247] dialects,
    abridged
dc:coverage                http://vocab.getty.edu/page/tgn/1009828
special:publisher_place    Leiden, The Netherlands
Path           Type               Rows
aligned.tsv    FormTable            53
languages.tsv  LanguageTable         3
```

The lack of output after the second command is a good thing: It means that no problems were found in our dataset. If there were errors in the word list, `cldf validate` would complain.

This dataset is now easy to visualize. Get the cookbook recipe and its dependencies (admittedly, getting `basemap` to work can be a bit of a hassle), and then a simple `python plot_representation.py Alorese-Lects-metadata.json alorese.png --cmap viridis_r` will generate a figure containing the three Alorese villages, each with the number of forms sampled from there. (The `viridis` color map is slightly greener, where the default `magma` cmap has a yellow that is even more similar to the land background color.)

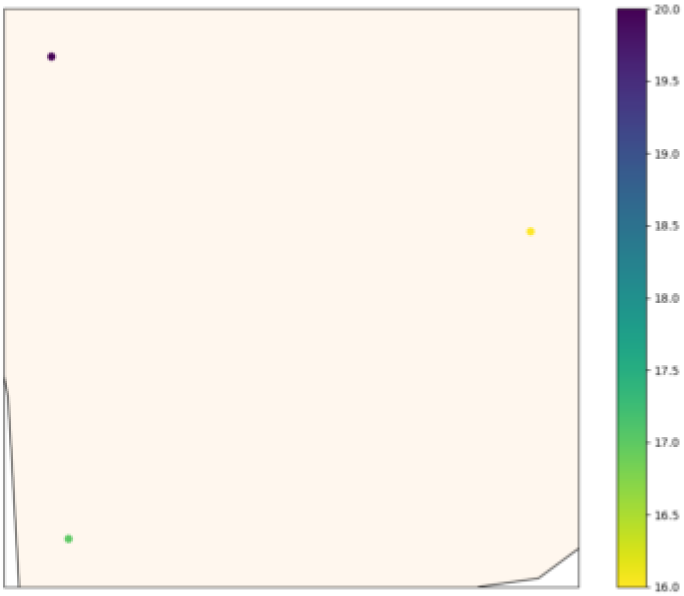

Figure 1: Number of forms given in the abridged Alorese dataset, for each of the three different dialects. The black line is the coastline of the birdshead peninsula of the island of Alor.

Another interesting tool to analyze CLDF wordlists comes in the Python library accompanying the LexiRumah dataset (Kaiping, Edwards & Klamer 2019). For creating orthographies for the languages in that dataset, we needed to know what sounds they use. The `pylexirumah.get_phonetic_inventories` module goes through the CLDF wordlist and counts the frequency of all segments that appear, both per-language and overall.

```
$ python -m pylexirumah.get_phonetic_inventories --dataset Alorese-Lects-metadata.json
alk
        a    11
        o    8
        i    8
        e    7
        m    5
        k    4
        n    4
        r    4
        f    3
        p    3
        h    2
        _    2
        g    2
        l    1
        u    1
dul
        a    16
        i    6
        e    5
        _    5
        n    5
        t    5
        r    4
        f    3
(...)
```

This again shows that the [full] data is not entirely clean: ; and h̃ are both unexpected as phonetic segments.

Any other CLDF Wordlist tool you might come along should also work with this dataset. For example, have a look at pylexibank (Forkel 2018), the python package for working with the Wordlists in the LexiBank project. The list of useful tools also includes the BEASTling tool for generating phylogenetic inference driver files, which we will work with in the next step.

References

Forkel, Robert. 2018. *pylexibank*. Python lexibank. https://github.com/lexibank/pylexibank (19 January, 2019).

Forkel, Robert, Sebastian Bank, Gereon A. Kaiping, Christoph Rzymski & Simon J. Greenhill. 2018. *pycldf*. Python. Cross-Linguistic Data Formats. https://github.com/cldf/pycldf (19 January, 2019).

Forkel, Robert, Christoph Rzymski, Gereon A. Kaiping & Mattis List. 2019. *The CLDF Cookbook*. Jupyter Notebook. Cross-Linguistic Data Formats. https://github.com/cldf/cookbook (19 January, 2019).

Kaiping, Gereon A., Owen Edwards & Marian Klamer. 2019. *LexiRumah 2.0.0*. Zenodo. doi: 10.5281/zenodo.2540954. https://zenodo.org/record/2540954#.XENYWaHrC00 (19 January, 2019).

List, Johann-Mattis, Michael Cysouw & Robert Forkel (eds.). 2016. *Concepticon*. Jena: Max Planck Institute for the Science of Human History. doi: 10.5281/zenodo.51259. http://concepticon.clld.org/.

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A Primer on Automatic Inference of Sound Correspondence Patterns I: Introduction

Johann-Mattis List (30/01/2019)

Categories: Primer

Tags: cognate detection, correspondence patterns, phonetic alignment, tutorial

After about three years of work on the matter, I have managed (with help of many colleagues who helped in testing) to develop a first approach for the *automatic inference of sound correspondence patterns*, which will soon be published with Computational Linguistics (List 2019). The key task which this algorithm solves is to take aligned data as input and to compute explicit *sound correspondence patterns* from the alignments.

Correspondence patterns are hereby understood as recurring alignment sites (i.e., columns per alignment) in a given dataset. In contrast to *regular sound correspondences* (or *systematic sound correspondences*, as Trask (2000) calls them), a correspondence pattern is a statement of sound correspondences across multiple languages, while regular sound correspondences are usually discussed for two languages only, at least in automatic (see Kondrak 2002) and formal approaches (see e.g., Hoenigswald 1960).

The result of an automatic correspondence pattern analysis can be thought of as some kind of a table, in which languages are placed in the columns, and correspondence patterns are placed in rows, with each cell indicating for each individual correspondence pattern, which reflex sound a given language shows for this pattern.

As an example, consider the following table, which shows four varieties of the Tableaux Phonétiques des Patois Suisses Romands (Gauchat et al. 1925), which were included as test set for the alignment algorithm presented in my thesis (List 2014).

Pattern	Frequency	Champéry	Lourtier	Plagne	Courtedoux
r	21	r	r	r	r
-(1)	8	--	--	ə	--
t	8	t	t	t	t
m	8	m	m	m	m
f	8	f	f	f	f
p	7	p	p	p	p
-(2)	4	--	--	--	ə
s	4	s	ʃ	s	s
k	3	k	k	k	tʲ

The table provides some ecclectic information (and I could easily provide more), namely some "identifier" for the pattern (which I created in an ad-hoc manner here), the frequency of attested alignment sites, where the pattern occurs, and the concrete reflexes in the four varieties.

While most of the patterns look boring, showing the same reflex in all varieties (which should not be surprising, given that we're dealing with dialect data here), some show some degree of variation, such as the two patterns which I label as *-(1) and *-(2), respectively, or the pattern *s and *ku. The first two patterns illustrate different degrees of metathesis across the varieties, as they surface in words like "du poivre", where prototypical reflexes would be Champéry [paːvro] as opposed to Plagne [paːvər] for the first, and Champéry [pɛrdy] as opposed to Courtedoux [prədʒy]. The *s pattern illustrates the pronunciation of original [s] as [ʃ] initials in Lourtrier, and the third pattern illustrates a specific palatalization process of velars in Courtedoux.

What is interesting and important about these data is how useful they are for additional tasks in historical linguistics. Correspondence patterns can, for example, be used to *predict* the pronunciation of missing reflexes in a given dataset (as I show in my forthcoming paper, List 2019), they can also be used to reconstruct a given ancestor form semi-automatically, given that all alignment sites which are assigned to the same correspondence pattern directly reflect the same common ancestor sound, and they can be used to investigate conditioning context, given that patterns that look very similar but differ regarding the reflexes of a few varieties often derive from the same proto-sound whose change was then modified in specific environments.

While correspondence patterns can be investigated manually, and people have been doing this in the past, the new computer-assisted methods which we have developed so far greatly facilitate the systematic investigation of correspondence patterns in historical linguistics. The only problem is that — in order to successfully carry out an automatic search for sound correspondence patterns, the data needs to be provided in a very good state, with a very high level of consistency and annotation.

In the following couple of weeks, I want to provide examples for different datasets, illustrating how these can be analyzed with help of the tools for automatic correspondence pattern detection, which have been developed in the past. In this context, I plan to select different datasets and show how they have to be prepared in order to properly analyze them. The posts will be accompanied by supplementary data and code, so that interested users can directly apply and test the examples discussed.

References

Gauchat, Louis and Jeanjaquet, Jules and Tappolet, Ernest (1925): *Tableaux phonétiques des patois suisses romands. Relevés comparatifs d'environ 500 mots dans 62 patois-types*. Publiés avec introduction, notes, carte et répertoires . Neuchâtel:Attinger.

Hoenigswald, Henry M. (1960): Phonetic similarity in internal reconstruction. *Language* 36.2. 191-192.

Kondrak, Grzegorz (2002): Determining Recurrent Sound Correspondences by Inducing Translation Models. In: *Nineteenth International Conference on Computational Linguistics (COLING 2002)*. 488-494.

List, Johann-Mattis (2014): *Sequence comparison in historical linguistics*. Düsseldorf:Düsseldorf University Press.

List, Johann-Mattis (forthcoming): Automatic inference of sound correspondence patterns across multiple languages. *Computational Linguistics* ?? 1-24.

Trask, Robert L. (2000): *The dictionary of historical and comparative linguistics*. Edinburgh:Edinburgh University Press.

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A Primer on Automatic Inference of Sound Correspondence Patterns II: Initial Experiments with Alignments from the Tableaux Phonétiques des Patois Suisses Romands

Johann-Mattis List (27/02/2019)

Categories: Analysis, Primer

Tags: Benchmark Database of Phonetic Alignments, correspondence patterns, EDICTOR, LingPy, Python, Tableaux Phonétiques des Patois Suisses Romands

Following up on my announcement to present in more detail how the algorithms for automatic correspondence pattern detection can be applied, this post introduces the preliminary preparations needed to run a first experiment with aligned data. In order to avoid that we have to align a dataset completely from scratch, we make use of already aligned data from the Tableaux Phonétiques des Patois Suisses Romands by Gauchat et al. (1925), which were originally aligned for the study in List (2014) and later published as part of the Benchmark Database of Phonetic Alignments (List and Prokić 2014). In this post, I will introduce how we can harvest the alignments from this dataset with help of LingPy, and later analyze them with help of the sound correspondence pattern algorithms.

The Tableaux Phonétiques des Patois Suisses Romands (Gauchat et al. 1925) is a large collection of dialect data on French dialects spoken in Switzerland. Originally collected by Gauchat and colleagues, it was digitized in a project by Hans Geisler (Heinrich Heine Universität Düsseldorf) but could by then not be published officially due to copyright restrictions. Fortunately, however, I could use parts of the data for my dissertation (List 2014), where I aligned 76 of the charts for as many as 62 dialect points. While the data in its form used by then can still be interactively searched from the website offering all supplementary material accompanying my dissertation, I figured later that it would be better to share it officially as part of a larger benchmark database of phonetic alignments, which I published together with Jelena Prokić, who contributed alignments for Bulgarian dialects to that sample (List and Prokić 2014). This Benchmark Database of Phonetic Alignments (BDPA) offers a potentially more convenient way of browsing and inspecting alignment data, although the data is not necessarily offered in a convenient form to reuse.

As of now, the original alignment data underlying the BDPA has also been submitted to Zenodo, from where it can still be downloaded. The data on the Zenodo repository is of a very simple structure, containing a bunch of zip-folders for each of the different datasets from which we harvested the alignments, along with two redundant master-folders, containing all 750 multiple sequence alignments. Each of the folders contains two sub-folders, one called `msa`, containing the multiple alignments in the so-called `msa-format`, which can be readily imported and processed by LingPy, as well as a `psa`-folder, containing all corresponding pairwise phonetic alignments (i.e., pairwise alignments automatically derived from the multiple alignments by extracting all possible pairs).

The `msa`-format is basically outdated, and we don't use it anymore, although LingPy still parses it. For testing purposes, this is quite useful, although we now usually tend to use alignments exclusively in wordlists, where we have more consistent ways of handling the data, and also doing more interesting analyses. The `msa`-format is described in detail on the LingPy website, so I will spare the readers and myself a closer description here. What is important to know is that we want to convert those files corresponding to the TPPSR in the

BDPA, asprovided in msa-format on Zenodo to the "normal" *wordlist-format*, as it is used by the LingPy package (see List et al. 2018 for a closer description) and also required in order to compute correspondence patterns with help of LingRex and the correspondence pattern recognition algorithm (List 2019).

Assuming that you have downloaded the data from Zenodo and unpacked the multiple.zip folder, placing the msa-folder in your current working directory (or cd-ing into it), we can now get started to convert the data. Our goal is to select some 15 representative dialects from the data, extract their alignments, and store them in the wordlist-format, so that we can later analyze the correspondence patterns in the data. We thus start by setting up our Python script in which we import the packages required:

```python
from lingpy import *
from glob import glob
import re
import tqdm
from lingpy.align.sca import normalize_alignment
```

We use glob to retrieve the paths of the files, and tqdm to have a status bar that informs us about the process. We further need the re module to retrieve some information about the data, lingpy in general, and the normalize_alignment function in specific. This latter function will delete all those columns from an alignment, which consist only of gaps. This can happen when taking only a small selection of language varieties from a larger selection of aligned words.

We can now retrieve all files with help of glob.

```python
files = glob('msa/*.msa')
```

To make sure that we find the varieties we want, I made a manual pre-selection, which we represent as a Python dictionary:

```
selection = {'Boudry': '46',
 'Cerneux-Péquignot': '53',
 'Champéry': '18',
 'Courtedoux': '62',
 'Courtepin': '41',
 'Côte-aux-Fées': '50',
 'Dompierre': '42',
 'Evoléne': '30',
 'Grimentz': '31',
 'Hermance': '36',
 'Lourtier': '22',
 '’LAuberson': '3',
 'Ormont-Dessus': '15',
 'Plagne': '56',
 }
```

We also represent our wordlist as a Python dictionary, where the `0`-key represents the column header.

```
D = {0: [
    'doculect',
    'language_id',
    'concept',
    'latin',
    'french',
    'form',
    'tokens',
    'alignment',
    'cogid'
    ]}
```

As we want to fill the wordlist with identifiers for the words themselves and for cognates consecutively, we set them now as variables.

```
idx, cogid = 1, 1
```

We also define a very lazy converter, since we want to replace all underscores in the alignments by a + symbol, which is now the standard marker for morpheme boundaries, which we decided for during the last year (but older versions have still the underscore _ as a marker for word boundaries).

```
converter = {
        '_': '+'
        }
```

We can now start by looping over all files and extracting the relevant data. In this loop, we open each of the msa-files with help of LingPy, and assess it's dataset property. If the dataset is French, we keep the file and try to process it further. We use a regular expression to parse the HTML-like coding of the so-called sequence identifier of the alignment, which is the counterpart of the aligned word forms in French and its projected ancestral form in Latin. Since the msa format does not specify how the dataset or the sequence identifier should be structured, the formats are pretty free, and by then, I used HTML-like tags for convenience (1).

Once we have extracted the dataset, made sure it is French, and also extracted the Latin and the French word form, we can extract the aligned data from the MSA-object, stored in the variable msa. Here, we iterate over its properties msa.taxa and msa.alignment and check if the name of the variety also occurs in our dictionary of pre-selected varieties. If this is the case, we retrieve the unaligned but segmented form (called tokens) by stripping off all dashes from the alignment, and we also retrieve the raw, unsegmented form by even deleting the spaces that would otherwise indicate the boundaries between the sound segments.

We can now add all data to our wordlist (or our dictionary, 3), but we should not forget to incremend the index for the word identifier (`idx`) and the cognate set identifier (`cogid`).

```
for f in tqdm.tqdm(files):
    # (1: initiate MSA object)
    msa = MSA(f)
    if msa.dataset == 'French':
        french, latin = re.findall(
                r'\*(.*?)\*',
                msa.seq_id
                )
        # (2: extract alignments)
        for taxon, alm in zip(msa.taxa,
                msa.alignment):
            taxon_id = selection.get(taxon, '')
            if taxon_id:
                tokens = [converter.get(
                    x,
                    x
                    ) for x in alm if x != '-']
                form = ''.join(tokens)
                # (3: add data to wordlist)
                D[idx] = [
                        taxon,
                        taxon_id,
                        french,
                        latin,
                        french,
                        form,
                        tokens,
                        alm,
                        cogid
                        ]
                idx += 1
        cogid += 1
```

Now that we have assembled the data readily, we can load it with help of LingPy's `Alignments` class, which we call by passing the dictionary with `cogid` as the keyword for the *reference* (`ref`), which we use to construct our alignments.

```
alms = Alignments(D, ref='cogid')
```

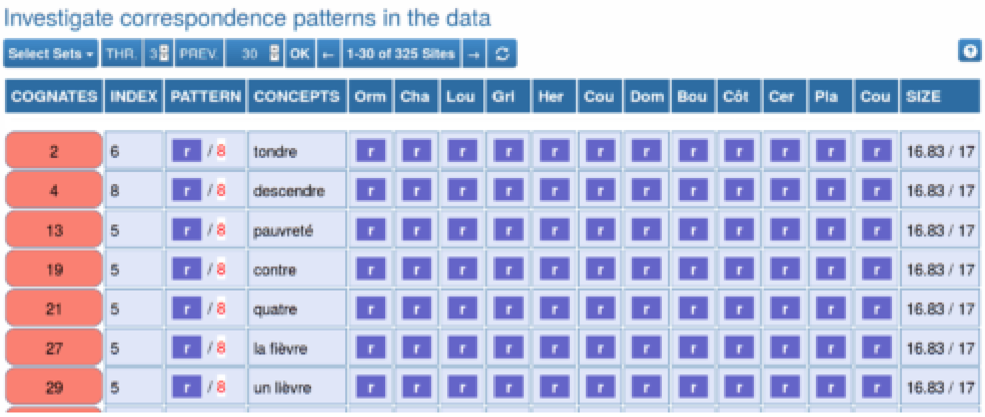
We need to do this in order to make sure that all alignments are “normalized”, i.e., they should not contain empty columns. We do this by iterating over all alignments in the `Alignments` object, which we can access as a dictionary, in which the key is the cognate identifier, and the value is a dictionary identical with the data needed to construct an `MSA` object. The normalization is now straightforward, and we re-write all individual alignments attached to individual word forms to make sure this is readily stored.

```
for cogid, msa in alms.msa['cogid'].items():
    for idx, alm in zip(
            msa['ID'],
            normalize_alignment(
                msa['alignment']
                )
            ):
        alms[idx, 'alignment'] = alm
```

We can now write the data to file. By passing the `prettify` keyword and setting it to `False`, we make sure that the data will be written to plain TSV format.

```
alms.output(
        'tsv',
        filename='tppsr-bdpa',
        prettify=False
        )
```

How we can use this file to calculate correspondence patterns with help of the correspondence pattern recognition algorithm described in List (2019) is something I will describe in more detail in a follow-up post. But what we can do already with the data by now is loading it into EDICTOR (List 2017), and use the built-in tool for correspondence pattern analyses. This tool is less accurate than the Python implementation in the LingRex package, since it is written in plain JavaScript. All it does is that it tries to sort the sound correspondences in a rather smart way, using JavaScripts rather convenient ways to sort arrays. This works — at least to some degree— surprisingly well, as you can see yourself, when opening the EDICTOR at http://edictor.digling.org and then either dragging the file `tppsr-bdpa.tsv` to the BROWSE button or selecting it by clicking on this button. You then click on ANALYZE in the menu, and select CORRESPONDENCE PATTERNS from there. Select "full cognates", as we are not dealing with partial cognates here, and press OK.



Investigate correspondence patterns in the data

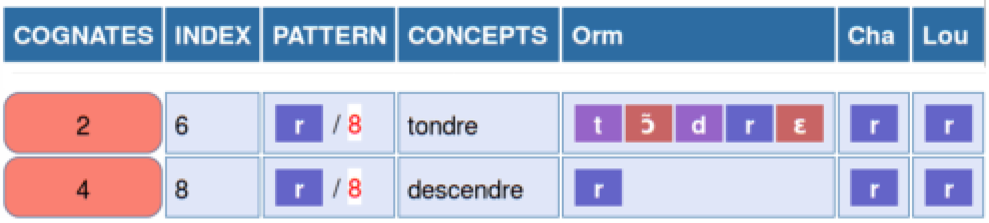
COGNATES	INDEX	PATTERN	CONCEPTS	Orm	Cha	Lou	Gri	Her	Cou	Dom	Bou	Côt	Cer	Pla	Cou	SIZE
2	6	r / 8	tondre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
4	8	r / 8	descendre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
13	5	r / 8	pauvreté	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
19	5	r / 8	contre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
21	5	r / 8	quatre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
27	5	r / 8	la fièvre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17
29	5	r / 8	un lièvre	r	r	r	r	r	r	r	r	r	r	r	r	16.83 / 17

Figure 1: Correspondence pattern display in EDICTOR

What you will see is a collection of all your correspondence patterns which EDICTOR's simple method extracts from the alignments.The arrangement is by language variety in the columns, and by cognate set (or alignemnt) in each row. By clicking on a given value, EDICTOR will show you the full word for that entry.

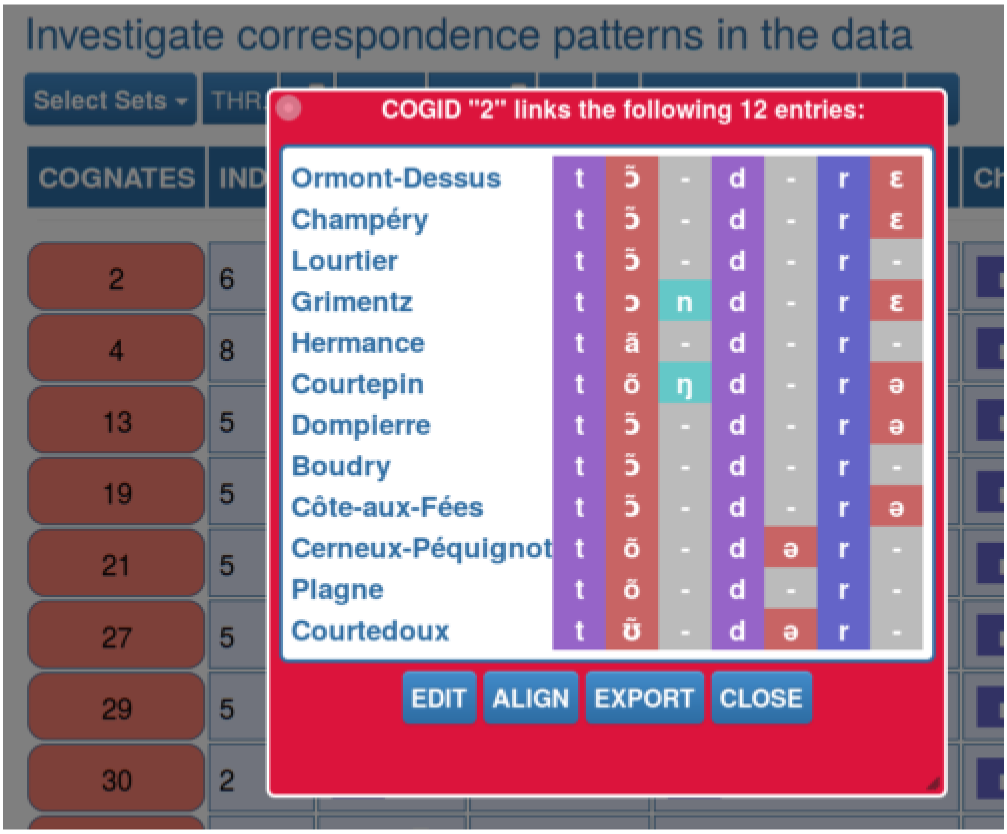
Clicking on the cognate ID on the very left, it will show you the alignment.

It would take too long to describe all possibilities for searching here, so I recommend those interested in exploring this further, to simply download the dataset, prepared with the script described here from the Github.Gist accompanying this



COGNATES	INDEX	PATTERN	CONCEPTS	Orm	Cha	Lou
2	6	r / 8	tondre	t ɔ̃ d r ɛ	r	r
4	8	r / 8	descendre	r	r	r

Figure 2: Viewing original words for a given correspondence pattern



COGID "2" links the following 12 entries:

Ormont-Dessus	t	ɔ̃	-	d	-	r	ɛ
Champéry	t	ɔ̃	-	d	-	r	ɛ
Lourtier	t	ɔ̃	-	d	-	r	-
Grimentz	t	ɔ	n	d	-	r	ɛ
Hermance	t	ã	-	d	-	r	-
Courtepin	t	õ	ŋ	d	-	r	ə
Dompierre	t	ɔ̃	-	d	-	r	ə
Boudry	t	ɔ̃	-	d	-	r	-
Côte-aux-Fées	t	ɔ̃	-	d	-	r	ə
Cerneux-Péquignot	t	õ	-	d	ə	r	-
Plagne	t	õ	-	d	-	r	-
Courtedoux	t	ʊ̃	-	d	ə	r	-

Figure 3: Alignment popups in EDICTOR's correspondence pattern viewer

tutorial, and see yourself what can be done. If you have ideas on how the tool could be enhanced, I would furthermore be happy about any kind of feedback or questions or suggestions, which you shoudl ideally share via our project page with GitHub/digling/edictor.

References

Gauchat, Louis and Jeanjaquet, Jules and Tappolet, Ernest (1925): *Tableaux phonétiques des patois suisses romands. Relevés comparatifs d'environ 500 mots dans 62 patois-types*. Publiés avec introduction, notes, carte et répertoires . Neuchâtel:Attinger.

List, Johann-Mattis (2014): *Sequence comparison in historical linguistics*. Düsseldorf:Düsseldorf University Press.

List, J.-M. and Prokić, J. (2014): A benchmark database of phonetic alignments in historical linguistics and dialectology. In: *Proceedings of the Ninth International Conference on Language Resources and Evaluation*. 288-294.

List, Johann-Mattis (2017): A web-based interactive tool for creating, inspecting, editing, and publishing etymological datasets. In: *Proceedings of the 15th Conference of the European Chapter of the Association for Computational Linguistics. System Demonstrations*. 9-12.

List, Johann-Mattis and Walworth, Mary and Greenhill, Simon J. and Tresoldi, Tiago and Forkel, Robert (2018): Sequence comparison in computational historical linguistics. *Journal of Language Evolution* 3.2. 130–144.

List, Johann-Mattis (2019): Automatic inference of sound correspondence patterns across multiple languages. *Computational Linguistics* 1.45. 1-24.

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A Primer on Automatic Inference of Sound Correspondence Patterns III: Extended Experiments with Alignments from the Tableaux Phonétiques des Patois Suisses Romands

Johann-Mattis List (27/03/2019)

Categories: Code, Primer

Tags: correspondence patterns, introduction, Python, TPPSR

Having illustrated how a quick correspondence pattern analysis can be done with help of readily formatted data and the EDICTOR tool alone, it is now time to show how we can use the LingRex package in order to carry out a full-fledged correspondence pattern analysis. While EDICTOR uses a simple algorithm that is based on sorting the patterns, the Python algorithm for correspondence pattern detection, which is described in detail in List (2019), uses a greedy approach inspired by the Welsh-Powell algorithm for graph coloring (Welsh and Powell 1967), in order to cluster all alignment sites in the data into clusters which are compatible with each other.

In the following, I will demonstrate how the LingRex package, which I plan to include into LingPy in the future, after sufficient tests have been written, can be used to apply the correspondence pattern detection algorithm, and how the results can — again — be investigated with help of EDICTOR. In order to get started, you should make sure to install the package with its dependencies. In order to do so, the easiest way is to download the package from GitHub or to clone it with GIT, and to install the depencencies with help of PIP.

