

Increasing Access To Bioinformatics Resources

Increase Community Curation by Increasing Your Community

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GBrowse User Introductory Tutorial

This suite is part of a larger set of tutorials funded in a large part by NHGRI. Additional free tutorials on model organism resources can be found at http://www.openhelix.com/model_organisms.shtml



Learn to use GBrowse, a web application that allows you to explore genomic sequences together with annotated data. GBrowse is rapidly becoming a genomic browser of choice amongst organism databases, because the browser is both universal and yet customizable. Once you learn to use GBrowse at one database, you'll be able to use it to view any genome. Results can be customized to show only the data you want to see. The tool is flexible to allow you to upload and incorporate your own unpublished data into the genomic viewer. You'll have fun as

you explore a variety of genomes (from paramecia to personal genomics) with the new perspective and detailed annotations that GBrowse provides.

You'll learn:

- the basic layout and search methods at GBrowse
- how to access detailed annotation data tied to genomic sequences
- · how to select and customize annotations using Tracks
- how to upload and incorporate your own data or other external data sources
- · take a tour of different GBrowsy databases



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More about the resource:

GBrowse stands for "Generic Genome Browser". It is a web application to view and explore annotated genomes. It was developed by GMOD, the Generic Model Organism Database, which is a community of biologists and computer programmers dedicated to the idea of making free, open-source software available to all model organism databases. or MODs, with the goal of simplifying and standardizing the appearance and usage of these MODs. When new genomes from different organisms are sequenced and a dedicated annotated database is created to serve that genome, the curators can use GBrowse to get their MOD up and running in no time.

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- Modular Flash tutorial with professionally recorded audio
- 2. PowerPoint slides with full script text included
- **Slide Handouts** for easy note taking
- Step-by-step exercises that lead user through hands-on experience
- **Link to Resource**

"Community Service" Efforts

Increase awareness of "bioinformatics" resources:

- OpenHelix Blog
- Resource Search Tool
- Act as a Community Bridge

This will increase the resource's user base, and thereby increase the community curation

(theoretically)

Funding largely from an NHGRI SBIR Phase II grant.

Increasing Community Curation:

600		Community_		Contribution_		Number of
ed 23 Apr 2009		<u>Size</u>	X	<u>Rate</u>	=	<u>contributors</u>
163.1 : Poste	by default:	500	X	1 %	=	5 people
38/npre.2009.31	increased rate:	500	X	5 %	=	25 people
ings : doi:10.103	increased community:	5000	X	1 %	=	50 people
ture Precedii	both approaches	s: 5000	X	5 %	=	250 people

Complementary Approaches to increasing community curation!

Sour Blog Community to Your Resource!

OH News

User Polls

RSS feeds from other great blogs



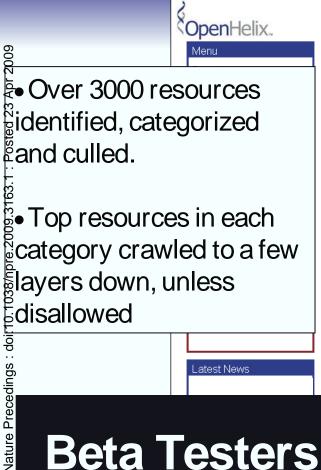
Regular Blog Features:

Tip of the Week (Wednesday)

What's Your Problem? open threads (Thursday)

Guest Posts

Research Search Tool



Beta Testers Appreciated!!



OpenHelix Blog posts relevant to your search

SeattleSNPs: http://pga.gs.washington.edu/

Easy keyword searching for bioinformatics resources; users can modify the criteria by which their search results are ranked



Pages hit on our blog

OpenHelix tutorial materials relevant to your search

H Web pages from the resource that were relevant to your search

Web pages from the resource that were relevant to your search

Training materials

a genetic variation discovery resource

No matches in the training materials for this resource

Links to hits within our trainings

OpenHelix Blog posts relevant to your search

Nature Precedings: doi:10.1038/npre.2009.3163.1: Posted 23 Apr 2009

Acting as a Bridge

" I don't want to ask a dumb question"

OpenHelix

I don't want to bother them"

" I doubt they' II do anything about my comments"

Etc.



User



Resource

Acknowledgements

Thanks for the invitation to talk.

Thanks VERY much to the organizers!

Any questions, suggestions or comments, feel free to email me:

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