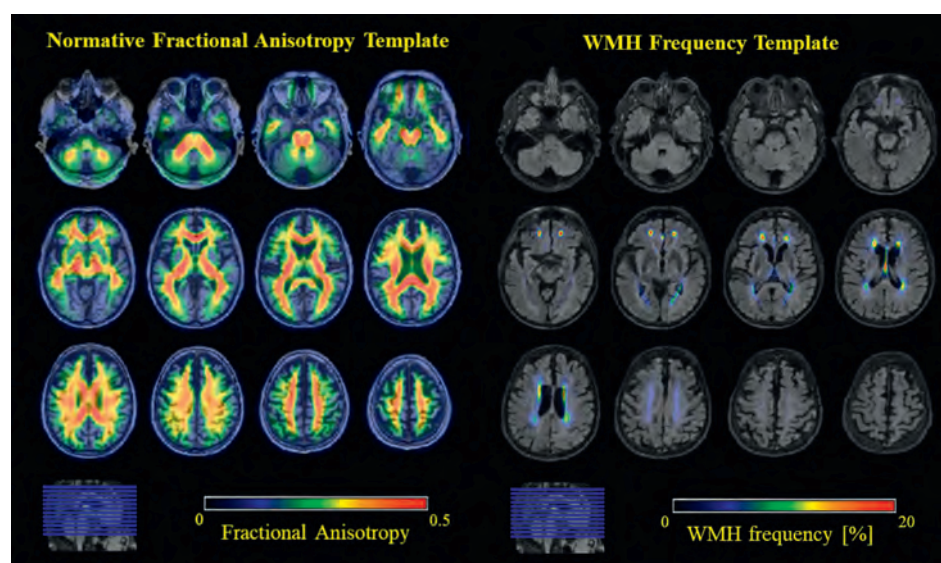


Harbinger of brain damage

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White matter hyperintensities (WMH) are areas of increased signal intensity in magnetic resonance imaging due to macrostructural changes in the white matter of the human brain. WMH have been linked to Alzheimer's disease, emotional and motoric dysfunction, and risk of later development of stroke. There has been recent interest in understanding the nature of the regional distribution of WMH and the extent to which WMH reflect restricted, discrete damage or a «tip-of-the-iceberg» phenomenon in which the abnormal signal is a harbinger of microstructural damage. In collaboration with the Columbia University, the

IAS investigates the hypothesis that regions with an intrinsically lower microstructure are most susceptible to develop WMH. Part of the ongoing project was to define a normative white matter microstructure template for young, healthy adults as well as a WMH frequency template in older adults. Microstructure is thereby reflected by the fractional anisotropy (FA) value of the water diffusion in the brain. First comparisons of the two templates show evidence supporting the postulated hypothesis. ■

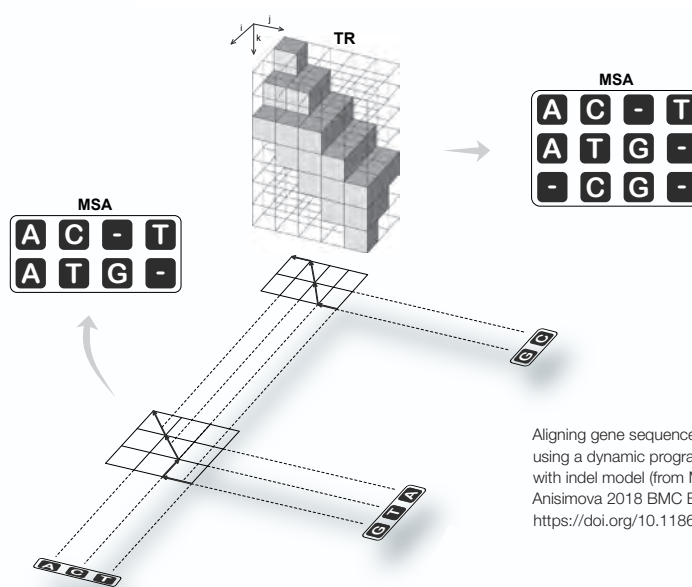


FA template (left) and WMH frequency template (right)

The history of genes

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The evolution of species can be traced back in history using the molecular changes in genes over time. This is modeled as a process of change along an evolutionary tree termed phylogeny. The two most important types of events are substitutions and indels (insertions and deletions) of nucleotides. Indel events are notoriously difficult to model and to reconstruct. Funded by SNSF grant 31003A_157064 (454 000 CHF between 2015–2018), Massimo Maiolo and Lorenzo Gatti – PhD students at the Applied Computational Genomics Team – have developed new methodology, which for the first time employs a mathematical indel model in order to find and align evolutionarily related gene sequences and to infer their phylogenies (fig. 1). Building on this work, the research will continue to tackle a joint reconstruction of ancestral gene sequences and the phylogenetic relationships. New funding of 800 000 CHF was secured for 4 years (2018–2022) provided by SNSF grant 31003A_176316. ■



Aligning gene sequences along a phylogeny using a dynamic programming approach with indel model (from Maiolo, Zhang, Gil, Anisimova 2018 BMC Bioinformatics <https://doi.org/10.1186/s12859-018-2357-1>)

Neue Projekte

Optimierung Recyclinghof-Logistik

Leitung: adrian.loetscher@zhaw.ch
Dauer: 1.3.18 – 31.12.19
Projektpartner: Stadt Zürich, ERZ Entsorgung + Recycling Zürich, Zürich

AGORA – The Art of Living the Good Life

Leitung: roland.gassmann@zhaw.ch
Dauer: 1.3.18 – 31.12.19
Beteiligte Institute: IAS, IUNR
Projektpartner: Schweizerischer Nationalfonds SNF, Bern

Bayesian parameter Inference for stochastic models (BISTOM)

Leitung: simone.ulzega@zhaw.ch
Dauer: 1.4.18 – 31.3.20
Projektpartner: Eawag, Dübendorf; Swiss Data Science Center (SDSC), Lausanne

Weitere Projekte

zhaw.ch/ias/projekte

Weiterbildung

Neue Kurse im Aufbau

- Artificial Intelligence for Non-Scientists
- Data Engineering in R and Python
- Data Structures and Programming for Data Sciences
- Deep Learning mit Tensorflow 2.0 und Keras
- Image Recognition for Life Sciences and Health
- Machine Learning Fundamentals
- Moderne Methoden zur Datenanalyse In R
- Moderne Methoden zur Datenanalyse mit Python
- Research Design and Project Management

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