```
$ git clone https://github.com/lingpy/lingrex.git
$ cd lingrex
$ pip install -r pip-requirements.txt
$ python setup.py develop
```

As data for testing, we will use the same dataset of 70 alignments taken from the *Tableaux Phonétiques des Patois Suisses Romands* (Gauchat et al. 1925), which were included as alignments in the *Benchmark Database for Phonetic Alignments* (http://alignments.lingpy.org, List and Prokić 2014). Now, that the data has already been prepared as a wordlist that can be accessed by LingPy and EDICTOR, we can directly access it from Python. Since LingRex uses LingPy's datastructures, it expects the same data as input. In fact, the major class that we will use to carry out the correspondence pattern detection is an extension of LingPy's `Alignments` class which can be used to handle alignments in wordlists. That means, that all the functions that are available as part of the `Alignments` class in LingPy are also available as part of the `CoPaR` class in LingRex. We thus start by loading the data.

```
from lingrex.copar import CoPaR
cop = CoPaR(
    'tppsr-bdpa.tsv',
    ref='cogid',
    segments='tokens'
)
print('{0} / {1} / {2}'.format(
    cop.height,
    cop.width,
    len(cop)
)
```

Now that we have imported the data, we need to add prosodic information to all sequences. This information serves as some kind of an initial clustering of the data, based on the prosodic environment of a given alignment site. In its simplest form, we treat all sites alike. But since we know, for example, that our alignments never place a vowel and a consonants into the same column, we can already use that information to make the task a little bit easier for the algorithm. This can be done by adding, what is called `structure` in the LingRex package.

```
cop.add_structure(model='cv', structure='structure')
```

This method will add another column to our data, in which each sound sequence is characterized by a string that indicates if the segment is a vowel or a consonant. The result of this can be seen when looking at the first ten entries of our wordlist, as shown in the table below.

ID	DOCULECT	TOKENS	STRUCTURE
1	Ormont-Dessus	ʃ e	C V
2	Champéry	ʃ i	C V
3	Lourtier	ʃ e	C V
4	Grimentz	ʃ aː	C V
5	Hermance	s e	C V
6	Courtepin	ʃ eː	C V
7	Dompierre	s e	C V
8	Boudry	s aː	C V
9	Côte-aux-Fées	s a	C V

ID	DOCULECT	TOKENS	STRUCTURE
10	Cerneux-Péquignot	s aː v u	C V C V

Now that we have added the `STRUCTURE` to our data, we can start with the real analysis. We start by retrieving the alignment sites with all relevant information, restricting the sites we consider to those which have at least two reflexes (indicated by the `minrefs` keyword).

```
cop.get_sites(minrefs=2, structure='structure')
```

This method will add a new attribute to our `CoPaR` object, called `sites`. These sites are organized as a dictionary, with tuples of the cognate identifier and the position in the alignment as a key, and the structure (if it is consonant or vowel, in our case) along with the concrete alignment site as a value. If a site contains missing entries, this is by default represented with help of the symbol `Ø`, which we use to denote missing data (in contrast to `-` denoting a gap in an alignment. The following table illustrates this for the cognate sets 31 and 63 in the data, which contain reflexes for the concepts *le chasseur* and *la hache*, with the latter being only reflected in 8 out of 12 varieties in our dataset. The alignment site column shows the reflex for each variety in alphabetical order by the variety name.

Now that we have stored the alignment sites, we can start clustering them.

```
cop.cluster_sites()
```

This analysis will add another property to our `CoPaR` object, called `clusters`. This is again a Python dictionary, consisting of the structure segment and the

COGID	POSITION	STRUCTURE	ALIGNMENT SITE
31	3	V	œː u œː u aː œ aː ou œ ɔː au u
31	4	C	r - - - - - - - - - - -
63	0	C	ʦ ʧ Ø ʧ ʦ ʦ ʦ Ø θ Ø Ø ʧ
63	1	V	- ɔ Ø ɑ ɛ - ɛ Ø õ Ø Ø a
63	2	C	- t Ø t t - t Ø - Ø Ø t
63	3	V	- ɛ Ø - a - a Ø - Ø Ø -

pattern as a key, and the alignment sites, represented by cognate identifier and position as value. If we now check in the data for the alignment sites for cognate set number 31 and 63, we can see that the initials in both cognate sets are assigned to the same pattern (as they are compatible), and that the last site in cognate set 31 is clustered with the last site in cognate set 50 (not shown here), while the rest of the sites are singletons, which do not recur anywhere else in the data. That we find a lot of singletons in the data is not surprising, given that we have a very limited number of cognate sets.

In order to analyze the clusters further, we can now make a secondary analysis, during which we compare all patterns that were inferred in this run with each alignment site a second time, this time assigning alignment sites to all patterns with which they are *compatible*. This may result in a fuzzy clustering, as one alignment site could easily be compatible with two or more patterns, provided it contains enough missing data.

```
cop.sites_to_pattern()
```

The results of this analysis are stored in the attribute `patterns` of the `CoPaR` object, and they are again provided in form of a Python dictionary, with the cognate set and the position as the key for the alignment site, and the patterns to which the site was assigned provided in a list as value, with each pattern represented by its size, its structure, and the pattern itself. In our analysis, only three sites occur, which could be assigned to more than one pattern. One of these is the second column of the alignment of cognate set 24 *m'appeler*, reflected in only three varieties. Given the large number of missing data in this alignment, it is compatible with seven different patterns in the data, shown below in the table.

Ø	Ø	Ø	Ø	Ø	Ø	Ø	r	r	Ø	r	Ø
r	r	r	r	r	r	r	r	r	r	r	r
l	r	r	r	r	r	r	r	r	r	r	r
r	r	r	**--**	r	r	r	r	r	r	r	**--**
r	r	**rː**	r	r	r	r	r	r	**ʁ**	r	r
--	r	r	Ø	r	r	r	r	r	r	r	Ø
r	r	**--**	r	r	r	r	Ø	r	Ø	Ø	r
Ø	Ø	r	Ø	Ø	Ø	r	r	Ø	**ʁ**	Ø	Ø

Since it is difficult to spot the differences between these patterns, I have marked all those sounds which are different from a normal *r* with bold font. We can see that the pattern is indeed compatible with all seven patterns, and that the seven patterns themselves are incompatible with each other. We can, however, also see that the differences are minor. There are different possibilities to explain the differences. They could be due to errors in the data or the alignments, they could be due to borrowing, due to individual *irregular* sound changes, or due to some specific phonetic environment that triggered a certain sound change in the individual varieties. What holds in all cases needs to be checked qualitatively, by investigating the variety in detail.

As a final step, we add the patterns to our wordlist, and write both the patterns and the wordlist to a new file.

```
cop.add_patterns(ref='patterns')
cop.output('tsv', filename='tppsr-copped')
cop.write_patterns('patterns.tsv')
```

This will result in two new files, the file `tppsr-copped.tsv` being a wordlist, which we can inspect in EDICTOR, and the file `patterns.tsv` being a spreadsheet that shows all patterns for each language variety along with the reflexes and the alignment sites. If you open the file `tppsr-copped.tsv` now with EDICTOR and inspect the correspondence patterns, as shown in the previous post, you will find, that EDICTOR displays the patterns inferred with the Python algorithm instead of using its own simple method. In this way, you can conveniently investigate the results with the interactive EDICTOR application that facilitates the detailed inspection of correspondence pattern data.

Instead of investigating the data further, I will end here, and leave it to interested readers to check the data and the results themselves. A script to run the analysis along with the data is available in form of a GitHub Gist, which you can find at https://gist.github.com/LinguList/6bd37f375c9715e3ecda395e23a17fcb.

References

Gauchat, Louis and Jeanjaquet, Jules and Tappolet, Ernest (1925): *Tableaux phonétiques des patois suisses romands. Relevés comparatifs dénviron 500 mots dans 62 patois-types*. Publiés avec introduction, notes, carte et répertoires . Neuchâtel:Attinger.

List, J.-M. and Prokić, J. (2014): A benchmark database of phonetic alignments in historical linguistics and dialectology. In: *Proceedings of the Ninth International Conference on Language Resources and Evaluation*. 288-294.

List, Johann-Mattis (2019): Automatic inference of sound correspondence patterns across multiple languages. *Computational Linguistics* 1.45. 137-161.

Welsh, D. J. A. and Powell, M. B. (1967): An upper bound for the chromatic number of a graph and its application to timetabling problems. *The Computer Journal* 10.1. 85-86.

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Using pyconcepticon to map concept lists I

Tiago Tresoldi (01/04/2019)

Categories: Analysis, Annotation

Tags: concepticon, concept mapping

A major problem for data reuse in computer-assisted historical linguistics, especially when employing data collected with no computational workflows in mind, is linking datasets in terms of the meanings of the words (or, technically, "forms") they carry. Just as linking languages across different datasets is not as straightforward as one might naively assume, demanding a complex reference catalog such as Glottolog, linking the concepts used in a wordlist (a "concept list") to our Concepticon project might well be the most intensive task in preparing a dataset for cross-linguistic studies.

We could discuss the more theoretical issues at hand, ranging from pragmatic lexicographic decisions to deep philosophical disputations on hermeneutics — even though it is always worth remembering, Concepticon is *not* an ontology, but a catalog for linking concept lists. However, for the time being, let's take a hard-headed view and look at the practical issues at play. Common issues are:

- Plain errors in the glosses, especially when OCR or typing from published sources is involved, such as in a recent concept list where I had a typo `barl` for `bark` (readers will note how "L" and "K" are next to each other in the most common keyboard layouts).
- Problems with homonyms where the meaning is not specified, such as in `bark` itself (which could be either a noun, the "skin" of a tree, or a

verb, "to bark") or in the recurring examples of `fly` (either the insect or the verb meaning "to move in the air") and of `dull` (either as opposed to "sharp" or to "smart").

- Problems with synonyms, such as in the case of a word being annotated as `eggplant` in one concept list but as AUBERGINE in Concepticon.
- Glosses given in a language other than English, and perhaps one you are not entirely familiar with, or sometimes in multiple languages (like Chinese *and* English) where the difference in semantics might be more of a hindrance than a help.

These problems alone would be enough to make concept mapping tedious, but most people involved in Concepticon would be happy if they were the only ones. Other common issues can lead almost to frustration are:

- The same dataset using slightly similar (and sometimes visually alike) glosses for the same concept, such as `dog` and `dog ` (note the trailing whitespace in the second one).
- Just like when reporting forms, authors including all kind of notes in their glosses, some useful for the mapping (like `fly (noun)`), some less so (such as `poor (dubious)`) some which would better be in a "Comments" column (like `happy [given by only one speaker]`).
- People never shy on coming up with different ways to annotate additional information, such as part-of-speech, hardly in a consistent way. Using the flying insect as a common denominator, our collection already includes specimens such as `fly (noun)` , `fly (n.)`, `fly (n)` , `fly noun`, `fly:n`, `fly [n.]`, `(N)fly`, `fly (insect)`, `the fly`, `a fly`, `the/a fly`, and `fly (mouche)`, besides mutations such as `FLY (n)` and `fly (noun` (note the missing close-parenthesis).

- Notations for polysemies being just as innovative and free, with commas (`hand,arm`), semicolons (`hand;arm`), slashes (`hand/arm`), or even nothing (`hand arm`), also allowing for inverted orders and spaces (e.g., `arm / hand`).
- The lists of basic vocabulary including, and for good reasons, terms which are very culture-specific or not colloquial in other languages, when it is not immediately obvious if the concept is already found in Concepticon (and, if not, whether it should be added) and under which gloss.

When facing repetitive tasks, programmers will immediately think of ways to facilitate and automate them. The Concepticon team did just that, with a set of tools from which we can gain a lot in terms of mapping speed and consistency, and it is fundamental to demonstrate such tools and make them known — after all, programmers also tend to have the bad habit of reinventing the wheel.

The first idea for mapping, and which can be used for some quick exploration, is probably to query the Concepticon catalog either online or from the command-line. For example, if we were to map a single coconut-related concept, we would likely think about querying for the string `coco` using the online catalog or just using the tool "grep" from the command line:

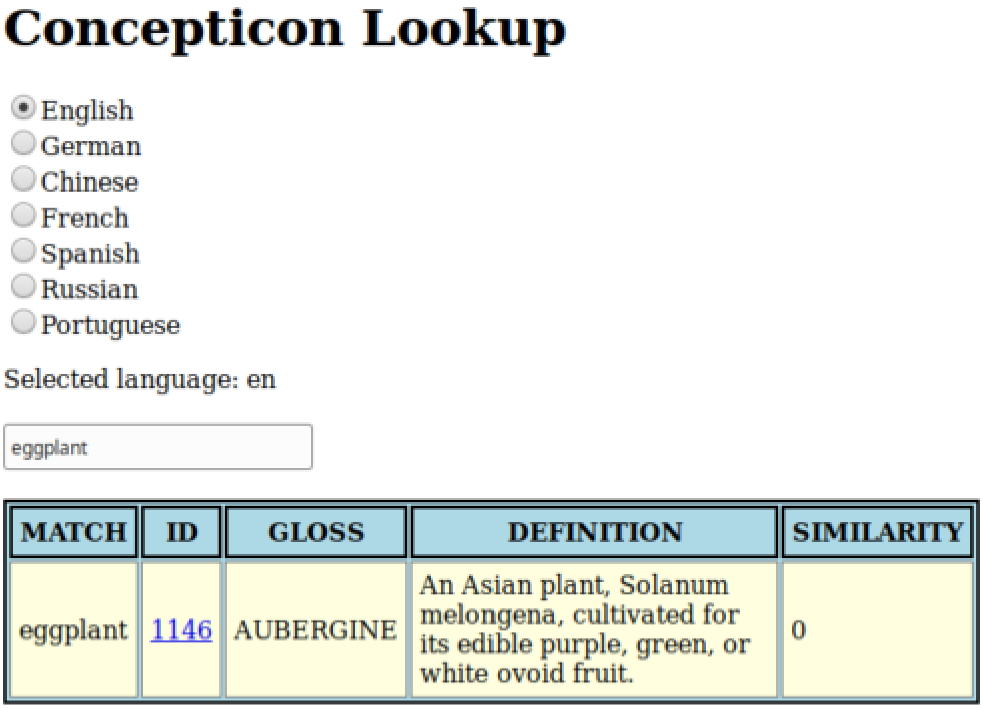
```
$ grep -i "coco" concepticondata/concepticon.tsv
147    COCONUT TREE    Agriculture and vegetation    A tropical tree with feathery leaves which bears coconuts.    Person/Thing
970    COCONUT    Agriculture and vegetation    The large hard-shelled oval nut with a fibrous husk of the cocos palm.    Person/Thing
1641    SILK    Clothing and grooming    One of the finest textiles, obtained from cocoons of certain species of caterpillars; it is soft, very strong and absorbent and has a brilliant sheen.    Person/Thing
2442    COCOA BEAN    Agriculture and vegetation    The dried and fully fermented fatty seed of Theobroma cacao, from which cocoa solids and cocoa butter are extracted.    Person/Thing
2649    COCONUT SHELL LADLE    Food and drink    A large spoon made from coconut shell.    Person/Thing
3034    GREEN COCONUT    Agriculture and vegetation    A green (i.e., not mature) oval nut with a fibrous husk of the cocos palm, used as source of coconut water.    Person/Thing
3035    RIPE COCONUT    Agriculture and vegetation    A ripe (i.e., mature) oval nut with a fibrous husk of the cocos palm, used as source of coconut meat.    Person/Thing
```

This strategy would work for straightforward cases, however missing most of the problems listed above, including homonyms, synonyms, and typos. Some could be circumvented by expanded strategies, such as by collecting synonyms (like the case of `eggplant`) in the more of 200 concept lists already mapped, checking to which Concepticon gloss the entries are mapped to. Once more, something far from practical.

The pyconcepticon library offers a much better alternative for this kind of query: a JavaScript library with pre-computed information (such as glosses from already mapped concepts lists, as just discussed) which also takes care of performing a number of string manipulations that we would probably need to perform by hand (in particular, all the common and not-so-common kinds of part-of-speech annotation). With pyconcepticon installed, just call

```
conceptícon app
```

from the command line, and a new browser-tab will be opened where you can run your queries, as in the images below. Alternatively, you can also visit http://calc.digling.org/concepticon/ where we store a version corresponding to the most recent release of the Concepticon. Note that, depending on how you installed pyconcepticon, you might need to pass as an argument the path to your Concepticon data repository, such as in `concepticon --repos /home/tresoldi/concepticon-data/ map_concepts conceptlist.tsv`.



Concepticon Lookup

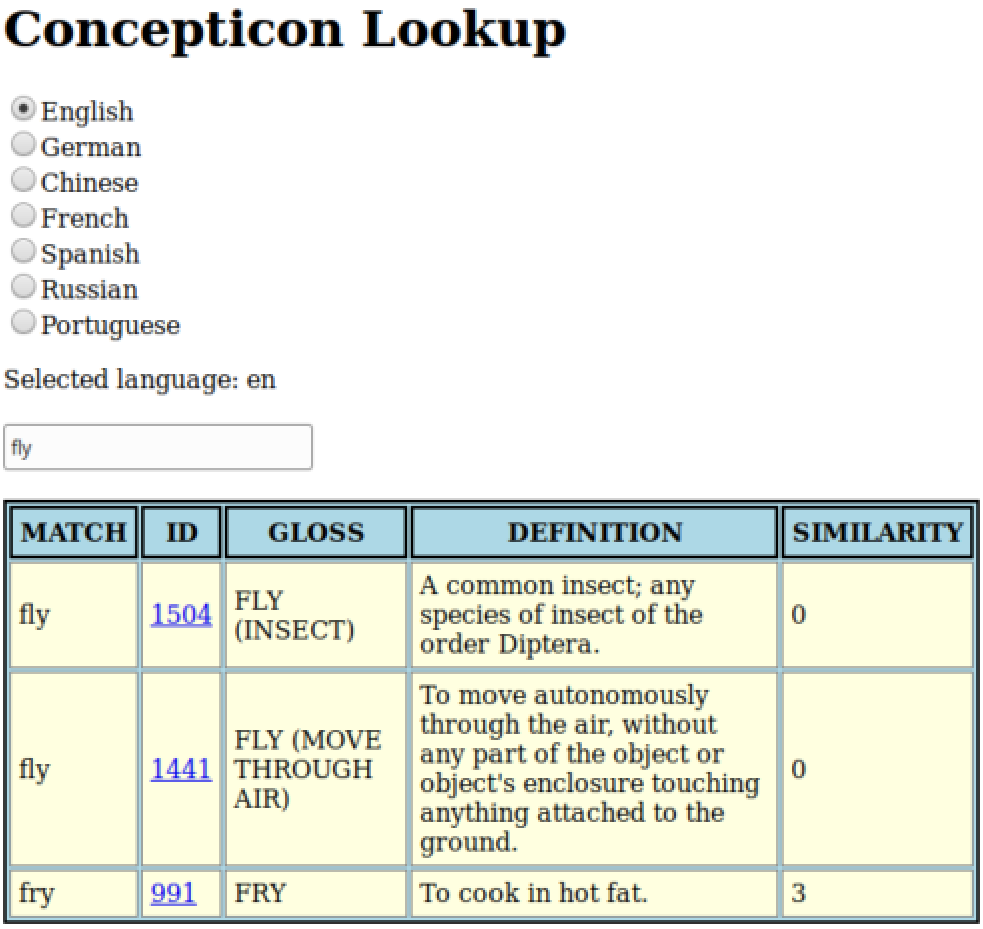
● English
○ German
○ Chinese
○ French
○ Spanish
○ Russian
○ Portuguese

Selected language: en

eggplant

MATCH	ID	GLOSS	DEFINITION	SIMILARITY
eggplant	1146	AUBERGINE	An Asian plant, Solanum melongena, cultivated for its edible purple, green, or white ovoid fruit.	0

You can see that with this application not only `eggplant` is matched to AUBERGINE as desired, but also that basic fuzzy matching is allowed, like in the query for `fly` returning a list of potential mappings FLY (INSECT), FLY (MOVE THROUGH AIR), and FRY. The output includes a similarity score



Concepticon Lookup

● English
○ German
○ Chinese
○ French
○ Spanish
○ Russian
○ Portuguese

Selected language: en

fly

MATCH	ID	GLOSS	DEFINITION	SIMILARITY
fly	1504	FLY (INSECT)	A common insect; any species of insect of the order Diptera.	0
fly	1441	FLY (MOVE THROUGH AIR)	To move autonomously through the air, without any part of the object or object's enclosure touching anything attached to the ground.	0
fry	991	FRY	To cook in hot fat.	3

which we might investigate in more detail in future posts, but in its essence the lower the score, the higher the match probability.

This tool is a great improvement on manual searching, but it would still be impractical for mapping entire concept lists, which usually range anywhere from 100 to 2,500 concepts. Thankfully, we already have a set of Python functions in pyconcepticon that allow automating this procedure, and which can be used from the command line. Let's create a fake concept list with different mapping issues (some clear-cut cases, but also glosses with annotations, colexified concepts, typing errors, etc.), which we store in a text file with one entry per line (note the mandatory `GLOSS` column name in the first line):

