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AmiGO 2: Welcome to the Beta

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Outline



2 The Current State of Things







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AmiGO 1

After years of clinging to a core relational database and SQL backend, the increasing number of tricks, extensions, and caches necessary to keep performance at an acceptable level has become too much.

Falling behind on:

- Complicated queries: enrichment, subsets, search, reports, etc.
- Handling larger amounts of data
- Providing services

AmiGO 2

The new architecture brings a lot to the table:

- Data as a document-making life simpler
- Our world is now pre-computed
- Can handle more data
- Easy tool creation, embedding, and widgets
- Direct remote data use (HTTP) and scripting (JavaScript API)

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Since Last Time

We now have:

- A stabilized instance (less downtime and oddities)
- Backend and libraries stabilized
- Frontend improvements
- Galaxy aware and kick out to GO Galaxy

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Bugs Now Considered Harmful

We're now entering beta-feedback is welcome.

• The AmiGO 2 Manual home: installation, links to more documentation, etc.

http://wiki.geneontology.org/index.php/AmiGO_2_Manual

- For interface and feature requests
 - Please contact me
 - Trackers are open for business (check here first) https://github.com/kltm/amigo
- For developer stuff: use of widgets, services, scripting, etc.
 - Mailing list home: for announcements, changes that may break things https://lists.lbl.gov/sympa/info/amigo2-dev

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- A new way of doing things. Relax...

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Collaboration and Integration

- Work with other groups on tools, schema, and library development
- Better consumption of aligned resources



QuickGO, GONUTS, Wikipedia, Plant Ontology, Virtual Fly Brain, Wikipedia...

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The Road to Production

Frontend

- Better documentation
- UI improvements (looking at ZFIN)
- More widgets as we get feedback
- Production
 - Jenkins loading
 - Scaling, server tuning, and the cloud
 - How many users will we have and how will they be using it?
 - How open do we want to be?
 - Analytics (user tracking) is now a lot harder
 - JS API, direct data, AmiGO 2
- Development
 - A few more backend tweaks (memory and traversal)

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Acknowledgments

- Berkeley Bioinformatics Open-source Projects
- The Gene Ontology Consortium
- Saccharomyces Genome Database
- All the users of AmiGO
- All the future users of AmiGO 2