AmiGO 2: Welcome to the Beta

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Outline

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)
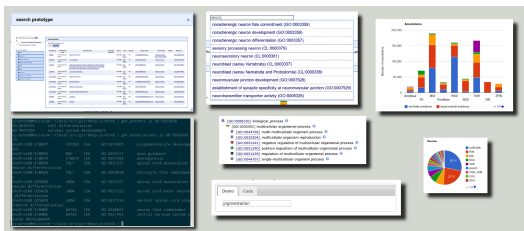
Since Last Time

We now have:

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

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…

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...

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)

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