```
GLOSS
dog
eggplant
fly (N)
to fly
hand/arm
dull
bambu
```

By running the command

```
concepticon map_concepts conceptlist.tsv
```

we obtain the following output:

```
GLOSS    CONCEPTICON_ID    CONCEPTICON_GLOSS    SIMILARITY
dog                2009    DOG                           2
eggplant           1146    AUBERGINE                     2
fly (N)            1504    FLY (INSECT)                  2
to fly             1441    FLY (MOVE THROUGH AIR)        1
hand/arm           2121    ARM OR HAND                   2
#<<<
dull               1518    STUPID                        2
dull                379    BLUNT                         2
#>>>
bambu               ???
#    6/7    86%
```

We can see that the method had no problem to map the five first entries, `dog` (a straightforward case), `eggplant` (using data already mapped), `fly (N)` (using an annotation for nouns), `to fly` (using an annotation for verbs), and `hand/arm` (using an annotation for colexifications). It was not possible to decide if `dull` should be linked to STUPID or to BLUNT (equal similarity scores), but the items are grouped together and clearly marked, so that review should be easy. Finally, a case of a typo or different orthography, such as `bambu`, was not mapped as the method does not try to be too clever, but the unmapped item is clearly identified as such with a triple question mark (a fall-back fuzzy string search for these cases might be implemented in the future). The method also informs us about how many concepts were mapped in the last line.

While glosses in English will perform better, due to its status as default language for glosses and a consequent higher count of entries, the same method can be used for other languages. For example, the concept list below, in Spanish:

```
GLOSS
perro
hombre
mujer
mano
mosca
hacer
```

can be linked with the same method by passing the `--language es` argument to `concepticon map_concepts`, with the output:

```
GLOSS    CONCEPTICON_ID    CONCEPTICON_GLOSS    SIMILARITY
perro              2009    DOG                           2
hombre             1554    MAN                           2
mujer               962    WOMAN                         2
mano               1277    HAND                          2
mosca              1504    FLY (INSECT)                  2
hacer              2575    DO OR MAKE                    2
#    6/6    100%
```

It is worth giving some notes on the inner workings of this method, also introducing the internals aspects of Concepticon. The `map_concepts` command wraps a call to the internal `api.map()` method, which will read entries from column `GLOSS` or `ENGLISH` and parse them with the `parse_gloss()` function. This helper method offered in the pyconcepticon library is used to extract the most important information from the “raw” gloss, along with its annotated part-of-speech (if any), as illustrated by the code snippet below:

```python
from pyconcepticon import glosses

for gloss in ['kill', 'kill (v)', 'to kill', 'to kill (somebody)']:
    parsed_gloss = glosses.parse_gloss(gloss)[0]
    print([gloss, parsed_gloss.main, parsed_gloss.pos])
```

Which returns:

```
['kill', 'kill', '']
['kill (v)', 'kill', 'verb']
['to kill', 'kill', 'verb']
['to kill (somebody)', 'kill', 'verb']
```

The main part of glosses and their part-of-speech tags are used in combination with mappings in already included concept lists, where each “raw” gloss is aligned to Concepticon as in the snippet below (a full list can be found in the repository tests):

```
1504    FLY (INSECT)///FLY  1
1504    FLY (INSECT)///Fly (n.) 1
1504    FLY (INSECT)///a fly    4
1504    FLY (INSECT)///blowfly/housefly 4
1504    FLY (INSECT)///fly  16
1504    FLY (INSECT)///fly (N)  1
1504    FLY (INSECT)///fly (animal) 1
1504    FLY (INSECT)///fly (insect) 5
1504    FLY (INSECT)///fly (n)  3
1504    FLY (INSECT)///fly (n.) 2
1504    FLY (INSECT)///fly (nn.)    1
1504    FLY (INSECT)///fly (noun)   1
1504    FLY (INSECT)///fly (sb.)    1
1504    FLY (INSECT)///fly_N    1
1504    FLY (INSECT)///housefly 2
1504    FLY (INSECT)///the fly  2
1504    FLY (INSECT)///the fly (insect) 46
1504    FLY (INSECT)///the fly (insect)s    46
1441    FLY (MOVE THROUGH AIR)///(the bird) flew    1
1441    FLY (MOVE THROUGH AIR)///FLY    1
1441    FLY (MOVE THROUGH AIR)///FLY (VERB) 1
1441    FLY (MOVE THROUGH AIR)///FLY (v.)   1
1441    FLY (MOVE THROUGH AIR)///Fly    2
1441    FLY (MOVE THROUGH AIR)///TO FLY 3
1441    FLY (MOVE THROUGH AIR)///To fly 1
1441    FLY (MOVE THROUGH AIR)///fly    59
1441    FLY (MOVE THROUGH AIR)///fly (as a bird)    1
1441    FLY (MOVE THROUGH AIR)///fly (of bird)  2
1441    FLY (MOVE THROUGH AIR)///fly (to)   1
1441    FLY (MOVE THROUGH AIR)///fly (v)    4
1441    FLY (MOVE THROUGH AIR)///fly (v.)   4
1441    FLY (MOVE THROUGH AIR)///fly (vb)   3
1441    FLY (MOVE THROUGH AIR)///fly (vb.)  2
1441    FLY (MOVE THROUGH AIR)///fly [vb]   1
1441    FLY (MOVE THROUGH AIR)///fly v. 4
1441    FLY (MOVE THROUGH AIR)///fly vb 1
1441    FLY (MOVE THROUGH AIR)///fly, to    2
1441    FLY (MOVE THROUGH AIR)///fly_V  1
1441    FLY (MOVE THROUGH AIR)///flying 2
```

This mapping does more than inform us that, say, the gloss `the fly (insect)` is mapped 46 times to the concept FLY (ANIMAL) or that `to fly` is mapped 26 times to FLY (MOVE THROUGH AIR). It also allows the algorithm to internally parse all the different glosses for "fly" as either a noun or a verb, so that it collects enough information to link any different and still unobserved gloss to the correct concept. We can also take a first glimpse at how pyconcepticon works under the hood, preparing for future blog posts where the internals will be explored in more detail.

Other commands in pyconcepticon might help the mapping process, such as `link` (to link concepts to a concept set, so that if either CONCEPTICON_GLOSS or CONCEPTICON_ID is given, the other is added) and `mergers` (which prints the Concepticon id of potential mergers), but `map_concepts` and `app` are the most important ones which cannot be lacking from your computer-assisted language comparison toolbox.

References

List, Johann Mattis & Cysouw, Michael & Greenhill, Simon & Forkel, Robert (eds.) 2018. *Concepticon*. Jena: Max Planck Institute for the Science of Human History. (Available online at http://concepticon.clld.org, Accessed on 2019-03-26.)

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Using pyconcepticon to map concept lists II

Tiago Tresoldi (08/04/2019)

Categories: Code

Tags: code example, concept mapping, Concepticon, Tucanoan languages

Mapping a given concept list to Concepticon can be done in a straight-forward way, even if automatic mappings need manual refinement. But what can we do when having to deal with larger datasets, say, a dictionary, from which we want to extract specific concepts, such as, for example, the ones in the classical Swadesh list of 100 items (Swadesh 1955)?

In the previous post on this topic, we discussed how the tools offered by the `pyconcepticon` library, in particular, the `concepticon` program that can be used from the command line or with a JavaScript interface, make concept mapping easier and more consistent. We also mentioned that they should be enough for automating many of the tasks that make up the mapping of a concept list to Concepticon, especially in those cases when programmers might be tempted to come up with half-baked implementations that are not reusable. Still, cases of one-time, dataset-specific solutions might be desirable or even necessary, such as when dealing with difficult concept lists that need to be pre-processed for manual intervention. While Concepticon, as part of the CLDF standard, is composed of plain-text files that could be loaded and manipulated with any programmer's favorite language or approach, in most cases it makes sense to use the internal component of the `pyconcepticon` library, wrapping them around our functions and workflows.

Let's illustrate this with an actual example, presented step-by-step. We recently had to start mapping a dataset for Barasana, a Tukanoan language spoken in Colombia. We had the following issues:

- Unlike most desirable cases for computer-assisted language comparison, at least in its more common current settings, the data does not come from lists of basic vocabulary (usually collected with the comparative method in mind), but from a bilingual Barasana-Spanish dictionary compiled by Jones and Jones (2009).
- The "dictionary" feature leads to two issues: first, most of the entries are far from comparable in the sense that they are too culture-specific or are clearly the output of word formation processes; second, second, the definitions, while occasionally similar to glosses, are in most cases long and complex lexicographic definitions.
- As the source is a bilingual *dictionary*, and not a bilingual *wordlist* or *vocabulary*, in many cases different words in our source language (Barasana) are translated with the same Spanish "gloss", especially in case of common vocabulary.
- The same definitions constitute our proxy to the forms glosses, but as mentioned they are given in Spanish, a language with less representation in Concepticon due to the majority of the concept lists already there using English or Mandarin for elicitation.
- For the purpose of the analysis, we did not want to map all possible concepts found in the data and already in Concepticon, but only the essential Swadesh-100 list, thus excluding entries with perfect matches like TELEPHONE.

Most of the issues above should be clear just from the first lines of our raw data:

```
$ head barasana.tsv
 SOURCE-ORTHOGRAPHY    SOURCE-PHONETIC SOURCE-WORD-CLASS   SOURCE-DEF
     ENGLISH-GLOSS   DIALECT-NOTE    GRAMMAR-NOTEʉ
 abarij á'ɑ    bɾ.i.ɨɦ́ Eɑ][ɑ́b'ɾ.í.ɨh J   s.v.inan.   cosa blanda (como
     tierra, fruta de árbol, coca pilada, herida, abdomen)
 abase á'ɑ    b.se Eɑ'][ɑ́b.sé J  v.i.    (ser/estar) blando, blanda (casabe
     , lodo)           ntg BARS,91 //aba// ‘’soft with the stative verb //
     aba// ‘to be ’soft is// aba-se// ‘that which is ’soft, no459; lf caus.
 abee ɑ'    béé   interj.     ¡ay no! (exclamación de amor frustrado)
                 ntg BARS,91 //Abe!// ‘expression of love for ’someone p40,
     2.27-2.30 Interjections, 2.29. Exclamatory;
 abi ɑ'    bí    interj.     ¡ay!            ntg BARS,91 //Abi!// ‘Oh, how
     small!/Oh, what a small quantity’!, p39, 2.29. Exclamatory. //Abo!//
     ‘oh, how big!; oh, what a huge quantity’! is an example of an
     exclamatory interjection. /o/ is used iconically for ‘’bigness and /i/
     is used for ‘’smallness. Thus, //Abi//! ‘oh, how small!; oh, what a
     small quantity’! We have recorded over thirty exclamatory interjections
     , many of which are synonymous, and most of which begin with /a/. Some
     of these are listed in (118);
 aboo ɑ'    bóo   interj.     ¡ah!         va abuu , ph ɑ'búúú ,   ntg BARS
     ,91 //Abo!// ‘Oh, how big!/Oh, what a huge quantity’!, p.39, 2.29.
     Exclamatory. is an example of an exclamatory interjection. o is used
     iconically for ‘’bigness and i is used for ‘’smallness. Thus, //Abi!//
     ‘oh, how small!; oh, what a small quantity’! We have recorded over
     thirty exclamatory interjections, many of which are synonymous, and
     most of which begin with a. Some of these are listed in (118);
 abore         v.caus.dep.     ser.blando-CAUS-nS         ntg BARS,91 //
     abo// (soft.CAUS) p70, no311;
```

No acceptable automatic mapping seems possible, which makes this one more supporting evidence for our insistence in computer- *assisted* language comparison: assisted mappings, where our algorithm does not try to be too clever but gives enough information for an expert decision later, *are* possible. We can demonstrate how such data can be generated, all while relying on previous work by means of the concept_map() and concept_map2() functions of pylexibank (briefly mentioned in the previous post).

While there are some differences in their inner workings, with concept_map() more a "full search" than concept_map2(), both mapping functions work similarly, requiring two lists of strings: - The first one, glosses, is a list of glosses or definitions we want to map, as found in the source data.- The second one, map_reference, is a list of reference points composed of Concepticon glosses and reference glosses, separated by triple slashes "///". Examples, as those provided in the previous post and available on-line in pre-compiled lists (such as this for English), are "FLY (INSECT)///fly (insect)" and "FLY (MOVE THROUGH AIR)///fly (as a bird)".

The items composing the glosses list can be pre-processed by the user in terms of textual manipulations, like removing leading and trailing spaces, or information extraction (such as obtaining the actual gloss from definitions with comments, like dog from the dog (noun)), but both functions take care of that by default. The map_reference list can also be compiled by the user as needed, but, in most cases, we will use pyconcepticon 's _get_map_for_language() function, which loads the precompiled, per-language references from concept lists mapped in the past, allowing us to quickly stand in the shoulders of past concept mappers.

Let's explore these data structures: we load our raw data using Python's default csv library, extract the glosses with a list comprehension, and build a reference map from the second element of each item of the value returned by _get_map_for_language() (readers are free to explore the additional information returned by this function; the "es" parameter is the language code for Spanish, which is necessary as pyconcepticon defaults to "en" for English).

```
# Imports the necessary libraries
import csv
import pyconcepticon.api

# Loads the Concepticon API with data from the specified path
# NOTE: REMEMBER TO SET YOUR OWN PATH IF NECESSARY!!!
CONCEPTICON_PATH = "/home/tresoldi/src/concepticon-data"
Concepticon = pyconcepticon.api.Concepticon(CONCEPTICON_PATH)

# Loads the raw data
with open('barasana.tsv') as csvfile:
    reader = csv.DictReader(csvfile, delimiter='\t')
    data = [row for row in reader]

# Loads the full language mapping, also setting the `lang`uage
lang = "es"
spanish_map = Concepticon._get_map_for_language(lang)

# Builds lists of glosses and references, and shows some contents
glosses = [entry.get('SOURCE-DEF') for entry in data]
map_reference = [entry[1] for entry in spanish_map]
print("glosses", glosses[:5])
print("map_reference", map_reference[:5])
```

Which returns:

```
glosses ['cosa blanda (como tierra, fruta de árbol, coca pilada, herida,
    abdomen)', '(ser/estar) blando, blanda (casabe, lodo) ', '¡ay no! (
    exclamación de amor frustrado) ', '¡ay! ', '¡ah! ']
map_reference ['ABACUS///Ábaco', 'ABSTAIN FROM FOOD///ayunar', 'ACCORDION
    ///Acordeón', 'ACCUSE///acusar, denunciar', 'ACHIOTE///achiote, bija']
```

We can now obtain the automatic mapping for each gloss, by calling either `concept_map()` or `concept_map2()` on the `glosses` list (from which we first remove any empty glosses); the differences between the methods will be explained in a future post, but it should be enough to know that they are essentially interchangeable, both returning a dictionary with the indexes in `glosses` as the keys and a tuple with the list of matched entries in `map_reference` and the similarity score as the values (`concept_map2()` return all entries with a similarity score lower than the requested one). Such formal description might be a bit unintuitive, so let's demonstrate with code:

```python
# Import the functions for the mapping
from pyconcepticon.glosses import concept_map, concept_map2

# Remove empty glosses
glosses = [gloss for gloss in glosses if gloss]

# Perform the mapping and show some of the entries (if they are found,
# otherwise print `None`)
mapping = concept_map(glosses, map_reference, language=lang,
    similarity_level=5)
for i in range(5):
    print([i, glosses[i], mapping.get(i, None)])
```

And, especially, with its results (also noting as some definitions, here "glosses", are not mapped as the algorithm is unable to find an acceptable match with the similarity range we requested), below. The first entry, `([1757], 4)`, means that a single match, of index 1757 and similarity score of 4, was found for the gloss starting with `cosa blanda...` ; gloss of indexes 2 to 4, all interjections such as `¡ay!` , had no match.

```
[0, 'cosa blanda (como tierra, fruta de árbol, coca pilada, herida, abdomen
    )', ([1757], 4)]
[1, '(ser/estar) blando, blanda (casabe, lodo) ', ([978], 4)]
[2, '¡ay no! (exclamación de amor frustrado) ', None]
[3, '¡ay! ', None]
[4, '¡ah! ', None]
```

As humans, we prefer textual representations to indexes of list indexes. The code should do us the heavy and boring work of mapping the latter to the former, so we collect the matched glosses by iterating over the `mapping` dictionary and extracting the part of the `reference` string found before the `"///"` delimiter— note that we do so by setting a default value `([], None)`, which indicates no matched concepts (its first element is an empty list) and, consequently, no similarity score (thus, `None`). As the list of matched elements will likely have repeated elements (because more than one reference gloss might be matched, and those will likely share their Concepticon ID), we also take a `set` of the elements before storing the results we care about in `mapped_glosses`. This programming logic could be done in a single Python list comprehension, but it is better to proceed stepwise here and collect each gloss match within a `for` loop.

```python
# Collect matched glosses and show some of them
mapped_glosses = {}
for gloss_idx, gloss in enumerate(glosses):
    match_idxs, sim = mapping.get(gloss_idx, ([], None))

    match_glosses = set([
        map_reference[match_idx].split('///')[0]
        for match_idx in match_idxs
    ])

    mapped_glosses[gloss] = list(match_glosses)

for item in sorted(mapped_glosses.items())[:10]:
    print(item)
```

The output shows that our code works and, once more, that most definitions will *not* be mapped.

```
('(ãno, semana) pasado', [])
('(estar) abierto, abierta', [])
('(estar) agotado, agotada (persona, animal) ', ['ANIMAL'])
('(estar) agotado, agotada (personas, animales) ', [])
('(estar) agotado, agotada (una persona, un animal) ', [])
('(estar) agrio, agria (limón, lulo, casabe hecho del almidón guardado por demasiado tiempo) ', ['SOUR'])
('(estar) alerto, alerta; ', [])
('(estar) apretado, apretada ', [])
('(estar) arrugada ', [])
('(estar) atrancado, atrancada; ', [])
```

At this point, we have our automatic mapping of all lexicographic definitions in the source as a list of potential matches in Concepticon with no, one, or multiple elements. We now need to filter only the entries with potential matches in the Swadesh 100 list.

As mentioned earlier, given that Concepticon data is stored in plain-text files, we could just read the raw `concepticon-data/concepticondata/conceptlists/Swadesh-1964-100.tsv` file and collect all its gloss under the `CONCEPTICON_GLOSS` column. However, `pyconcepticon` already has functions in place for iterating over the properties of a concept list, so that it is easier and faster for us to just wrap it in our own code. Considering that we need to perform some checks and operations, and especially that such code might be useful in the future, we can write our own function for collecting the glosses of an existing concept list.

```python
# Define a function for obtaining the glosses of a concept list
def glosses_from_list(list_id):
    """
    Returns a list with the Concepticon glosses for a given conceptlist.

    Takes care of removing duplicates, empty entries, etc.

    Parameters
    ----------
    list_id : str
        The unique identifier for the list, as used in Concepticon, such
        as "Swadesh-1964-100".
    """

    # Obtain the concept list with a list comprehension; note the [0]
    # subsetting for getting the first element of the comprehension
    concept_list = [
        cl for cl in Concepticon.conceptlists.values()
        if cl.id == list_id
    ][0]

    # Obtain all the Concepticon glosses in the list; remember that they
    # glosses might be duplicated or empty at this point
    glosses = [
        concept.concepticon_gloss for concept
        in concept_list.concepts.values()
    ]

    # Remove any empty (i.e., non mapped) glosses and make sure there are
    # no duplicates (using `set`)
    glosses = set([gloss for gloss in glosses if gloss])

    # Return as a list
    return sorted(glosses)

# Obtain the glosses from the Swadesh 100 list and show some of them
swadesh = glosses_from_list("Swadesh-1964-100")
print(swadesh[:10])
```

Which works as expected:

```
['ALL', 'ASH', 'BARK', 'BELLY', 'BIG', 'BIRD', 'BITE', 'BLACK', 'BLOOD', '
    BONE']
```

We are now ready to generate our results, iterating over the data we collected earlier and writing to a `barasana-swadesh.tsv` file the rows that hold potential Swadesh entries. A better output than the one coded below could be provided, making the reviewing task even easier— for example, by sorting entries by similarity score, listing glosses alphabetically, or already including the Concepticon ID. However, this should be easy to any Python programmer and is beyond our scope of illustrating the inner working of `pyconcepticon`.

```python
# Write the output
with open('barasana-swadesh.tsv', 'w') as handler:
    # Write headers
    handler.write('FORM\tPHONETIC\tDEFINITION\tGLOSSES\tNOTES\n')

    # Iterate over all rows looking for potential Swadesh data
    for row in data:
        # Extract the list of glosses per form, defaulting to an empty list
        glosses = mapped_glosses.get(row['SOURCE-DEF'], [])

        # Get the subset of glosses that are in Swadesh 100
        glosses = [gloss for gloss in glosses if gloss in swadesh]

        # If there is at least one Swadesh gloss, build a buffer from the
        # row, adding an information on all potential glosses (separated with a
        # vertical bar in case of multiple glosses), and print it
        if glosses:
            buf = [
                row['SOURCE-ORTHOGRAPHY'],
                row['SOURCE-PHONETIC'],
                row['SOURCE-DEF'],
                '|'.join(glosses),
                row['GRAMMAR-NOTE'],
            ]

            handler.write('%s\n' % '\t'.join(buf))
```

We can finally inspect the results and confirm that the code is working, such as in good potential matches as ãmo for HAND and baáre for EAT. We can already spot problems, as well: adocʉ̃ was mapped to PERSON due to the parsing of its definition, and baásãare, clearly a word formation including the baáre above, is also mapped to EAT (which was expected in our logic, as both have the same Spanish gloss "comer"). Nevertheless, we surely saved a lot of time for the linguists that would correct this first mapping, also gaining much in terms of consistency. Even better, once the results will be finished and included in Concepticon, the new concept list from Barasana with Spanish definitions will improve the results for future semi-automatic and automatic mappings, especially in case of other datasets with glosses in Spanish (thus helping, for example, to include more Native American Languages in Lexibank).

```
$ head barasana-swadesh.tsv
 FORM    PHONETIC    DEFINITION  GLOSSES NOTESʉ̃
 adoc ɑ'     dó.ɨk̆   este tamaño de (animal, persona)    PERSON
 ãmo 'ɑ̃    mõ E'ɑ̃][ő̃m J  mano    HANDʉ
 ãma ɑ̃'ɨɑ̃    m E'ɑ̃][ɨɑ̃m J  cuello (ser humano, botella)    NECKʉ
 ãmtutu ɑ̃ɨ˜   m.'tutú Eɑ̃]['ɨm̃.túti J     cuello (ser humano, botella)
    NECK
 baare 'ɑ́ɑ́    bɾ.e E']][ɑ́ɑ́bɾ.é J    nadar   SWIM
 baáre 'ɑɑ́    bɾ.e    comer   EAT ntg BARS,91 //ba// ‘’eat no4;
 baásãare 'ɑɑ́    b.ɑ̃ɑ̃sɾẽ. E']][ɑɑ́b.ɑ̃ɑ̃sɾẽ. J   comer   EAT
 bajirocare ɑ'    bhíɾ.óɑkɾ.e   morir (una persona)     DIE ntg BARS,91 p
    .23, 2.4. Verbs with only a subject argument, p.24,  Verbs which agree
    in number with the subject. A very productive verb used in verb
    compounds, both transitive and intransitive, is roka 'to move down/away
     (s)'; roka becomes rea  with plural subjects. For example, baji roka '
    to die (s)' and baji rea 'to die (p)';ʉ
 boag, boago '    bóɑ́.ɨg    (ser/estar) podrido, podrida (animal, persona)
     PERSON
```

The entire source code here developed is available as a GitHub Gist.

References

Barasana Literacy Committee, Paula S. Jones and Wendell H. Jones (compilers). 2009. *Diccionario bilingüe: Eduria & Barasana-Español, Español-Eduria & Barasana*. Bogotá, D.C.: Editorial Fundación para el Desarrollo de los Pueblos Marginados. 613pp.

Swadesh, M. (1955): *Towards greater accuracy in lexicostatistic dating. International Journal of American Linguistics*. 21.2. 121-137.

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Behind the Sino-Tibetan Database of Lexical Cognates: Introductory remarks

Johann-Mattis List (13/05/2019)

Categories: Primer

Tags: data curation, database, EDICTOR, lexical cognates, lexicostatistics

One of the major efforts behind our recently published paper on the origin and spread of the Sino-Tibetan languages (Sagart et al. 2019) was the creation of a database of lexical cognates which was used to run the phylogenetic analyses. The creation of this database started about four years ago, when I joined the Centre des Recherches Linguistiques sur l'Asie Oriental in Paris as a research fellow in January 2015, and Guillaume Jacques and Laurent Sagart approached me with the idea of making a phylogenetic study of Sino-Tibetan languages. In December 2017, almost three years after having started, our database consisted of 180 concepts translated into 50 different languages. Since creating the database was not directly straightforward from the beginning, with quite a few situations in which we realized we had to re-arrange the data or the procedure, I thought it might be useful to share our experience in a series of blog posts, as it might be interesting for scholars who wish to create their own database.

A database of lexical cognates is nothing else than a comparative wordlist in which cognate relations between words from different languages are annotated. For the database itself, no specific software is needed, and spreadsheet editors like LibreOffice, Excel, or Google Sheets can easily be used for this purpose. As a minimal requirement, such a database provides information on how a given *language* expresses a given *concept* and with which other *words* the word denoting this concept in the language is etymologically related. Ideally, more information should be supplied, of course, for example, regarding the source of information (be it a reference or original fieldwork), if the word has been borrowed or not, or how the word is pronounced. If one wants to be very detailed, one can also indicate who made the respective cognate judgments, or even supply alignments that indicate where the experts think that the words are cognate.

While it sounds rather straightforward to create such a database at a first glance, there are many pitfalls one should better be aware of before starting to build one from scratch. There is a large amount of potential problems one can encounter during the creation process. It can turn out that the data for a key language is insufficient, key collaborators may leave the project, coding data may turn out to require much more time than estimated, and the results may also be disappointing in the end.

In order to be prepared for what can happen, it would be ideal, if we had some kind of a guideline on how to create datesets of lexical cognates. Given large projects of datasets that were prominently used in the past, such as ABVD (Greenhill et al. 2008), IELex (Dunn et al. 2012), or the datasets published as part of the Global Lexicostatistical Database project (Starostin and Krylov 2011), one might even think that this problem has been discussed long enough, so that scholars who want to build a new database on their own should not have a hard time to find enough guidance on how to get started. Unfortunately, when going from theory to practice, our own experience in working with lexical data from different scholars as part of large data aggregation projects like CLICS^2 (List et al. 2018) has shown that this is usually not the case. While fieldworkers have their toolbox to create dictionaries, there is no equivalent for historical linguists working on comparative databases of lexical cognates. As a result, scholars who start datasets from scratch often reinvent many wheels, and the wheels they reinvent may be squared at times.

Our experience with building the Sino-Tibetan Database of Lexical Cognates underlying the study by Sagart et al. (2019) does not solve these problems. We were making use of tools like EDICTOR (List 2017), which facilitate the process of cognate coding and making alignments of the data, but in order to get the data in a first instance, we mostly relied on the fact that we had people (mostly also myself) in our team who could quickly prepare custom scripts to parse available data and extract the data we needed. We also profited much from the fact that some projects, especially STEDT (Matisoff 2015), but also Tower of Babel, had been digitizing large amounts of data in a rather regular form in the past. We were also lucky to have people in our team who have done original fieldwork (which enabled them to quickly fill in a list of certain varieties, consulting informants where data was missing), and to have external collaborators who generously shared their data and answered our queries on specific items (see the list of acknowledgments in Sagart et al. 2019 for details).

The way in which we assembled the data for our study was not straightforward, but rather a winding road of many dead-ends, some surprises, lots of discussions, some disappointments, and a lot of lessons we learned for the future. We did not reach our (or maybe preliminary my) initial goal of providing a database of cognates that would provide fully aligned cognate sets and list all correspondence patterns in an indisputable way, so that it could be inspected, challenged, and improved by our colleagues in all kind of details one could think of as a historical linguist. But we achieved to provide a dataset of 180 concepts translated into 50 different varieties of Sino-Tibetan, along with an interface to easily inspect the data which goes beyond many of the datasets that have been published in the past.

Our data is open, scholars can easily inspect it in detail from its URL, and they can even correct the cognate judgments, add alignments, and further expand or correct it. In order to do so, however, one needs to learn a bit about the way in which we (1) assembled the data, (2) coded the data, and (3) how the tools for data curation and annotation can be used. In order to make it easier to understand what was going on *behind* the *Sino-Tibetan Database of Lexical Cognates,* we plan to write a couple of blog posts in which we will explain how the data was assembled, curated, and analyzed.

References

Dunn, Michael (2012): Indo–European Lexical Cognacy Database (IELex). Hosted at https://ielex.mpi.nl/.

Greenhill, Simon J. and Blust, Robert and Gray, Russell D. (2008): The Austronesian Basic Vocabulary Database: From bioinformatics to lexomics. *Evolutionary Bioinformatics* 4. 271-283.

List, Johann-Mattis (2017): A web-based interactive tool for creating, inspecting, editing, and publishing etymological datasets. In: *Proceedings of the 15th Conference of the European Chapter of the Association for Computational Linguistics*. System Demonstrations. 9-12.

List, Johann-Mattis and Simon Greenhill and Cormac Anderson and Thomas Mayer and Tiago Tresoldi and Robert Forkel (eds.) (2018): *CLICS: Database of Cross-Linguistic Colexifications*. Max Planck Institute for the Science of Human History. Jena: http://clics.clld.org/.

Matisoff, James A. (2015): *The Sino-Tibetan Etymological Dictionary and Thesaurus project*. Berkeley: University of California.

Sagart, Laurent and Jacques, Guillaume and Lai, Yunfan and Ryder, Robin and Thouzeau, Valentin and Greenhill, Simon J. and List, Johann-Mattis (2019): Dated language phylogenies shed light on the ancestry of Sino-Tibetan. *Proceedings of the National Academy of Science of the United States of America*. 1-6. DOI: 10.1073/pnas.1817972116

Starostin, George S. and Krylov, Phil (eds.) (2011): *The Global Lexicostatistical Database. Compiling, clarifying, connecting basic vocabulary around the world: From free-form to tree-form*. http://starling.rinet.ru/new100/main.htm.

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Biological metaphors and methods in historical linguistics I: Introduction

Nathanael E. Schweikhard (15/05/2019)

Categories: Methodology

Tags: biology, discussion, interdisciplinary research, metaphors, methodological transfer

Evolutionary biology and historical linguistics share a long history of scientific exchange, reflected both not only in the sharing and transfer of metaphors but more recently also in the transfer of methods. Already Charles Darwin claimed that both species and languages evolve in tree-like patterns, and linguists, like Wilhelm Meyer-Lübke, used terms like "sprachliche[n] Biologie" ("linguistic biology") when referring to the history of languages (Meyer-Lübke 1890, x). While the discipline of historical-comparative linguistics allowed biologists to adopt evolutionary thought against religious dogma in the late 19th century (Wells 1987: 54), it was biological applications which opened up the possibility of large quantitative studies in linguistics based on computational approaches (Geisler and List 2013, 111).

Many articles and essays have been written listing possible similarities between the disciplines (for recent ones see for example Pagel 2016 or List et al. 2016). Yet biology is considered a natural science, while linguistics is thought to belong to the humanities. One could even say that their research objects belong to two different worlds, the objective universe, on the one hand, and the world of the products of the subjective mind, on the other hand (Geisler and List 2013:

121). Therefore, one may rightfully ask what it is that makes the exchange of ideas so fruitful.

Both disciplines deal with historical processes and can therefore be seen as belonging to the wider field of historical sciences which are dealing with the past and how it lead to the present by "analyz[ing] persistence with modification of systems ('descent with modification')" (Stevick 1963, 160). In other words, they describe and reconstruct earlier stages of their research objects, proposing ancestral character states in biology or proto-forms in linguistics (Atkinson and Gray 2005, 519), or investigate earlier stages directly, where they are still attested as fossils or in form of manuscripts and inscriptions (ibid: 514). Additionally, both disciplines propose theories that seek to explain the transmission of their research objects, be it vertical (in form of inheritance) or horizontal (in form of direct exchange).

Change in linguistics and biology can be studied from different perspectives. One can restrict oneself to study only one language or species at the same time, investigating its internal history from its oldest attestations to the present, or one can compare several languages or species, which form a family, and investigate how they separated and interacted after separation.

In addition, one can also carry out a general comparison of languages and species in order to find the general laws and tendencies by which they change, which is part of the typologogical approach in linguistics. Both fields are thus based on the assumption that all languages and species change through time. Already August Schleicher stated that "Sprachen sich verändern so lange sie leben" (Schleicher 1863: 18, "Languages change as long as they are alive"). There is some debate among scholars as to whether the principles of change might also change with time or whether they remain constant.

Considering these similarities, but also the obvious differences between the fields, looking at historical linguistics against the contrast of evolutionary biology is of particular benefit when modeling language history as it forces one to be explicit about one's assumptions. This inspired us to start a series of blogposts on comparisons between biology and linguistics. In future posts we will describe in more detail which correspondences and differences there are between the research objects of biology and linguistics and what needs to be taken into account when using methods from evolutionary biology to tackle problems in historical linguistics.

References

Atkinson, Quentin D., and Russell D. Gray. 2005. "Curious Parallels and Curious Connections: Phylogenetic Thinking in Biology and Historical Linguistics." *Systematic Biology* 54 (4): 513–26. http://www.jstor.org/stable/20061257.

Geisler, H., and J.-M. List. 2013. "Do Languages Grow on Trees? The Tree Metaphor in the History of Linguistics." In *Classification and Evolution in Biology, Linguistics and the History of Science. Concepts– Methods – Visualization*, edited by Heiner Fangerau, Hans Geisler, Thorsten Halling, and William Martin, 111–24. Stuttgart: Franz Steiner Verlag.

Gray, Russell D., Simon J. Greenhill, and Malcolm D. Ross. 2007. "The Pleasures and Perils of Darwinzing Culture (with Phylogenies)." *Biological Theory* 2 (4): 360–75.

List, Johann-Mattis, Jananan Sylvestre Pathmanathan, Philippe Lopez, and Eric Bapteste. 2016. "Unity and Disunity in Evolutionary Sciences: Process-Based Analogies Open Common Research Avenues for Biology and Linguistics." *Biology Direct*, nos. 39, 11: 1–17.

Meyer-Lübke, Wilhelm. 1890. *Italienische Grammatik*. Leipzig: Verlag von O. R. Reisland.

Pagel, Mark. 2016. "Darwinian Perspectives on the Evolution of Human Languages." *Psychonomic Bulletin & Review*, 1–7. https://doi.org/10.3758/s13423-016-1072-z.

Schleicher, August. 1863.] [*Die darwinsche Theorie und die Sprachwissenschaft*. Weimar: Hermann Böhlau.

Stevick, Robert D. 1963. "The Biological Model and Historical Linguistics." *Language*, nos. 2, 39: 159–69. https://www.jstor.org/stable/411199.

Wells, Rulon S. 1987. "The Life and Growth of Language: Metaphors in Biology and Linguistics." In *Biological Metaphor and Cladistic Classification: An Interdisciplinary Perspective; [Papers from Symposium on Biological Metaphor Outside Biology (1982.03.04-05, Philadelphia) Interdisciplinary Round-Table on Cladistics and Other Graph Theoretical Representations (1983.04.28-29, Philadelphia)]*, edited by Henry Max Hoenigswald, 39–80. Philadelphia: Univ. of Pennsylvania Pr.

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Rooting MADness

Gerhard Jäger (22/05/2019)

Categories: Analysis

Tags: phylogenetic reconstruction, rooting

Rooting of phylogenetic trees is an important task, not only in evolutionary biology, but also in historical linguistics. So far, however, different rooting methods have not yet been sufficiently tested on linguistics data. Given that a new method for the automatic rooting of phylogenetic trees has been presented recently in biology, it seemed to be a good occasion to test in detail how well this new method works in comparison with alternative methods.

A few months ago, Mattis List pointed my attention to a (relatively) novel method for rooting phylogenetic trees with branch lengths: *Minimal Ancestor Deviation* rooting (Kümmel Tria et al. 2017). I will not go into the details of that algorithm here; the interested reader is referred to the mentioned article. Suffice it to give two quotations:

> *"The MAD method operates on binary unrooted trees and assumes that branch lengths are additive and that OTUs are contemporaneous." (Kümmel Tria et al. 2017:1)*

and

> *Branch ancestor deviations quantify the departure from strict clock-like behaviour, reflecting the level of rate heterogeneity among lineages. Wrong positioning of the root will lead to erroneous iden- tification of ancestor nodes, and apparent deviations will tend to be larger. We therefore infer*

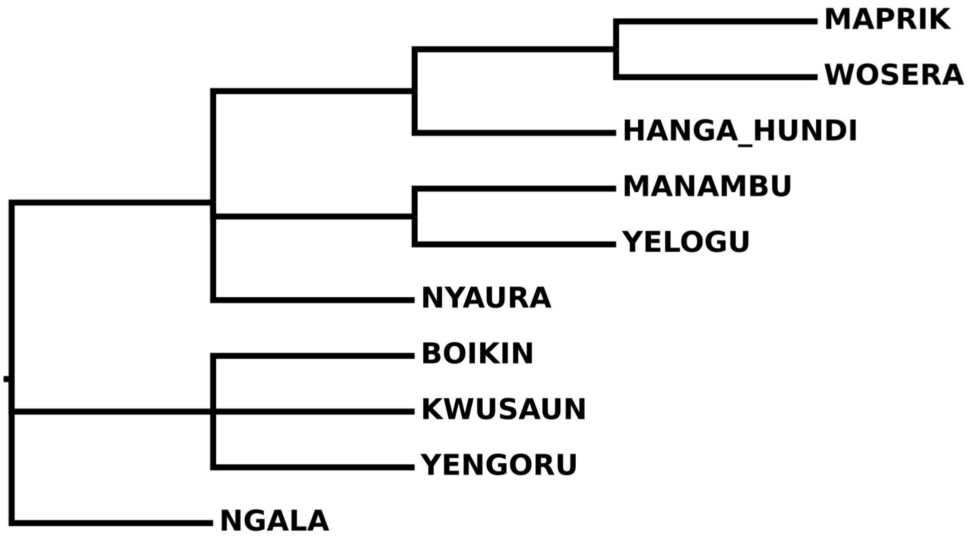
> *the MAD root as the branch and position that minimizes the ancestor deviation [...]. (Kümmel Tria et al. 2017: 2)*

Several standard algorithms for phylogenetic infernce (e.g., Neighbor Joining, most off-the-shelf implementations of Maximum Likelihood) produce unrooted trees with branch lengths, and one needs to perform rooting as a separate step. So if this new kid in town is better than standard techniques such as midpoint rooting or outgroup rooting, this might come in handy.

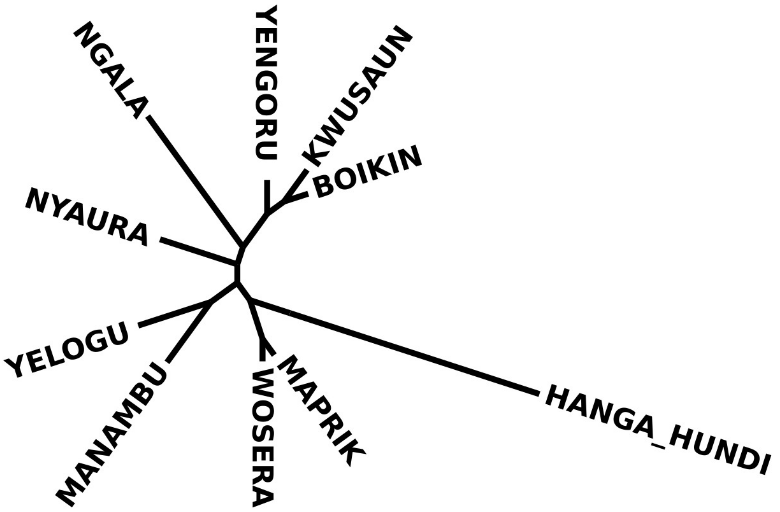
Mattis and me were interested in how well this method performs in comparison to other rooting methods when applied to language trees derived from word lists. So I did a little experiment.

In Jäger (2018), I describe a method to apply automatic cognate detection to the data from the ASJP project (Wichmann et al. 2016), to extract character matrices and to apply Maximum Likelihood (ML) phylogenetic inference (Data and code are available at https://osf.io/cufv7/). In the meantime I have updated my database to ASJP v. 18. I used those data to infer ML trees for all Glottolog families for which ASJP contains at least 10 contemporaneous doculects, using the Glottolog classification as constraint tree. This gave me 64 unrooted trees. (To my dismay, I noticed along the way that the Glottolog classification that is shipped with ASJP is incomplete, so I extracted the Glottolog classification from the Glottolog website.)

I will use Ndu (a language family spoken in Papua New Guinea; traditionally considered as part of the Sepik family) as my running example. The Glottolog classification looks like this:

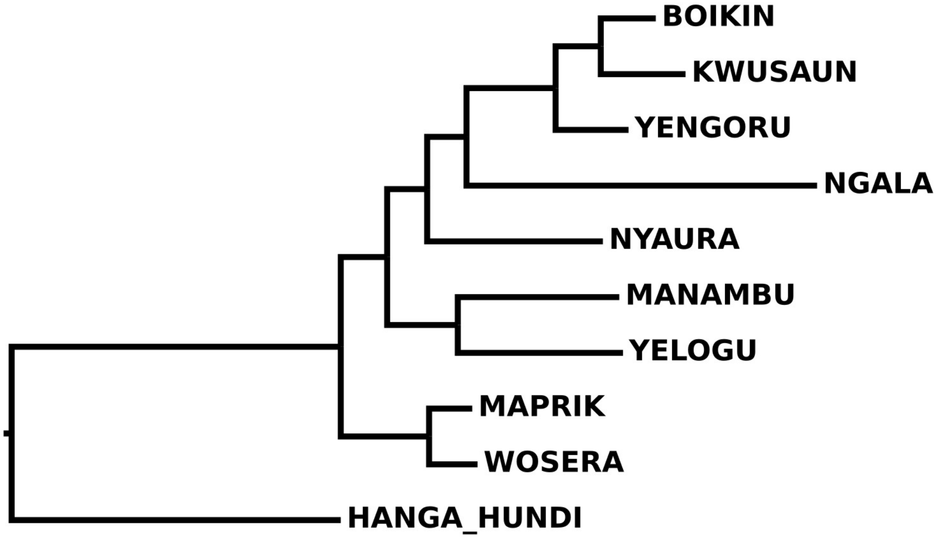


My ML-tree (obtained using the great software RAxML) is here:



The task is to find the correct root of the unrooted tree. However, the goldstandard does not identify a unique root, as Glottolog identifies three subgroups (Boikin, Ngala, and Nuclear Ndu).

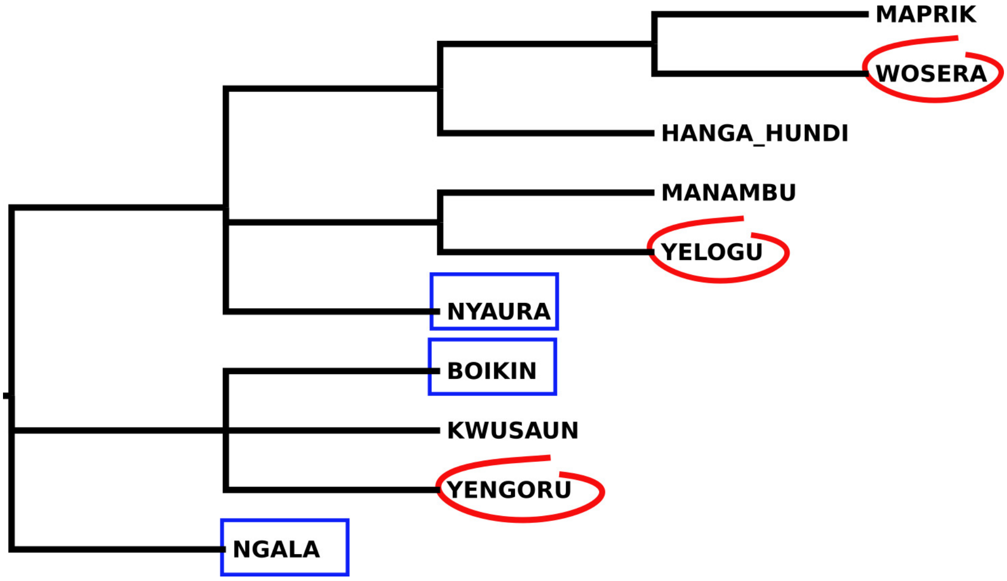
Consider, e.g., the midpoint-rooted version of the ML tree:



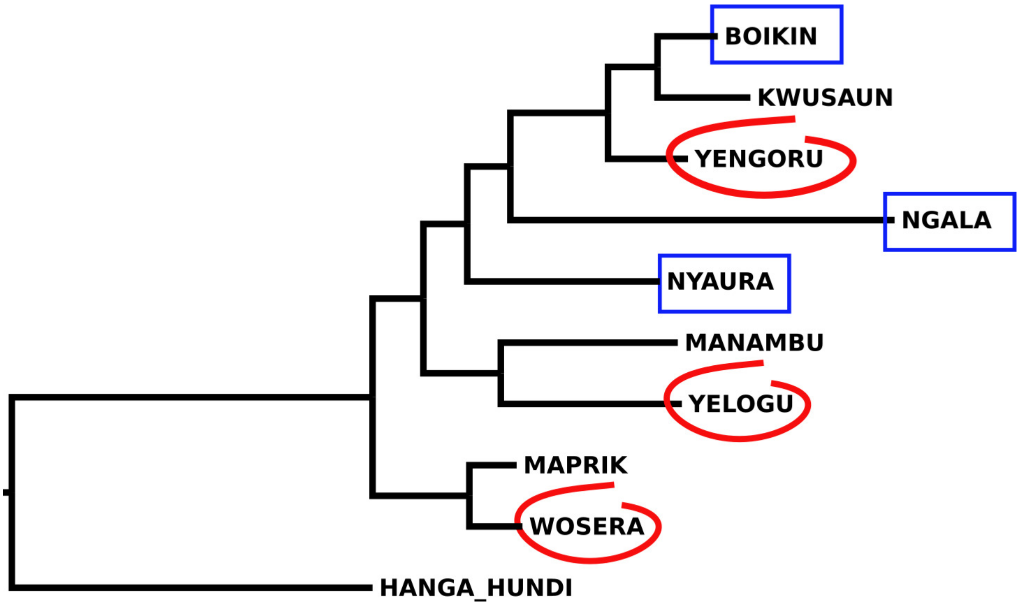
This looks pretty bad, but can we quantify how bad it is?

One way to do it is to harness the *triplet distance* (Sand et al. 2014) between the rooted tree and the Glottolog goldstandard.

To see what this is about, consider the triplet (Yengoru, Yelogu, Wosera). In the goldstandard tree, it is grouped as (Yengoru, (Yelogu, Wosera)).



In the midpoint rooted tree, the grouping is (Wosera, (Yelogu, Yengoru)).



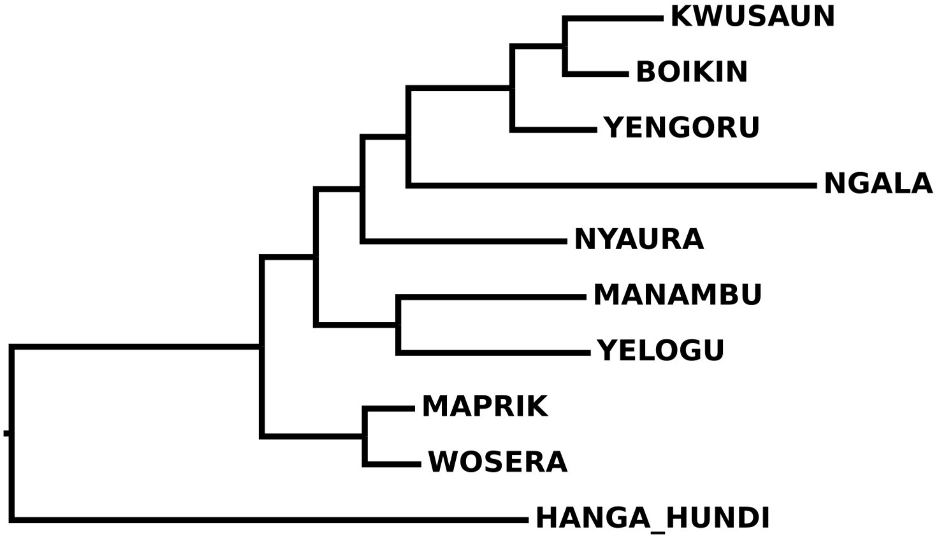
So this triplet is mis-classified by midpoint rooting. This evaluation is performed for each triplet of doculects. We disregard triplets like (Ngala, Boikin, Nyaura), which remain unresolved in the goldstandard. I call the number of misclassified triplets, divided by the number of goldstandard-resolved triplets, the *Generalized Triplet Distance* (GTD) between the rooted binary-branching tree and the goldstandard tree. (This is inspired by the *Generalized Quartet Distance* from Pompei et al. 2011).

I compared four rooting methods:

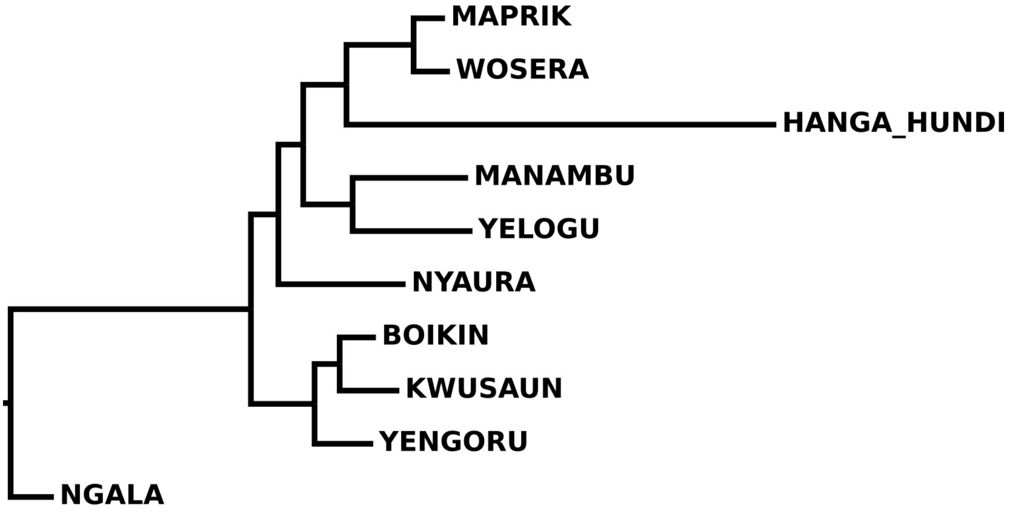
1. **MAD rooting.**
2. **Midpoint rooting.**
3. **Outgroup rooting.** For this I created an artificial outgroup, with a character vector consisting entirely of 0s.
4. **Yule rooting.** This method is derived from (Steel and McKenzie 2001). They give a formula to compute the likelihood of a rooted tree *topology* under the assumption that it was generated by a Yule process. The tree is rooted by calculating this likelihood for each possible root location and

picking the one with the maximal likelihood. If there was a tie between different branches, I picked one at random.

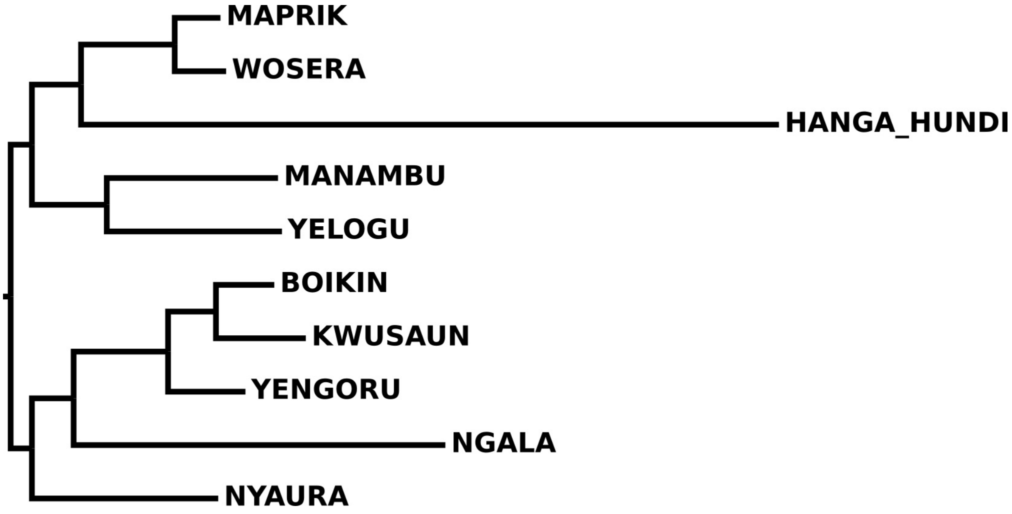
Here is the MAD rooted tree for Ndu (which happens to be identical to the midpoint rooted version here):



The outgroup-rooted tree:



And the Yule-rooted version:



Outgroup rooting is the only method here that produces a tree consistent with the goldstandard. The GTDs are

1. MAD: 0.61
2. midpoint: 061
3. outgroup: 0.00
4. Yule: 0.21

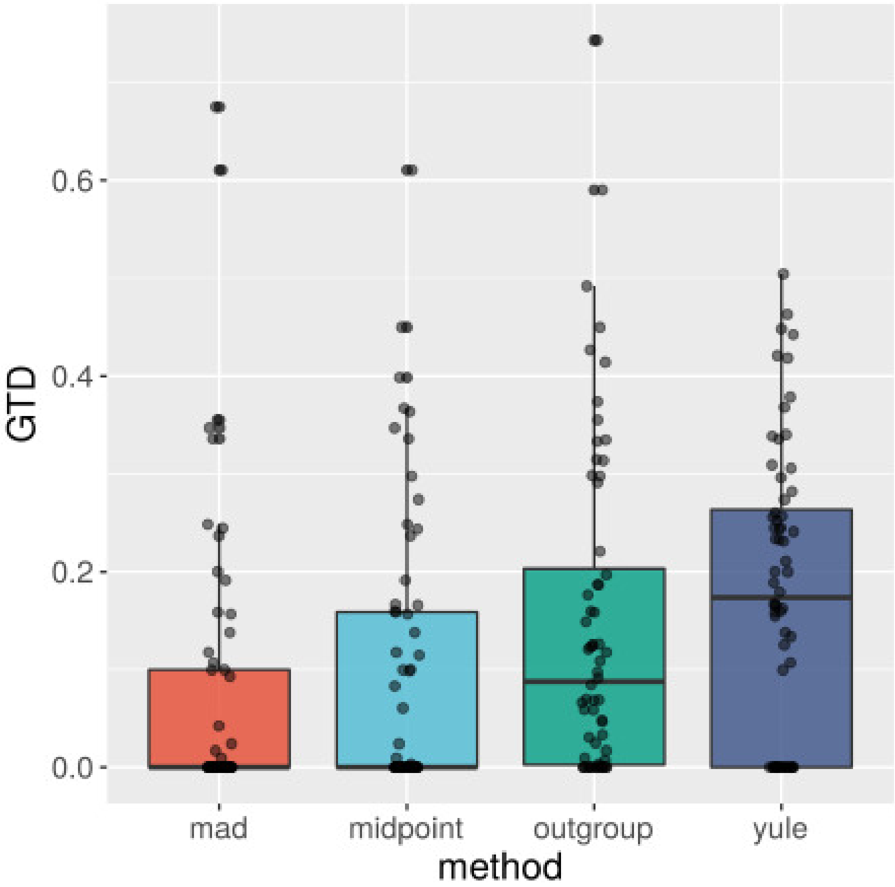
It seems that both MAD and midpoint rooting are thrown off-stride here by the extra-long branch extending to Hanga Hundi.

When we perform this comparison over all 64 families, we get a different picture though:

mean	GTD
MAD	0.0704
midpoint	0.0941
outgroup	0.1437
Yule	0.1771

These numbers indicate quite clearly that MAD and midpoint rooting are superior to both outgroup and Yule rooting. The difference between MAD and midpoint rooting seems to be small, but closer examination reveals that MAD is in fact substantially better than midpoint rooting. - MAD rooting achieved a GTD of 0.0 (meaning: finds a root fully consistent with the goldstandard) for 42 families (66%), but midpoint rooting only for 35 families (55%).- Both MAD and midpoints rooting have a median of 0, but the 75th quantile for MAD is at 0.10, and for midpoint at 0.16).

The difference is also clearly visible in the boxplots:



To conclude, *Minimal Ancestor Deviation* rooting seems to be better suited to root language phylogenies than more established methods. The usual disclaimers apply – we cannot be sure how much of these results depend on the particular data and phylogenetic inference method I used here. Different data might produce different results. Still, MAD rooting deserves to be included into the standard toolbox of phylogenetic linguistics.

Code and data, including all trees and the complete evaluation results, are available at https://github.com/gerhardJaeger/competititiveRooting.git.

References

Jäger, G. (2018): Global-scale phylogenetic linguistic inference from lexical resources, *Scientific Data* 5, 180189. URL: https://doi.org/10.1038/sdata.2018.189

Kümmel Tria, F. D., Landan, G., and T. Dagan (2017): Phylogenetic rooting using minimal ancestor deviation. *Nature Ecology and Evolution*. URL: http://dx.doi.org/10.1038/s41559-017-0193

Pompei, S., Loreto, V., & Kümmel Tria, F. D. (2011): On the accuracy of language trees. *PloS one*, *6* (6), e20109.

Steel, M., & McKenzie, A. (2001): Properties of phylogenetic trees generated by Yule-type speciation models. *Mathematical biosciences*, *170* (1), 91-112.

Sand et al. (2014): tqDist: a library for computing the quartet and triplet distances between binary or general trees, *Bioinformatics*, 30.14, 2079–2080.

Wichmann, Søren, Eric W. Holman, and Cecil H. Brown, eds., 2016. *The ASJP Database*, version 17. URL: https://asjp.clld.org

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Behind the Sino-Tibetan Database of Lexical Cognates: Concept selection

Johann-Mattis List (26/06/2019)

Categories: Primer

Tags: code example, concept list, Concepticon, database, Sino-Tibetan

One of the crucial steps in creating a database of lexical cognates is the selection of concepts one wants to use for a given study. While many scholars use the classical Swadesh list of 200 items) (Swadesh 1952) for this purpose, or the combined list of 207 items, in which the former has been merged with Swadesh's updated list of 100 items (Swadesh 1955), and which is often mistakenly attributed to Swadesh himself, although the first official reference seems to be Comrie (1977), it is useful to give the selection of concepts some more thought initially.

What scholars underestimate usually in this context is that there are quite different reasons why the classical Swadesh lists, or any pre-compiled concept lists, may not be apt for the investigation of a given language family. Apart from the obvious reason that a concept list may contain terms that cannot be found in the target languages, additional problems resulting from concept choice result from language-specific characteristics of lexical typology, such as: (A) sound symbolism, which may differ across languages, (B) compoundhood, which also shows language-specific patterns, (C) polysemy or homophony, which both may show areal or family-specific aspects.

In addition, one should not underestimate the importance of data availability. Given that the majority of lexical databases are not compiled from scratch, but derived from existing data collections which serve as some kind of the backbone of the database, one should make sure to check which concepts have been recorded in the major sources upon which one wants to base the database.

When compiling the Sino-Tibetan Database of Lexical Cognates for our study on the origin of Sino-Tibetan (Sagart et al. 2019 , we had to struggle with all of the above-mentioned points. Since our initial goal was to create a database of *high mutual coverage* in terms of attested words per language (see List et al. 2018 for a discussion of this concept), we had to pay specific attention to the problem of data availability. For this reason, we started from an initial comparison of concepts available different sources (including those digitized by the STEDT project, Matisoff 2015). To compare the concepts available in the different sources, we made use of the Concepticon project (concepticon.clld.org, List et al. 2016, see List 2018 for an introduction to the goals of the project) and the `pyconcepticon` library, which offers quick access to the resources offered by Concepticon.

When having installed the `pyconcepticon` package, following the instructions provided at the project's GitHub repository , one can easily check the overlap between several concept lists using the `intersection` command that can be invoked from the terminal (you have to replace `PATH` with the path to your local Concepticon repository):

```
$ concepticon --repos=PATH intersection Yakhontov-1991-35 Swadesh-1952-200 Swadesh-1955-100 Dolgopolsky-1964-15
1 EYE [1248]
2 I [1209]
3 LOUSE [1392]
4 NAME [1405]
5 THOU [1215]
6 TONGUE [1205]
7 TOOTH [1380]
8 TWO [1498]
9 WATER [948]
```

This code example checks which of the concepts given in the concept lists by Swadesh (100 and 200) plus the lists by Yakhontov (published in Starostin 1991) and Dolgopolsky (1964) recur in all lists, and outputs them both with their Concepticon Gloss, and their Concepticon IDs. Note that you do not need to use the lists that are provided by Concepticon alone, you can also compare with your own concept lists, and this is exactly what we did, as we wanted to work with data that was not yet officially linked to Concepticon (see the tutorial by List 2017 for more information).

While our first concept list consisted of as many as 250 concepts, we had to reduce it further, once we started to add more languages to our sample. Often, we ran into simple coverage problems, as some of the concepts we thought would be useful turned out to be missing from sources, and other concepts, like, e.g., MOSQUITO, were not lexified in some regions of the Himalaya.

As a result, our final "master list", which we used for the phylogenetic analyses, only comprises 180 concepts. The criteria for exclusion of concepts was strictly technical. We ranked all concepts by their coverage with respect to the languages in our sample, and set up a coverage of at least 80% (each concept should be reflected in at least 80% of our languages). We further removed some remaining concepts from the list which had been shown to be problematic with respect to compoundhood, sound symbolism, and polysemy.

Using Concepticon to check for coverage and overlap across concept lists turned out to be very efficient, as it helped us to avoid to include data into our database which did not provide enough coverage. To illustrate how this can be done, we can compare the coverage of our current list of 250 concepts in the database with the coverage of a resource that we might want to add to our database in the future. This resource is the database of cognates in Kho-Bwa languages, compiled by T. A. Bodt (available from Bodt and List 2019). As Bodt's data and our data are linked to Concepticon (following the recommendations of the CLDF initiative, Forkel et al. 2018), we can compare their intersection with a simple command from the terminal, in which we combine the original `intersection` command of `pyconcepticon` with the `wc` command shipped with all Unix terminals by using the famous and incredibly useful `pipe` `|` :

```
$ concepticon --repos=PATH intersection Sagart-2018-250.tsv Bodt-2019-664.tsv | wc -l
202
```

To run this code as illustrated here, the concept lists need to show a certain format. You can check this out yourself by installing `pyconcepticon`, downloading the Concepticon data, and the two concept lists, which I have all uploaded to this GitHub Gist.

References

Bodt, Timotheus A. and List, Johann-Mattis (2019): Testing the predictive strength of the comparative method: An ongoing experiment on unattested words in Western Kho-Bwa langauges. *Papers in Historical Phonology* 4.1. 22-44.

Comrie, Bernard and Smith, Norval (1977): Lingua Descriptive Series: Questionnaire. *Lingua* 42. 1-72.

Dolgopolsky, Aron B. (1964): Gipoteza drevnejšego rodstva jazykovych semej Severnoj Evrazii s verojatnostej točky zrenija [A probabilistic hypothesis concering the oldest relationships among the language families of Northern Eurasia]. Voprosy Jazykoznanija 2. 53-63.

Forkel, Robert and List, Johann-Mattis and Greenhill, Simon J. and Rzymski, Christoph and Bank, Sebastian and Cysouw, Michael and Hammarström, Harald and Haspelmath, Martin and Kaiping, Gereon A. and Gray, Russell D. (2018): Cross-Linguistic Data Formats, advancing data sharing and re-use in comparative linguistics. *Scientific Data* 5.180205. 1-10.

List, Johann-Mattis and Cysouw, Michael and Forkel, Robert (2016): Concepticon. A resource for the linking of concept lists. In: *Proceedings of the Tenth International Conference on Language Resources and Evaluation*. 2393-2400.

List, Johann-Mattis (2017): *Historical Language Comparison with LingPy and EDICTOR* [Historischer Sprachvergleich mit LingPy und EDICTOR]. Department of Linguistic and Cultural Evolution: Max-Planck Institute for the Science of Human History.

List, Johann-Mattis and Walworth, Mary and Greenhill, Simon J. and Tresoldi, Tiago and Forkel, Robert (2018): Sequence comparison in computational historical linguistics. *Journal of Language Evolution* 3.2. 130–144.

List, Johann-Mattis (2018): Towards a history of concept list compilation in historical linguistics. *History and Philosophy of the Language Sciences* 5.10. 1-14.

Matisoff, James A. (2015): *The Sino-Tibetan Etymological Dictionary and Thesaurus project*. Berkeley:University of California.

Sagart, Laurent and Jacques, Guillaume and Lai, Yunfan and Ryder, Robin and Thouzeau, Valentin and Greenhill, Simon J. and List, Johann-Mattis (2019): Dated language phylogenies shed light on the ancestry of Sino-Tibetan. *Proceedings of the National Academy of Science of the United States of America* 116. 10317–10322. DOI: 10.1073/pnas.1817972116

Swadesh, Morris (1952): Lexico-statistic dating of prehistoric ethnic contacts. With special reference to North American Indians and Eskimos. *Proceedings of the American Philosophical Society* 96.4. 452-463.

Swadesh, Morris (1955): *Towards greater accuracy in lexicostatistic dating*. International Journal of American Linguistics 21.2. 121-137.

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Using the Waterman-Eggert algorithm for sentence alignment

Johann-Mattis List (15/07/2019)

Categories: Code

Tags: code snippet, sentence alignment, sequence alignment, Waterman-Eggert algorithm

During the 24th International Conference of Historical Linguistics, I was asked by a colleague whether I would know a good way to align and scores sentences available in form of phonetic transcriptions. While it is clear that one can roughly compare the difference between sequences rather easily by aligning them, and calculating, for example, the edit distance between them, it is clear that the task of sentence alignment could be done in a somewhat more subtle way.

The first obstacle that we may meet when trying to align sentences is that a completely linear alignment may yield problems, since sentences may contain the same or similar words, but differ with respect to word order. The first alignment algorithm that comes to mind when trying to deal with this question is the so-called Waterman-Eggert algorithm, first proposed and named after Waterman and Eggert (1987).

Long time ago, I provided an implementation of this algorithm as part of the LingPy package. The basic idea compared to traditional alignment algorithms is to expand upon local alignment when searching for optimal subsequences between two strings. While local alignment stops after having identified the longest similar subsequence between two strings, the Waterman-Eggert algorithm does not stop, but instead continuous searching for more similar subsequences in the data, just until all of them have been readily identified.

This is not the place to get into the details of the algorithmics here. For those interested in the topic, I recommend to have a look at List (2014), where the major algorithms for alignment analyses have been rdescribed and discussed for usability in linguistic applications. To get a sbrief glimpse at the crucial difference between Waterman-Eggert and the famous local alignment algorithm by Smith-Waterman (Smith and Waterman 1981), let us open a terminal and test the Waterman-Eggert algorithm in a short LingPy session (List et al. 2018).

```
>>> from lingpy import *
>>> for a, b, c in we_align('abcd', 'cdab'):
...     print(' '.join(a))
...     print(' '.join(b))
...     print('-')
a b
a b
-
c d
c d
```

What should be clear from this illustration is that the algorithm does not simply align strings locally, but instead that it searches for substring matches. This is internally done by identifying the highest-scoring subsequence in the alignment matrix at first, and then searching again for the next-high-scoring subsequence, until none are left.

To use this for sentence alignment of sentences provided in phonetic transcription, we can write a wrapper function that makes use the Waterman-Eggert implementation given in LingPy. In addition to simply aligning two sentences, however, we would also like to score them, and we will soon see how this can be done. We first start by loading a patch for the Waterman-Eggert algorithm, since I realized that the current LingPy implementation contains a bug. This patch is provided along with the code in a GitHub-Gist accompanying this post.

We start our script by loading the libraries. Here, we load LingPy, the patch (which will soon be included when we do the next update), and the `product` function from itertools, which we need to populate our scoring dictionary.

```python
from lingpy import *
from patch_we_align import we_align
from itertools import product
```

We now start by defining our function. It has a rather simple call signature with a few parameters. The first parameters are the sentences, which should be given in IPA transcription without any punctuation marks. The gap penalty is the classical gap penalty passed to the alignment algorithm. The model refers to the sound class model, i.e., it determines how we represent sounds internally in our function. The default is the `sca` model also widely used in LingPy. The limit-argument tells the function which subsequences it should still accept as matches. I think, for initial tests, subsequences of length two seem like a good start here.

```python
def salign(
        senA,
        senB,
        gap=-1,
        model='sca',
        limit=2
        ):
    """Align and score two sentences"""
```

In the next step, we convert the sentences into sound classes, using the sound class model. To do so, we first tokenize them, i.e., we determine what should count as a sound. This function will treat combinations of base-letters and diacritics as one sound. If you do not want to use it, just provide your data already in space-segmented form, and this function won't do anything. We then convert the segmented data (a Python list as data type) into sound class representations.

```python
# retrieve sound class model
if not hasattr('scorer', model):
    model = Model(model)
# convert to sound classes
tokA, tokB = list(map(
    lambda x: ipa2tokens(
        x.replace(' ', '_')),
    [senA, senB]))

# assume segmentation by underscore
clsA, clsB = list(map(
    lambda x: tokens2class(
        x,
        model
        ),
    [tokA, tokB]
    ))
```

Before we can now align the data with the Waterman-Eggert algorithm, we need to create a scorer that tells the algorithm how segments should be compared with each other. Here, we simply use the built-in scorer provided along with the LingPy package, setting the matching of `_` with itself to `0` , because we do not want to enourage the algorithm to align too many boundary markers with each other.

```
scorer = {(a, b): -1 if \
        (a != b or '_' in (a, b)) \
        else 1 for a, b in product(
        set(clsA+clsB),
        set(clsA+clsB))
    }
# make sure boundaries don't score
scorer['_', '_'] = 0
```

We can now start to compute the alignments. While doing so, we iterate over each identified segment and store their similarity in a specific list, so we can later used it for scoring the similarity of the sentences. Our patch has the advantage of offering a detailed index of which elements have been aligned (different from the original call signature). We use this to extract the original transcriptions as alignments, rather than the aligned sound classes.

```
out, scores = [], []
for a, b, score, iA, iB in we_align(
    clsA, clsB, scorer=scorer, gap=gap
    ):
    if len(a) < limit:
        pass
    else:
        out += [
                (a, b, score)
                ]
        scores += [score]
```

While we could already output the data as is, it would be useful to score the data as well, in order to offer us a way to retrieve some general distance between the two sentences. In order to do so, we just follow Downey et al. (2008) in computing a normalized distance score from the similarity scores that we retrieve for each aligned subsequence in comparison with the alignments of each sentence with itself.

```
        # compute self-scores
        sA = sum([scorer[a, a] for a in clsA])
        sB = sum([scorer[a, a] for a in clsB])
        sAB = sum(scores) / len(scores)

        score = 1 - (2 * sAB / (sA + sB))
        return out, score
```

Equipped with this code, we can now carry out our first sentence alignment. Let's compare two random sentences from German with each other in which we deliberately re-arrange some words.

```
alms, scores = salign(
        'əʁːmainuɪ.ɪɛ͡sthnsainhrts',
        'ɛ͡ʁːhrtsmainuə.sain',
        gap=-2
        )
for a, b, score in alms:
    print(' '.join(a))
    print(' '.join(b))
    print('{0:.2f}'.format(score))
print('{0:.2f}'.format(scores))
```

The output of this comparison (the first sentence is inspired by Goethe's "Meine Ruh' ist hin") yields the following results:

```
H E R C
H E R C
4.00
S A N
S A N
3.00
M A N E R Y
M A N - R Y
3.00
0.38
```

In total, the algorithm yields three blocks, which correspond to four words in the original data, with the third block (corresponding to “meine Ruh”) showing the same order in both test sequences. The last score, 0.38, is the overall distance of the two sequences, which is rather low, given the high number of words occuring in the sequence.

It is clear that more can be done to arrive at a good sentence alignment. This post was not meant to present a complete solution to the problem, it was rather intended to illustrate how we can use the tools we offer in libraries such as LingPy to carry out quick tests on new topics that have so far not yet been thoroughly discussed in the field of comparative linguistics. Code and patch are available in form of a GitHub Gist, which you can download from here.

References

Downey, Sean S. and Hallmark, Brian and Cox, Murray P. and Norquest, Peter and Lansing, Stephen (2008): Computational feature-sensitive reconstruction of language relationships: developing the ALINE distance for comparative historical linguistic reconstruction. *Journal of Quantitative Linguistics* 15.4. 340-369.

List, Johann-Mattis (2014): *Sequence comparison in historical linguistics*. Düsseldorf:Düsseldorf University Press.

List, Johann-Mattis and Greenhill, Simon and Tresoldi, Tiago and Forkel, Robert (2018): *LingPy. A Python library for quantitative tasks in historical linguistics*. Max Planck Institute for the Science of Human History. Jena: http://lingpy.org.

Smith, T. F. and Waterman, M. S. (1981): Identification of common molecular subsequences. *Journal of Molecular Biology* 1. 195-197.

Waterman, M. S. and Eggert, M. (1987): A new algorithm for best subsequence alignments with application to tRNA-rRNA comparisons. *Journal of Molecular Biology* 197. 723-728.

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Feature-Based Alignment Analyses with LingPy and CLTS I

Johann-Mattis List (19/08/2019)

Categories: Code

Tags: alignment, cross-linguistic transcription systems, distinctive features, phonetic alignment, Python, scoring function

In the past, people have repeatedly asked me how they could use their own scoring functions in combination with LingPy's alignment algorithms. Their major concern was that the sound-class-based scoring systems we use in LingPy might fail to reflect true phonetic similarity of sounds, specifically also because they are not informed by classical ideas about distinctive features in phonology. As described in detail in List (2014), LingPy converts sounds in phonetic transcription to an internal alphabet of less than 30 letters, to which the alignment algorithms are then applied in a second stage.

What my colleagues wanted to do instead was to test feature-based scoring systems (e.g. Chomsky and Halle 1968) and then use these features to derive distance or similarity scores between phonetic segments which would then be used to carry out the alignment analysis. In addition, some colleagues had created their own similarity matrix, and wanted to apply it more flexibly to other datasets (see, for example, Jäger 2015). My answer was usually, that this could be done in principle, but that it would require some amount of data preprocessing, depending on what data one wants to align. Not many colleagues asked me a second time, maybe because they thought it would be too complicated to use their own distance or similarity scores in LingPy.

When I recently started working on a modified alignment algorithm myself, I had to work on the same question again, and I figured, that it is in fact not that difficult to use a custom scoring function in Lingpy. Most of the things one needs to use LingPy along with custom scoring functions are already in place. Furthermore, with our recently published pyclts package, underlying the Database of Cross-Linguistic Transcription Systems (see Anderson et al. (2018) for an overwiew), there is now even a large collection of sounds for which we have distinctive feature sets. The major reason why I never tested feature-based alignment methods so far, was that I could not find a feature-system that would offer feature for all the sounds I usually find in linguistic datasets. Even datasets like Phoible (Moran et al. 2014), which offers huge amounts of transcriptions barely touch the surface of the variation one encounters when working with real transcriptions.

Luckily, our CLTS system has shown to be very robust so far. It understands some 8000 different phonetic segments, including clicks, tones, dipththongs, and certain consonant clusters, and we have developed first approaches to convert a given dataset into a form of IPA that CLTS accepts. For the conversion, we now use *orthography profiles* (Moran and Cysouw 2018), which I have presented in past tutorials (List 2017), and for which I recently also wrote an implementation in JavaScript, called SegmentsJS.

I therefore think that it is time to get back to my colleagues' request and illustrate how one can first create a custom, feature-based scoring function with help of CLTS, and then use this scoring function to carry out pairwise alignments of phonetic sequences. Given my limited time to write tutorial blogposts, I furthermore decided to divide this post into two (potentially three) posts, and discuss the creation of the scoring function in this post, while I will get back to the question of how to use LingPy's methods for sequence comparison in one or two follow-up posts.

Before we start with the actual code, it is important to understand how scoring functions work. Basically there are two different kinds of scoring functions: those based on *distances* between segments, and those based on *similarities* between segments. One may intuitively think that there is no real difference with respect to the use of similarities or distances. When looking closer into the algorithmics underlying the sequence alignment problem, however, this assumption is not correct, since only similarity-based scoring functions allow for both semi-global and local alignment analyses (for details on these problems, compare List 2014, where all algorithms are described in detail).

For this reason, it is not useful to start from the computation distance scores for phonetic segments. Instead, I recommend everybody who wishes to work seriously on phonetic alignment algorithms to work with those algorithms that make use of similarities between segments. While distance scores are probably easy to understand, since we can think of them in form of distance in space, or distance along pathways, or distance in trees. Distance between identical objects is always 0, and the more dissimilar two objcts become, the higher the distance score between them. Similarity scores, on the other hand, assume some high score for the identity of objects, which may vary, depending on the object under question, and smaller scores for dissimilar objects, with scores beyond zero being reserved for those objects that have almost nothing in common.

In order to derive a *distance score* between two sound segments which are defined by a given feature system, the easiest and seemingly most straightforward way (recommended and defended by some colleagues in personal communication) is to compute the so-called *Hamming distance* (Hamming 1950). This distance reflects the proportion of features where two segments differ. Turning the Hamming distance into a similarity score is straightforward, since we only need to calculate the proportion of features where two segments are identical.

If we look at the CLTS feature system, we find 37 features in total, which cover three major classes of sounds, *consonants*, *vowels*, and *tones*, which themselves may vary with respect to the features that define them. The features themselves can be binary or have multiple values. Retrieving the features of a given sound linked to the CLTS system is straightforward. The features can be found in the `featuredict` attribute of a `Sound` object.

```python
from pyclts import TranscriptionSystem
bipa = TranscriptionSystem('bipa')
sound = bipa['ts']
for i, (k, v) in enumerate(sorted(sound.featuredict.items())):
    print('{0:5} | {1:22} | {2:10}'.format(i+1, k, v or '-'))
```

When you type in this code in your commandline (provided you have installed the pyclts package, e.g., with help of `pip`, by typing `pip install pyclts`), you will receive the output shown in the following table in text form.

No.	Feature	Value
1	articulation	–
2	aspiration	–
3	breathiness	–
4	creakiness	–
5	duration	–
6	ejection	–
7	glottalization	–
8	labialization	–
9	laminality	–
10	laterality	–

No.	Feature	Value
11	manner	affricate
12	nasalization	–
13	palatalization	–
14	pharyngealization	–
15	phonation	voiceless
16	place	alveolar
17	preceding	–
18	raising	–
19	relative _ articulation –	
20	release	–
21	sibilancy	sibilant
22	syllabicity	–
23	velarization	–
24	voicing	–

We can see from the output that CLTS currently uses as many as 24 different features to define consonants, which mostly reflect the traditional way in which sounds are defined by the International Phonetic Alphabet (IPA 1999). You can apply the same procedure to check for the vowel and the tone features applied by CLTS, by replacing the line `sound = bipa['ts']` by the line `sound = bipa['a']` or `sound = bipa['55']`, respectively.

With our feature vector and a system like CLTS which offers feature values, it is straightforward to write a short function that allows us to compare the hamming distance between different sounds transcribed in *Broad IPA* (`bipa`) system offered by the CLTS database.

We start by defining our function for scoring two sound segments. This function accepts two paremeters (the sound segments, passed as strings), and three keywords, `bipa` (referring to the `bipa` transcription system offered by the `pyclts` package), `classes` (a function that defines to which score we want to normalize our Hamming similarities), and `features`, the list of feature vectors, as offered per class in our transcription system.

```
from pyclts.transcriptionsystem import TranscriptionSystem
from itertools import combinations

def score_sounds(
        a,
        b,
        features=None,
        classes=None,
        bipa=None
        ):
    """
    Score sounds with Hamming distance from feature system.
    """
    # load bipa object
    bipa = bipa or TranscriptionSystem('bipa')

    # define the features
    features = features or {
        "consonant": list(
            bipa['t'].featuredict),
        "vowel": list(
            bipa['a'].featuredict),
        "tone": list(
            bipa['⁵⁵'].featuredict)
        }
    # define base score for the classes
    classes = classes or {
        "consonant": 1,
        "vowel": 1,
        "tone": 1
        }
```

You can see from this first code block that I was lazy and did not spell out the feature systems, but retrieved them from dummy sounds. As we will see later, however, we will usually create our feature vectors before and pass them to the method via the keywords, also to avoid that the Broad IPA is loaded on every call, which will drastically influence the performance of this method.

Our next step consists in the conversion of our sounds to our `TranscriptionSystem` in CLTS, and to check for dipthongs or clusters. Dipthongs and clusters are not defined by their own features in CLTS, but rather have separate features for the first and the second sound, which can be accessed through their attributes `from_sound` and `to_sound`. To keep the demonstration simple for the time being, we will for now simply represent the complex sounds by their first sound.

```
    # convert sounds to transcription system
    sA, sB = bipa(a+' '+b)

    # check for diphthongs or clusters
    if hasattr(sA, 'from_sound'):
        sA = sA.from_sound
    if hasattr(sB, 'from_sound'):
        sB = sB.from_sound
```

Now we make sure to return a high negative value in those cases where the base classes for all sounds in CLTS turn out to be different. This score is in fact arbitrary, as long as it is low enough, since we want to avoid no matter what, that alignments mix the sound classes (some colleagues were not happy with this decision in the past, but my experience clearly shows that not separating classes leads to an unexpected alignment behavior that is extremely difficult to control).

```
    # return -10 if classes don't match
    if sA.type != sB.type:
        return -10
```

Now, we are almost done with our function that calculates segment similarities based on distinctive feature systems. In order to compute the Hamming similarity, we first define the base similarity, which is reflecting the size of the feature vector, and then calculate the factor needed to normalize the data consistently. According to our defaults, which we wrote into the function, the highest similarity score for all sound classes is 1, so normalization will yield scores between 0 and 1 for our Hamming similarities.

```
    # base score is the number of features
    sim = len(features[sA.type])

    # normalization factor
    normalize = classes[sA.type] / sim

    # return in case of identity
    if a == b:
        return sim * normalize

    # reduce similarity in case of mismatch
    for feature in features[sA.type]:
        if sA.featuredict[feature] != sB.featuredict[feature]:
            sim -= 1
    return sim * normalize
```

Now that we can compute our Hamming similarities, we can test this function directly by feeding it different sounds. In order to get a full-fledged scoring dictionary, however, which we will need to carry out a phonetic alignment analysis, it is useful to write another function that takes a couple of sounds as input and returns a scoring dictionary in which all sounds are compared with each other. The function takes a bunch of letters as parameter, and also the three keywords, which we already defined for the `score_sounds` function.

```
def get_scorer(
        letters,
        bipa=None,
        classes=None,
        features=None
        ):
    """
    Retrieve a scoring dictionary for alignment algorithms.
    """
    # load bipa object
    bipa = bipa or TranscriptionSystem('bipa')

    # define the features
    features = features or {
        "consonant": list(
            bipa['t'].featuredict),
        "vowel": list(
            bipa['a'].featuredict),
        "tone": list(
            bipa['⁵⁵'].featuredict)
        }
    # define base score for the classes
    classes = classes or {
        "consonant": 1,
        "vowel": 1,
        "tone": 1
        }
```

After this boring part, where we repeat the same code (this may definitely be enhanced further, but for demonstration purposes, it is surely enough), we can now compute the scorer. This can be done in a very straightforward way with help of the `combinations` method offered by the `itertools` module, which is part of Python.

```
    scorer = {}
    bipa = bipa or TranscriptionSystem('bipa')
    for a, b in combinations(letters, r=2):
        scorer[a, b] = scorer[b, a] = score_sounds(a, b, bipa=bipa)
        scorer[a, a] = score_sounds(a, a, bipa=bipa)
        scorer[b, b] = score_sounds(b, b, bipa=bipa)

    return scorer
```

Now, we can finally start and see, how well this approach works. For convenience, I use the tabulate package for printing of tables, and define a couple of sounds whose similarity I want to investigate.

```
from tabulate import tabulate
cons = ['p', 't', 'b', 'd', 'ʰp', 'ʰt']
vows = ['a', 'e', 'i', 'o', 'u']
scorer = get_scorer(cons+vows)
```

When retrieving the similarity matrix from the scorer now, we can easily construct a matrix, which illustrates the difference between the sounds in our sample.

```
matrix = [[1 for x in cons] for y in cons]
for (i, a), (j, b) in combinations(enumerate(cons), r=2):
    matrix[i][j] = matrix[j][i] = round(scorer[a, b], 2)
for i, (c, r) in enumerate(zip(cons, matrix)):
    matrix[i] = [c]+r
print(tabulate(matrix, headers=cons, tablefmt='pipe'))
```

The matrix for the consonants in our sample is shown in the following table.

	p	**t**	**b**	**d**	**p**	**t**
p	1	0.96	0.96	0.92	0.96	0.92
t	0.96	1	0.92	0.96	0.92	0.96
b	0.96	0.92	1	0.96	0.92	0.88

d	0.92	0.96	0.96	1	0.88	0.92
p	0.96	0.92	0.92	0.88	1	0.96
t	0.92	0.96	0.88	0.92	0.96	1

By replacing the `cons` variable by `vows`, we can produce the same matrix for our vowels.

	a	**e**	**i**	**o**	**u**
a	1	0.95	0.95	0.85	0.85
e	0.95	1	0.95	0.9	0.85
i	0.95	0.95	1	0.85	0.9
o	0.85	0.9	0.85	1	0.95
u	0.85	0.85	0.9	0.95	1

Those experienced in phonetics and distinctive features and historical sound change may find the results strange, especially those for the consonants. We see that `[p]` is as similar to a `[t]` as to a `[b]`, although most scholars would usually say that `[p]` and `[b]` are much closer to each other. The problem, and this is also one of the challenges when using feature systems for alignment analyses, is that all features are given the same weight by our Hamming similarity approach. When comparing the features by which `[p]`, `[t]`, and `[d]` differ, according to the CLTS feature system, we can see that `[p]` and `[t]` differ by one feature ("place"), and `[p]` and `[b]` differ by another feature ("voicing"). Since the similarity measure presented here does not allow for a differential weighting of features and feature values, it yields the same similarity of 0.96, since both sounds differ in one out of 24 features.

References

Anderson, Cormac and Tresoldi, Tiago and Chacon, Thiago Costa and Fehn, Anne-Maria and Walworth, Mary and Forkel, Robert and List, Johann-Mattis (2018): A Cross-Linguistic Database of Phonetic Transcription Systems. *Yearbook of the Poznań Linguistic Meeting* 4.1. 21-53.

Chomsky, Noam and Halle, Morris (1968): *The sound pattern of English*. New York and Evanston and London: Harper and Row.

Hamming, Richard W. (1950): Error detection and error detection codes. *Bell System Technical Journal* 29.2. 147–160.

Jäger, Gerhard (2015): Support for linguistic macrofamilies from weighted alignment. *Proceedings of the National Academy of Sciences* 112.41. 12752–12757.

List, Johann-Mattis (2014): *Sequence comparison in historical linguistics*. Düsseldorf: Düsseldorf University Press.

List, Johann-Mattis (2017): Historical Language Comparison with LingPy and EDICTOR [Historischer Sprachvergleich mit LingPy und EDICTOR]. Department of Linguistic and Cultural Evolution: Max-Planck Institute for the Science of Human History.

Steven Moran and Daniel McCloy and Richard Wright (eds.) (2014): *PHOIBLE Online*. Max Planck Institute for Evolutionary Anthropology. Leipzig: http://phoible.org/.

Moran, Steven and Cysouw, Michael (2018): *The Unicode Cookbook for Linguists: Managing writing systems using orthography profiles*. Berlin:Language Science Press.

Supplementary Information

The code demonstrated here can be found on this GitHub Gist.

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Feature-Based Alignment Analyses with LingPy and CLTS II

Johann-Mattis List (16/09/2019)

Categories: Code

Tags: algorithm, distinctive features, phonetic alignment

Having seen how we can obtain a simple scorer derived from the feature system in CLTS (List et al. 2019) in last month's post, what is missing now, in order to use the scorer for alignment analyses, is an alignment function which can take the scorer as an argument. If one does not have higher ambitions with respect to the alignment function itself, this step can be achieved in a very straightforward way with help of LingPy's (List et al. 2018) `nw_align()` or `sw_align()` method. As can be seen from the documentation, this method takes as input two sequences (i.e., lists of sounds), along with a scoring function. Obviously, all we need to do now is to create our specific scorer based on the CLTS features, and then pass this scoring function along with our sequences to the function.

Let's test this by writing a small function that takes two sequences as input and then (a) creates the scorer using the procedure we illustrated in the preceding post, and (b) aligns the sequences, using either the Needleman-Wunsch algorithm (Needleman and Wunsch 1970) for global alignment, or the Smith-Waterman algorithm (Smith and Waterman 1981) for local alignment. We start by importing the `malign` package of LingPy which offers simple alignment methods, as well as LingPy proper, and adding this to the start of our file `features.py` which we used last time.

```
from lingpy.algorithm.cython import malign
```

We can now define our alignment function. Following general LingPy nomenclature, we distinguish between global and local alignment as different *alignment modes* (see List 2014 for details on alignment modes). We just write this function below the functions for scoring elements and for creating the scorer in our script.

```
def feature_align(seqA, seqB, mode='global', gap=-1):
    if mode == 'global':
        align = malign.nw_align
    elif mode == 'local':
        align = malign.sw_align
    scorer = get_scorer(list(set(seqA+seqB)))
    return align(seqA, seqB, scorer, gap)
```

In order to run this function, we must input the data as a list. This can be done by splitting IPA sequences with help of LingPy's `ipa2tokens` function, or by using software specifically devoted to segmentation, such as the segments package, that uses *orthography profiles* to split data into segments (Moran and Cysouw 2018), of which I recently produced a JavaScript version for demonstration purposes, called SegmentsJS.

For a first test, we simply segment the data directly.

```
seqA = 'ʰt ɔ x t ɐ'.split()
seqB = 'd ɔː t ə r'.split()
almA, almB, score = feature_align(seqA, seqB)
print('\t'.join(almA))
print('\t'.join(almB))
print('{0:.2f}'.format(score))
```

From the output, we can see, that the method correctly aligns the two sequences.

```
tʰ    ɔ   x  t  ɐ  -
d     ɔː  -  t  ə  r
-1.00
```

What you may find to be strange is the negative score for this alignment. But as the alignment itself is correct, we do not need to worry about this too much. The alignment has two gaps, and our gap penalty is `-1`. This will result in a score of `-2` for the gaps alone. Since each perfect match scores with `1` as well, and we have only one perfect match, the rest of the scores cannot outweigh the penalties introduced by the gap score. This shows, as we will try to look at in a follow-up post, that we need to re-design our scoring function to account more properly for the specific needs of alignment algorithms.

But let us now make a general test of the feature-based alignment method by using it to align all the sequences in a benchmark. Here, we use the benchmark proposed by Covington (1996), which is available from the Benchmark Database of Phonetic Alignments (BDPA, List and Prokić 2014). We use this dataset for convenience, because it is small, and can therefore easily be added to a GitHub Gist repository. Interested users can easily obtain the more elaborated and larger benchmark data from the BDPA and test the algorithm on more and more challenging datasets.

To load the data from the benchmark, we first download the data and extract the file `covington.psa`, which contains the alignments in the "PSA" format that LingPy uses for partial alignments. This format is outdated for different reasons. First, because the main interest of LingPy's algorithms has now shifted to cognate detection and multiple alignments, and pairwise alignments are no more considered the key task of the library. Second, with new standards such as CLDF (Forkel et al. 2018), we are generally re-evaluating the usefulness of formats that are too idiosyncratic. Third, with LingPy's wordlist format, that has been offering for a long time now the possibility to store multiple alignments, and to also edit them with the EDICTOR tool (List 2017), we do no longer need specific formats, but could render the same data without problem in a multi-lingual wordlist, even if it only consists of aligned pairs. But since LingPy has not yet abandoned the PSA format and can readily read it, we can use it now to read in the file, align the data, and check if the alignment matches the gold standard. To evaluate the alignments, we simply score the number of *perfect alignments* which are identical with the gold standard.

```
psa = PSA('covington.psa')
scores = []
for i, (seqA, seqB) in enumerate(psa.tokens):
almA, almB, score = feature_align(seqA, seqB)
if almA == psa.alignments[i][0] and almB == psa.alignments[i][1]:
    scores += [1]
else:
    scores += [0]
print('{0:.2f}'.format(sum(scores)/len(scores)))
```

As we can see from the output, the algorithm reaches a score of 0.82, that is, 82% of the alignments are identical with the gold standard. In total, these are 67 out of 82 alignments in the benchmark. With this score, the feature-based alignment in this form shows a very mediocre performance, as we can see when comparing with scores reported for other alignment algorithms, specifically SCA (List 2014) with 80 perfect alignments (98%), Kondrak's ALINE (Kondrak 2000 with 78 perfect alignments (95%), or Covington's algorithm (1996) with 68.8 perfect alignments (84%).

From these results, we can thus see what was already mentioned in last month's post: by simply computing the Hamming distances of distinctive feature systems, we do not necessarily arrive at linguistically meaningful alignments, similarities, or distances. In a follow-up blog post, I will try to show what we can do to cope with the problems introduced by naive Hamming distances for feature vectors. The code accompanying this post is again available in form of a GitHub Gist repository.

References

List, Johann-Mattis and Anderson, Cormac and Tresoldi, Tiago and Rzymski, Christoph and Greenhill, Simon and Forkel, Robert (2019): *Cross-Linguistic Transcription Systems*. Jena:Max Planck Institute for the Science of Human History.

Covington, Michael A. (1996): An algorithm to align words for historical comparison. *Computational Linguistics* 22.4. 481-496.

Forkel, Robert and List, Johann-Mattis and Greenhill, Simon J. and Rzymski, Christoph and Bank, Sebastian and Cysouw, Michael and Hammarström, Harald and Haspelmath, Martin and Kaiping, Gereon A. and Gray, Russell D. (2018): Cross-Linguistic Data Formats, advancing data sharing and re-use in comparative linguistics. *Scientific Data* 5.180205. 1-10.

Kondrak, Grzegorz (2000): A new algorithm for the alignment of phonetic sequences. In: *Proceedings of the 1st North American chapter of the Association for Computational Linguistics conference*. 288-295.

List, Johann-Mattis and Greenhill, Simon and Tresoldi, Tiago and Forkel, Robert (2018): *LingPy. A Python library for quantitative tasks in historical linguistics*. Version 2.6.4. Max Planck Institute for the Science of Human History. Jena: http://lingpy.org.

List, Johann-Mattis (2014): *Sequence comparison in historical linguistics*. Düsseldorf:Düsseldorf University Press.

List, J.-M. and Prokić, Jel (2014): A benchmark database of phonetic alignments in historical linguistics and dialectology. In: *Proceedings of the Ninth International Conference on Language Resources and Evaluation*. 288-294.

List, Johann-Mattis (2017): A web-based interactive tool for creating, inspecting, editing, and publishing etymological datasets. In: Proceedings of the 15th Conference of the European Chapter of the Association for Computational Linguistics. *System Demonstrations*. 9-12.

Moran, Steven and Cysouw, Michael (2018): *The Unicode Cookbook for Linguists: Managing writing systems using orthography profiles*. Berlin:Language Science Press.

Needleman, Saul B. and Wunsch, Christan D. (1970): A gene method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of Molecular Biology* 48. 443-453.

Smith, T. F. and Waterman, M. S. (1981): Identification of common molecular subsequences. *Journal of Molecular Biology* 1. 195-197.

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Biological metaphors and methods in historical linguistics II: Words and genes

Nathanael E. Schweikhard (18/09/2019)

Categories: Theory

Tags: analogies, biology, historical linguistics

As was mentioned in the introduction to this series of blogposts, both species and languages are often presented in a tree model. In biology, trees of each individual gene are created in order to account for horizontal transmission and other processes in which the history of a gene differs from the general history of its genome. From the sum of these trees, the species trees are then derived, a method called *gene tree reconciliation* (Nakhleh 2013). In linguistics on the other hand, phylogenetic trees normally are built on cognate sets of related words, from which the most likely tree of the languages is calculated. A closer equivalent however would be to describe the history of each individual word or word form, including regular sound change, irregular changes to its form, semantic changes, borrowings, and processes of word formation, and to derive the language tree based on the sum of the word histories (Gray, Greenhill, and Ross 2007, 15). Unlike its biological equivalent, this is normally done manually.

While anthropological, including linguistic, data behaves more like phenotype data than like genotype data in biology (Morrison 2014), the mechanisms themselves seem much more directly comparable between genes and language data since phenotypes would add an unnecessary layer of complexity, being expressions of genes, while genes are what is replicated from one generation to the next.

Similarly, Stevick, while maintaining the general equation between species and languages, suggests that it would be better to compare actual utterances with individual organisms (Stevick 1963, 161) or their genomes, since language is replicated through its use in communication. In this model, gene replication with mutation corresponds to communication (i.e. word exchange) with innovation (Pagel 2009, 406, 408).

One obvious difference is that in genetic, i.e. sexual, reproduction, the whole genome is recombined, whereas in each instance of communication, only part of the mental lexicon is typically affected, an exception being systemic changes like the change of one set of phonemes to another set. These systemic changes are another difference: in the genome, most genes are fairly independent, but a change to one word in the lexicon can easily reflect a wide-reaching change to many parts of the lexicon as in regular sound change.

Besides these systemic changes, words in the lexicon can also influence each other and cause sporadic changes called *analogy*, which is typically based on the meanings of the words. This is comparable to linked loci in the genome, even if the underlying mechanisms are — of course — entirely different (Nakhleh 2013, 720, 726). From this, one can conclude that word-meaning-pairs (what Gévaudan 2007 refers to as “lexikalische Einheit”, i.e., “lexical unit”, on page 28), and not word forms on their own, correspond to individual genes coupled either with their function or with their position in the genome.

While individuals and not whole species reproduce, evolutionary biology normally treats the samples taken from individuals as representing the species as a whole. Similarly, linguists normally talk about language stages being derived from previous language stages spoken at least a generation before, more typically several centuries: they do not put much focus on how language usage changes during the course of the life of a person beyond the language acquisition phase (but see e.g. Labov 1981 as an influential exception).

To go even a level deeper, some scholars compare the amino acids that make up a gene with the phonemes that make up a given word (Hruschka et al. 2015, 1), but while this may seem to make sense in the context of the other metaphors mentioned, I have not yet found a way to apply this equation in our research. More interesting in this regard is that the distribution of morphemes in a given language can be modeled in a similar manner as the distribution of protein domains within genomes (Keller and Schultz 2014).

At times, whole sequences of genes have been likened to words. This is a methodologically valid comparison, as in both disciplines, sequences of genes on the one hand and sequences of sound strings denoting the same concept on the other hand can be aligned in order to gain insights into the likelihood that a given gene or word is orthologous or cognate with another (Koonin 2005, 217f; List et al. 2016, 6), even if it otherwise does not fit well into the metaphors employed here. An important difference in that regard is also that while gene sequences consist of the same four nucleotides, words of different languages more typically make use of different sets of phonemes. For example click sounds famously can be found in some languages of southern Africa, but are almost missing in most other parts of the world (Trask 2007, 12).

Overall, one can conclude that despite some similarities, the research objects of linguists and biology are obviously very different and it therefore should depend on the fruitfulness of the research method whether adopting a given metaphor makes sense or not. Nevertheless, thinking about these metaphors can support finding potential methods to adopt, also by pointing out which approaches one takes for granted in one's own field but which might be handled differently in another.

References

Gévaudan, Paul. 2007. *Typologie des lexikalischen Wandels: Bedeutungswandel, Wortbildung und Entlehnung am Beispiel der romanischen Sprachen*. Stauffenburg-Linguistik ; 45. Tübingen: Stauffenburg.

Gray, Russell D., Simon J. Greenhill, and Malcolm D. Ross. 2007. "The Pleasures and Perils of Darwinzing Culture (with Phylogenies)." *Biological Theory* 2 (4): 360–75.

Hruschka, D. J., S. Branford, E. D. Smith, J. Wilkins, A. Meade, M. Pagel, and T. Bhattacharya. 2015. "Detecting Regular Sound Changes in Linguistics as Events of Concerted Evolution." *Current Biology* 25 (1): 1–9.

Keller, Daniela Barbara, and Jörg Schultz. 2014. "Word Formation Is Aware of Morpheme Family Size." *PLoS ONE*.

Koonin, Eugene V. 2005. "Orthologs, Paralogs, and Evolutionary Genomics." *Annual Review of Genetics* 39: 309–38. https://doi.org/ [10.1146/annurev.genet.39.073003.114725]

Labov, William. 1981. "Resolving the Neogrammarian Controversy." Language 57(2): 267–308. JSTOR: 413692.

List, Johann-Mattis, Jananan Sylvestre Pathmanathan, Philippe Lopez, and Eric Bapteste. 2016. "Unity and Disunity in Evolutionary Sciences: Process-Based Analogies Open Common Research Avenues for Biology and Linguistics." *Biology Direct* 11 (39): 1–17.

Morrison, David A. 2014. "Are Phylogenetic Patterns the Same in Anthropology and Biology?" *bioRxiv*. https://doi.org/10.1101/006486.

Nakhleh, Luay. 2013. "Computational Approaches to Species Phylogeny Inference and Gene Tree Reconciliation." *Trends in Ecology and Evolution* 28 (12): 719–28.

Pagel, Mark. 2009. "Human Language as a Culturally Transmitted Replicator." *Nature Reviews. Genetics* 10: 405–15.

Stevick, Robert D. 1963. "The Biological Model and Historical Linguistics." *Language* 39 (2): 159–69. https://www.jstor.org/stable/411199.

Trask, Robert L. 2007. *Language and Linguistics: The Key Concepts.* Abingdon: Routledge.

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Illustrating linguistic data reuse: a modest database for semantic distance

Tiago Tresoldi (30/10/2019)

Categories: Code, Dataset, Organization

Tags: colexification network, fair data, semantic distance

Besides new algorithms and tools that facilitate established workflows, one change prompted by computer-assisted approaches to language comparison is a distinct relationship between scientists and their data. A critical part of our work, and perhaps the one with the most lasting impact, is to promote an approach in which the data life-cycle is not constrained within the limits of planning and publishing a study. Data are organized and planned for reuse in investigations perhaps not even considered during collection, with the output of one project becoming the input of another.

An ongoing project at our department, the Cross-Linguistic Data Formats (CLDF) initiative (Forkel et al. 2018), embodies this life cycle of data in line with the FAIR principles of data management (Wilkinson et al., 2016). Part of the ambitious umbrella project Glottobank, a global research consortium to document and understand linguistic diversity and evolution, datasets collected in CLDF formats can be quickly aggregated from different sources to form new datasets. An example of how CLDF stands at the heart of a data life-cycle is our CLICS project (Rzymski, Tresoldi et al., 2019), in which we carry out a comprehensive analysis of colexifications (i.e., words used to express two different concepts, either due to polysemy or to homonymy), automatically inferred from lexical sources that we converted to CLDF format and aggregated. CLICS is a derivative database, and the success and interest among the public, from psycholinguists to conlangers, also owes to the coding framework that backs it. Using the Python APIs that we have developed, anybody can recompute the network of colexifications and its clusters, experiment with other designs and algorithms, or apply the published network to alternative objectives.

We can illustrate this progression with the case of a less ambitious personal project in which, for two distinct goals, I lacked some measure of semantic distance (however approximate) between pairs of concepts from our Concepticon project (List et al. 2019). I needed distances both for predicting the prevalence of accidental resemblances (Tresoldi, 2019), and for simulating linguistic change to test novel phylogenetic techniques. There are several interpretations of "semantic distance," as in hierarchic or otherwise structural ontologies (for example, the amount of nodes that needs to be traversed in WordNet, cf. Princeton University, 2010) or in complementary occurrences in corpora (as in vogue with word vectors, in the often repeated "king – man + woman = queen" equation, but see Nissim 2019). Neither method was adequate because, more as with typologies presented in semantics and semiology (cf. Traugott & Dasher 2001, Bloomfield 1933, Blank 1999), I needed an approximate probability for a word changing its meaning following a given "semantic path" (as in "awesome", formerly "inspiring awe" and now "exciting", or "villain", formerly "countryman" and now "vile") as well as the chance for apparently unrelated lexemes having a common, albeit remote, source (such as "mouse" and "muscle"). A network linking all concepts, but where the path between WOOD and TREE was shorter than the one between CUSHION and COOKING.

Before running community detection algorithms such as "infomap" (Rosvall et al. 2009), CLICS first normalizes lexeme transcriptions and then imposes thresholds of occurrence. These steps and limits are helpful in a study for establishing global and areal patterns, but results in a graph with singletons (words not linked to any other) and independent subgraphs. There is no guarantee that it will link all concept pairs, no matter how long the path between them. Likewise, edge weights are computed for the same goal of community identification rather than for approximate semantic closeness.

As a tool developed with principles of FAIR data in mind, the CLICS library allows to deal with the first issue by allowing to collect any and every occurrence of colexification. The table below presents a sample of the output, with each pair of concepts followed by its counts, ranging from the most common, MOON/MONTH, to spurious associations (like LOOK/BURNING, but notice how, among the minimum counts, we find semantically similar concepts, such as FLOWER/SPROUT (VERB)):

Concept A	Concept B	Families	Languages	Words
MOON	MONTH	57	320	328
WOOD	TREE	57	298	405
CLAW	FINGERNAIL	55	217	225
...	...	...	...	...
LOOK	BURNING	1	1	1
STEPDAUGHTER	CHILD-IN-LAW	1	1	1
FLOWER	SPROUT (VERB)	1	1	1

This new output, in a textual tabular format, can be combined with the communities published with CLICS to get the desired distance matrix. With the script available on GitHub, we can define different correction parameters for the counts of each pair (favoring families over languages, and languages over words), as well as reducing the distance between concepts of the same cluster. The result is what we call for: a graph of which all Concepticon concepts are a part (i.e., a partially connected network), with edge weights based on colexification counts and corrected according to cluster membership. The hypothesis is that meanings change according to semantic distance, with changes within the same cluster meaning more likely. Our script generates a file in standard GML format, available here which can be explored with ordinary graph tools.

Despite not all concept pairs being linked by means of a single edge, it is now possible to find a path between every pair, with the distance between the concepts, taken as a surrogate for the semantic distance, corresponding to the sum of the edge weights involved. We can obtain the shortest and best path, or even sub-optimal ones, with pathfinding algorithms such as the ones of Dijkstra (1959) and Yen (1971). Computing the shortest path for the over 3 million pairs in this experiment is not particularly useful, as many of the links would be spurious and an actual account would need to look for the mean distance of non-overlapping shortest path (as performed in network analysis). However, it is still fun to play and look for the distance between a handful of random pairs (here the defined as the mean distance of the three shortest paths), along with the best overall solution for each pair:

Concept A	Concept B	Distance	Steps
BALL	HALF	36.70	2
FODDER	MAPLE TREE	188.73	2
COCONUT	FINE (PENALTY)	154.25	2
BOLT (MOVE IN HASTE)	CABBAGE	326.74	3
BRAID (VERB)	SLEEP	155.17	1

While these semantic distances are tentative and far from ideal, as a quick exploration can confirm, it is worth looking at how FAIR data made it feasible to promptly and easily obtain a database to test both the prototypes mentioned in the beginning. As part of a scientific cycle, it not only suggested that it was worth to continue investing both ideas, but it further allowed to generate data that other scientists can use just as promptly and quickly, spending even less time in data collection and processing (thus also saving computing power). We could use these data, for example, to bootstrap projects for developing similar but better data, perhaps combining the different approaches to "semantic distance" mentioned above, and which likewise would not need to be restricted within the boundaries of a single publication.

References

Blank, Andreas. 1999. "Why do new meanings occur? A cognitive typology of the motivations for lexical semantic change" in Blank, Andreas; Koch, Peter (eds.), *Historical Semantics and Cognition*. Berlin/New York: Mouton de Gruyter, pp. 61-90.

Bloomfield, Leonard. 1933. *Language*. New York: Allen & Unwin.

Dijkstra, Edsger W. 1959. "A note on two problems in connexion with graphs." *Numerische mathematik* 1, no. 1: 269-271.

Forkel, Robert; List, Johann-Mattis; Greenhill, Simon J.; Rzymski, Christoph; Bank, Sebastian; Cysouw, Michael; ammarström, Harald; Haspelmath, Martin; Kaiping, Gereon A.; and Gray, Russell D. 2018. "Cross-Linguistic Data Formats, advancing data sharing and re-use in comparative linguistics." *Scientific data* 5.

List, Johann Mattis; Greenhill, Simon J.; Rzymski, Christoph; Schweikhard, Nathanael; Forkel, Robert (eds.). 2019. Concepticon 2.1.0. Jena: Max Planck Institute for the Science of

Human History. (Available online at http://concepticon.clld.org, Accessed on 2019-10-28.)

Nissim, Malvina; van Noord, Rik; van der Goot, Rob. 2019. *Fair is Better than Sensational:Man is to Doctor as Woman is to Doctor*. arXiv:1905.09866

Princeton University "About WordNet." *WordNet*. Princeton University. 2010.

Rosvall, Martin; Axelsson, Daniel; and Bergstrom, Carl T. 2009. "The map equation." in *The European Physical Journal Special Topics* 178, no. 1: 13-23.

Rzymski, C., T. Tresoldi, S. Greenhill, M. Wu, N. Schweikhard, M. Koptjevskaja-Tamm, V. Gast, T. Bodt, A. Hantgan, G. Kaiping, S. Chang, Y. Lai, N. Morozova, H. Arjava, N. Hübler, E. Koile, S. Pepper, M. Proos, B. Epps, I. Blanco, C. Hundt, S. Monakhov, K. Pianykh, S. Ramesh, R. Gray, R. Forkel, and J. List. 2019. The Database of Cross-Linguistic Colexifications, reproducible analysis of cross-linguistic polysemies. Manuscript. 1-24. Preprint, currently under review.

Traugott, Elizabeth C.; Dasher, Richard B. 2001. *Regularity in Semantic Change*. Cambridge: Cambridge University Press.

Tresoldi, T. 2019. "A cross-linguistic computational approach on chance resemblances". Presented at the workshop *Computer-assisted approaches in historical and typological language comparison, organized as part of the Annual Meeting of the Societas Linguistica Europea* (2019/08/21-24, Leipzig).

Wilkinson, Mark D., Dumontier, Michel; Aalbersberg, IJsbrand J.; Appleton, Gabrielle; Axton, Myles; Baak, Arie; Blomberg Niklas et al. 2016. "The FAIR Guiding Principles for scientific data management and stewardship." in *Scientific data*, 3.

Yen, Jin Y. 1971. "Finding the k shortest loopless paths in a network." *Management Science* 17, no. 11: 712-716.

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Biological metaphors and methods in historical linguistics III: Homology and homoplasy

Nathanael E. Schweikhard (20/11/2019)

Categories: Theory

Tags: analogies, language change, phylogenetic reconstruction, word formation, word trees

As we have seen in previous instances of this blog post series, there are many parallels but also many differences between the evolutionary branches of biology and of linguistics. In the following, I will present a comparison of the causes due to which two related inheritable entities (e.g. two words or two genes of different languages or species) may differ from each other, or two unrelated ones resemble each other. The linguistic categories presented here can also be found in List (2016) whereas the biological categories are largely based on Koonin (2005).

Common ancestry

Genes that are related to each other are called homologues. There is no well-established linguistic catch-all term for words that are related to each other, but they could be said to have an *etymological relation*. The most common causes due to which such related entities differ from each other in related languages or species are the processes of regular sound change and random gene mutation, respectively. Both of these happen all the time, and affect all words or genes in the same way (with certain exceptions), and can therefore be considered the default baseline process that does not demand a different name for the type of homology (Gévaudan 2007, 14). Only their absence (as in for example certain iconic words that did not take part in regular sound change, like English *peep* /piːp/ having retained its Middle English form instead of turning into /paɪp/ (Flaksman 2017, 17)) or irregular cases of sound change caused by frequency effects (Bybee 2017) or analogy, or areas of the genome especially prone to mutation may warrant new terms.

There are also other processes that can be involved in the relation between individual genes or words but they are quite different from each other in the different fields and cannot as easily be equated with each other. For language, there are the various kinds of *word formation* processes in which a new word is derived based on existing words. The closest counterpart in genetics is *gene duplication* (List 2014, 40), in which the same gene is included twice, thereby increasing the amount of genes in the genome. As with word formation products, duplicate genes then continue evolving more or less independently from each other but still may have an influence on each other's future evolution. This is related to their functional similarity in the genome (Koonin 2005, 318, 323), and to processes of analogy in the lexicon.

However, a product of word formation rarely has the same shape as the word it is derived from (the only exception being the process of conversion), whereas duplicated genes initially are the same, only later they may diverge by mutation. Additionally, word formation processes normally involve either more than one word or morpheme as the input (e.g. in compounding or affixation) or at least combine a word with a pattern to derive the new word. The processes in biology most similar to that are *fusion* and *fission*, i.e. the merger of two genes and the split of a gene into two, but here the original genes cease to exist, whereas for example compounding does not cause the simplexes to stop being part of the lexicon. These different processes nevertheless share the fact that they challenge the established types of homology (Koonin 2005, 327) and cognacy, respectively.

Xenology is a special type of homology in which a horizontal transmission was involved (Koonin 2005, 315). This happens either in the context of hybridization, when genomes of different species are combined by interspecies reproduction, or, in microbes, by a variety of mechanisms. In the tree model it leads to reticulation. Its obvious linguistic equivalent are *borrowings* from one language to another (Atkinson and Gray 2005, 513). Hybrids could be likened to creole languages (Gray et al. 2007, 10).

In natural species there are normally only four letters of the genetic alphabet, the four chemicals guanine, cytosine, adenine and thymine. Yet also artificial new letters have been created (Hoshika et al. 2019). Once these molecules undergo reproduction, the replication mechanism might encounter problems interpreting them and treat them like errors (Ledbetter et al. 2018). Similar things happen in language: Since different languages normally have different phoneme systems, the shape of a borrowed word is typically adapted to the phoneme system of the borrowing language (see for example Lin (2008) on the adaptation of English words borrowed into Mandarin). Yet overall linguistic change is much less restricted.

To summarize, in regards to homology, only a few corresponding processes can be found when comparing evolutionary genetics and linguistics, even though the basic ideas are the same.

Other factors of similarity

Common ancestry is not the only possible cause of similarities. Two of the causes most frequently considered are *chance resemblances* and universal tendencies. Both of these are called *homoplasy*, making this the complement term to homology as it describes similarity independent of common ancestry.

If languages or species are only very distantly related, similarities between them are usually considered *chance resemblances*. In languages, words can with reasonable certainty be proven to go back to a common ancestor by searching for patterns of regular sound correspondences between the languages (Lass 1997, 129). Failing to find any regular sound correspondences that would explain the similarity between two words does however not necessarily disprove their relatedness as it can be confounded by processes of analogy and word formation. On the other hand, in some cases actual homoplasies are not purely due to chance, but may result from *universal tendencies* (List 2016, 120), e.g. high vowels being associated with smallness (Sidhu and Pexman 2018) or words derived from baby-talk having simple syllable structures. As a third possibility, a borrowing can be postulated as the cause.

In a comparable way to linguists putting their trust in regular sound correspondences over surface similarity, biologists tend to trust comparisons on the genetic more than comparisons on the phenetic (morphological) level, the latter of which tend to suffer from increased degrees of homoplasy, as in the very basic example of both birds and bats developing wings. Also in the evolution of species, universal tendencies are at play, meaning the same evolutionary development might occur independently in different species based on universal or environment-specific demands on natural life. Therefore, phenetic similarity is mainly considered in those cases where genetic data is not available (e.g. in fossiles).

But also closely related languages or species may share characteristics independent of any of the causes mentioned thus far even though it is known that their common ancestor did not have them. This is called *parallel evolution*, or, in linguistics, *drift*. It means that both descendants changed an ancestral characteristic in a *parallel* fashion. This is believed to be caused by interdependencies within the *system* of a given language or genome that cause them to evolve in similar directions independent from each other, combined with universal tendencies (List et al. 2016, 9f). One basic linguistic example for this are processes of word formation. The same derivation, especially in the case of the ubiquitous process of compounding, can easily be formed independently in the same manner in two related languages and it is often difficult to determine whether the word formation in question was already created in the ancestor or only in the daughter languages (or both).

What may result in a pattern in the data similar to homoplasy is the phenomenon of *incomplete lineage sorting*. Here, a *polymorphism* (i.e. different members of a population having partially different genes) in the ancestor species is resolved in different directions in daughter species (Nakhleh 2013, 721; List et al. 2016, 6f; Jacques and List 2019, see also the recent post by Jacques) which can mean that more distantly related branches share homologous characteristics that their respective closer relatives are missing.

This has been thus far mostly ignored in computational linguistics even though examples for polymorphisms can also be found in language evolution. A language may have two synonymous words, while each of its two daughter languages loses a different synonym. Or it may have suppletive forms in a paradigm that either end up spreading out onto the whole paradigm and removing the regular word forms, or getting replaced by regular word forms. Unlike in species, the polymorphism occurs not in different organisms but within the same lexicon, potentially within the same utterance. A polymorphism between different mental lexicons of the same population on the other hand is exhibited by sociolects, in which speakers utilize slightly different languages depending on the social context.

If these reasons for similarities can be excluded, the shared innovations may be interpreted to point towards a closer relationship between the descendants sharing them.

Conclusion

Linguistics tends to work with much less data than genetics, so shortcomings of the model that genetics can simply skip over due to the large amount of data they have will come much more to the forefront in linguistics, forcing us to be very clear in what we are actually trying to model. Whether we adopt biological methods in linguistics or develop linguistic models for computational approaches independently, describing the differences and similarities in the way I tried to do in this blogpost can serve as a new perspective to see which aspects may have been neglected.

References

Atkinson, Quentin D., and Russell D. Gray. 2005. "Curious Parallels and Curious Connections: Phylogenetic Thinking in Biology and Historical Linguistics." *Systematic Biology* 54 (4): 513–26. http://www.jstor.org/stable/20061257.

Bybee, Joan L. 2017. "Grammatical and Lexical Factors in Sound Change: A Usage-Based Approach." *Language Variation and Change* 29: 273–300.

Flaksman, Maria. 2017. "Iconic Treadmill Hypothesis: The Reasons Behind Continuous Onomatopoeic Coinage." In *Dimensions of Iconicity*, edited by Angelika Zirker, Matthias

Bauer, Olga Fischer, and Christina Ljungberg, 15–38. John Benjamins Publishing Company. https://doi.org/10.1075/ill.15.02fla.

Gévaudan, Paul. 2007. *Typologie des lexikalischen Wandels: Bedeutungswandel, Wortbildung und Entlehnung am Beispiel der romanischen Sprachen*. Stauffenburg-Linguistik ; 45. Tübingen: Stauffenburg.

Gray, Russell D., Simon J. Greenhill, and Malcolm D. Ross. 2007. "The Pleasures and Perils of Darwinzing Culture (with Phylogenies)." *Biological Theory* 2 (4): 360–75.

Hoshika, Shuichi, Nicole A. Leal, Myong-Jung Kim, Myong-Sang Kim, Nilesh B. Karalkar, Hyo-Joong Kim, Alison M. Bates, et al. 2019. "Hachimoji DNA and RNA: A Genetic System with Eight Building Blocks." *Synthetic Biology* 363: 884–87.

Jacques, Guillaume, and Johann-Mattis List. 2019. "Save the Trees: Why We Need Tree Models in Linguistic Reconstruction (and When We Should Apply Them)." *Journal of Historical Linguistics* 9 (1): 128–67. https://doi.org/10.1075/jhl.17008.mat.

Koonin, Eugene V. 2005. "Orthologs, Paralogs, and Evolutionary Genomics." *Annual Review of Genetics* 39: 309–38. https://doi.org/10.1146/annurev.genet.39.073003.114725.

Lass, Roger. 1997. *Historical Linguistics and Language Change*. Cambridge: Cambridge University Press.

Ledbetter, Michael P., Rebekah J. Karadeema, and Floyd E. Romesberg. 2018. "Reprograming the Replisome of a Semisynthetic Organism for the Expansion of the Genetic Alphabet." *Journal of the American Chemical Society* 140: 758–65.

Lin, Yen-Hwei. 2008. "Patterned Vowel Variation in Mandarin Loanword Adaptation: Evidence from a Dictionary Corpus." In *Proceedings of the 20th North American Conference on*

Chinese Linguistics (Naccl-20), edited by Marjorie K. M. Chan and Hana Kang, 1:175–87. Columbus, Ohio.

List, Johann-Mattis. 2014. "Sequence Comparison in Historical Linguistics." PhD thesis, Heinrich-Heine Universität Düsseldorf.

List, Johann-Mattis. 2016. "Beyond Cognacy: Historical Relations Between Words and Their Implication for Phylogenetic Reconstruction." *Journal of Language Evolution* 1 (2): 119–36. https://doi.org/10.1093/jole/lzw006.

List, Johann-Mattis, Jananan Sylvestre Pathmanathan, Philippe Lopez, and Eric Bapteste. 2016. "Unity and Disunity in Evolutionary Sciences: Process-Based Analogies Open Common Research Avenues for Biology and Linguistics." *Biology Direct* 11 (39): 1–17.

Nakhleh, Luay. 2013. "Computational Approaches to Species Phylogeny Inference and Gene Tree Reconciliation." *Trends in Ecology and Evolution* 28 (12): 719–28.

Sidhu, David M., and Penny M. Pexman. 2018. "Five Mechanisms of Sound Symbolic Association." *Psychon Bull Rev* 25: 1619–43.

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Linguists love plants, too!

Yunfan Lai (20/11/2019)

Categories: Methodology

Tags: Anthropology, Ethnobotany, fieldwork, Rgyalrongic, Sino-Tibetan

Linguists can never solely concentrate on language. This is especially true for field linguists who document a previously unknown language. Unveiling the charm of an undocumented language requires the researcher to explore as much as possible about the people, the society, and of course, the nature around them.

Linguists sometimes (well, sometimes always) do better than anthropologists when it comes to the interaction between linguistics and anthropology (change my mind!). Studies on kinship systems are a good example. A lot of linguists have done researches in this domain, like Loungsbury (1956), who did a thorough study on Pawnee (Caddoan) kinship terms, published in Language; Harry Hoijer, a student of Edward Sapir, published in the same year a paper on Athapaskan kinship terms (Hoijer 1956). Returning from the good old days, recent years see the emergence of interest in anthropological issues among linguists who study Sino-Tibetan languages. Guillaume Jacques published a paper in 2012, on the kinship system in Tangut, an extinct language once spoken in Today's Ningxia, China (Jacques 2012). Another exciting work comes from my colleague, Zhang Shuya, has been interested in Kinship systems of Rgyalrong languages (Sino-Tibetan, spoken in Sichuan, China). Rgyalrong languages in general exhibit complex phonology (see the descriptions in Hsie 1999, Jacques 2004 and Jacques 2008), and for untrained ears, distinguishing phonemes with subtle differences would be a pain in the neck. In Bragbar Situ (an Eastern Rgyalrong language), kinship terms are full of similar but distinctive phonemes that if we aren’t able to make the distinction, we risk making serious errors.

For example, the prefixes *t* - and *ta*- are different in that their vocalisms annotate the gender, *t* - for female and *ta*- for male: *t* -“*tsi-pu* ’mother’s sister’s brother”* *vs* ta-kə-pō* “mother’s brother’s sister”. Further, historical linguistic analyses can help us understand how kinship systems changed in time, comparing the different systems of a few dialects and observing the semantic changes of cognates. I would doubt that an anthropologist can figure all these things out without collaborating with an experienced field linguist. If you are interested in this study, please wait impatiently for Shuya’s forthcoming paper, Brag-bar kinship system in synchronic and diachronic perspectives, to appear next year in BSOAS.

This post, however, is not about kinship terms, but about plant terms, which is arguably a greater challenge than kinship terms. This summer (June – August 2019), I went on a field trip with Shuya to document plant terms in two of the Rgyalrongic languages, Brag-bar Situ and Siyuewu Khroskyabs Khroskyabs.

The languages in question are spoken in the mountainous regions in the highlands of Western Sichuan. The area is covered by two vegetation zones, the mid-mountain vegetation zone in the southeast margin and the alpine canyon vegetation zone in the southeast. You can find a good number of species there, from evergreen broad-leaved forests to alpine shrub meadows. The high botanical diversity are pretty much comparable to the linguistic diversity there. Native speakers, quite imaginably, live in interactions with the natural environment, and their minds could well be an encyclopedia of local plants.

Figure 1: The Siyuewu village

We are both botany laymen, so we collaborated with botanists from Yunnan University of Traditional Chinese Medicine, in order to accomplish our goal.

We went into the mountains together and learn from one another. The field work is generally accompanied by one or several native speaker(s), who identify plants and tell us about them: the name in the local language, the morphology, and the uses.

The botanists help us collect specimens, and teach us how to conserve them. Normally, it is best to have flowers or fruits on the specimens, so the botanists can make accurate identifications. But not everyone of them happens to bloom

Figure 1: Shuya taking notes from native speakers

or bear fruit within a given period of a year, and that means we need field trips in different seasons. Summer is good enough, anyway, as you can see most of the flowers and the weather is pleasant.

Figure 2: A bsang gsol (bsang offering)

The specimens were then brought back to Yunnan, where the botanists are based. They may have some secret weapon to help identify the species and report us back with the scientific names. And us, the linguists, stayed in the Rgyalrongic speaking regions to do our job: recording and transcribing. Several native consultants are needed, as they might make mistakes with the plant terms.

Some terms are quite funny. The burdock (*Arctium lappa L.*), is called *pə ə-rtsôs* in Brag-bar Situ. Literally, *pə ə̄* means "mouse" and *rtsôs* means "to touch", so the term globally means "touch by the mouse".

The Khroskyabs term *m^venono*, literally meaning "grandmother's breasts", designates the flower of Salvia przewalskii Maxim, as the purple flowers, accordingly, look like female breasts with ptosis as they age.

Figure 3: Me making specimens

So, what could we do with linguistic ethnobotany? There could be many benefits, both synchronically and diachronically, linguistically and non-linguistically.

Figure 4: Shuya learning from the botanists

By comparing cognates between plant terms, we may get a better idea about the sound correspondences across different Rgyalrongic languages and improve our understanding of Rgyalrongic historical linguistics. That some of the terms

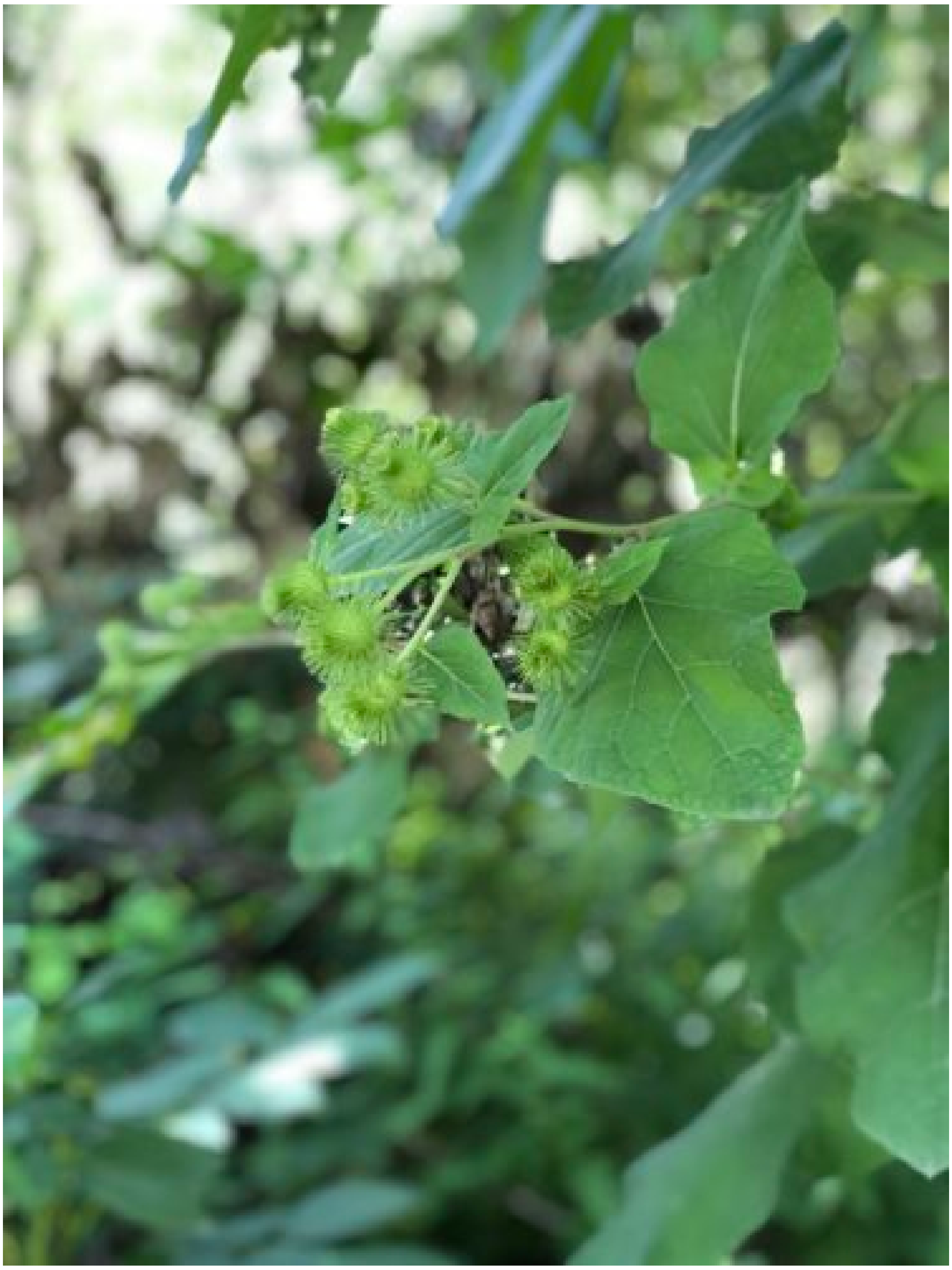


Figure 5: Burdock

can be reconstructed into the proto-language implies that the ancestors of all Rgyalrongic people already knew and probably made use of those plants. Terms borrowed from other languages can be sorted by layers, according to different

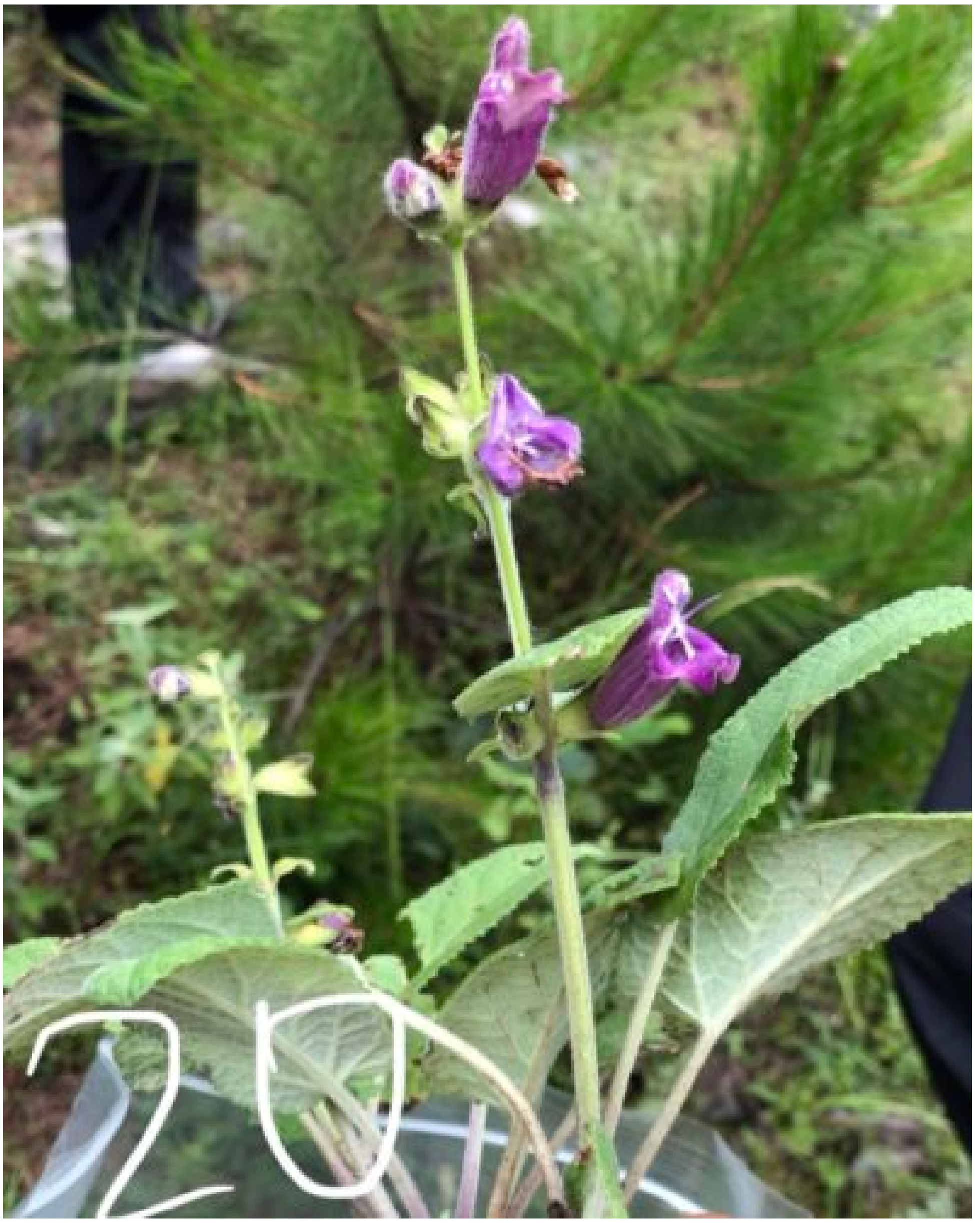


Figure 6: Salvia przewalskii Maxim

stages of sound change. We know that sound correspondences are always messy in Sino-Tibetan languages, but plant term comparisons may tidy up the mess, and we can also implement automatic methods (see for example [this post]) So it is not impossible to know the relative chronology of plants known by native speakers. Inference of the Proto-Rgyalrongic life could well be made based on historical linguistic analyses (of course, we need more cognates!). The table below shows the cognates found in the field work this year.

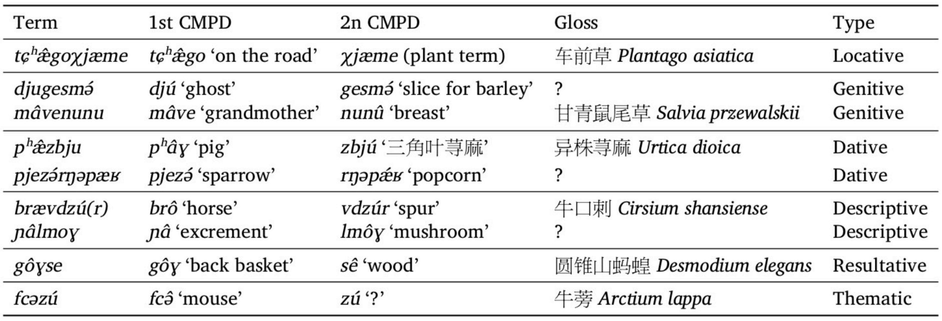
Table: Cognates between Bragbar and Khroskyabs

Bragbar	Siyuewu	Chinese	Latin
*cankēk-**camiê***	*tɕʰæ̂go**χjæme***	车前草	*Plantago asiatica*
rbəɟə̄p	***lbəvé***	藜	*Chenopodium album*
ʐɐkōk	*ʐeké*	苦苣菜	*Sonchus oleraceus*
tə-mtō, tə-mtɐ-ɕē	*təmtóse*	黄杨木	*Buxus sinica*
səɟōk	*sjôɣ*	柏树	*Cupressaceae*
mtʰɐlō	*tʰêle*	云南松	*Pinus yunnanensis*
ʐgalō	*qʰêle*	胡桃	*Juglans*
sāj	*fsəsê*	白杨	*Populus alba*
***jʐbrə**-prə̂m*	***zbrə́**se*	杨属	*Populus*
***mdɐ**tsū*	***ldæ̂**ve*	蕨苔	*Pteridium aquilinum*
kʰərdɐ̂j	*χté*	野高粱	*Bistorta vivipara*
ɕkō	*skû*	葱	*Allium fistulosum*
*ta-**jmōk***	*lmôɣ*	菌类	*Fungi*

Plant terms are a key to synchronic analyses of nominal constructions in the modern languages. They cover nearly all kinds of nominal morphology, commonly or rarely found in other nominals. From unanalysable terms, to various types of compounding. Shuya and I gave a talk on this subject in Tianjin this year (Lai and Zhang 2019). I am also looking forward to use the method of word formation handling, when I have enough material, developed by Nathanael, with his excellent paper accepted, Schweikhard and List (forthcoming). The table below shows the cases of Tatpuruṣa in Siyuewu Khroskyabs.

The fruits produced from this project are not only to feed us, the researchers, but also to be given back to the native speakers and the entire society. We plan to publish an encyclopedia of local plants with names, descriptions and sound files in Rgyalrongic languages (Hopefully three languages, including Guillaume Jacques' Japhug).

Table: Tatpuruṣa in Siyuewu Khroskyabs



Term	1st CMPD	2n CMPD	Gloss	Type
tɕ^{h}ǣgoχjæme	*tɕ^{h}ǣgo* ‘on the road’	*χjæme* (plant term)	车前草 *Plantago asiatica*	Locative
djugesmə́	*djú* ‘ghost’	*gesmə́* ‘slice for barley’	?	Genitive
mâvenunu	*mâve* ‘grandmother’	*nunû* ‘breast’	甘青鼠尾草 *Salvia przewalskii*	Genitive
p^{h}ǣzbju	*p^{h}âɣ* ‘pig’	*zbjú* ‘三角叶荨麻’	异株荨麻 *Urtica dioica*	Dative
pjezə́rŋəpæʁ	*pjezə́* ‘sparrow’	*rŋəpǽʁ* ‘popcorn’	?	Dative
brævdzú(r)	*brô* ‘horse’	*vdzúr* ‘spur’	牛口刺 *Cirsium shansiense*	Descriptive
ɲâlmoɣ	*ɲâ* ‘excrement’	*lmôɣ* ‘mushroom’	?	Descriptive
gôɣse	*gôɣ* ‘back basket’	*sê* ‘wood’	圆锥山蚂蝗 *Desmodium elegans*	Resultative
fcəzú	*fcə̂* ‘mouse’	*zú* ‘?’	牛蒡 *Arctium lappa*	Thematic

References

Lounsbury, Floyd G. 1956. A Semantic Analysis of the Pawnee Kinship Usage. Language 32 (1): 158-194.

Hoijer, Harry. 1956. “Athapaskan kinship systems”. American Anthropologist. 58 (2): 309–333.

Jacques, Guillaume. 2012d. The Tangut kinship system in Qiangic per-spective. In Nathan W. Hill (ed.), Medieval Tibeto-Burman Languages IV, 211–258. Leiden: Brill.

Hsieh, Feng-fan. 1999. Theoretical Aspects of Zhuokeji rGyalrong Phonology. National Tsing Hua University, Taiwan MA thesis.

Lai, Yunfan and Zhang Shuya. 2019. Plant terms as key to nominal morphology in Rgyalrongic languages. Paper presented at the he Fourth Workshop on Sino-Tibetan Languages of Southwest China. August 2019.

Schweikhard, Nathanael and Johann-Mattis List. under review. Handling word formation in comparative linguistics.

Zhang, Shuya. forthcoming. Brag-bar kinship system in synchronic and diachronic perspectives. Bulletin of the School of Oriental and African Studies.

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