

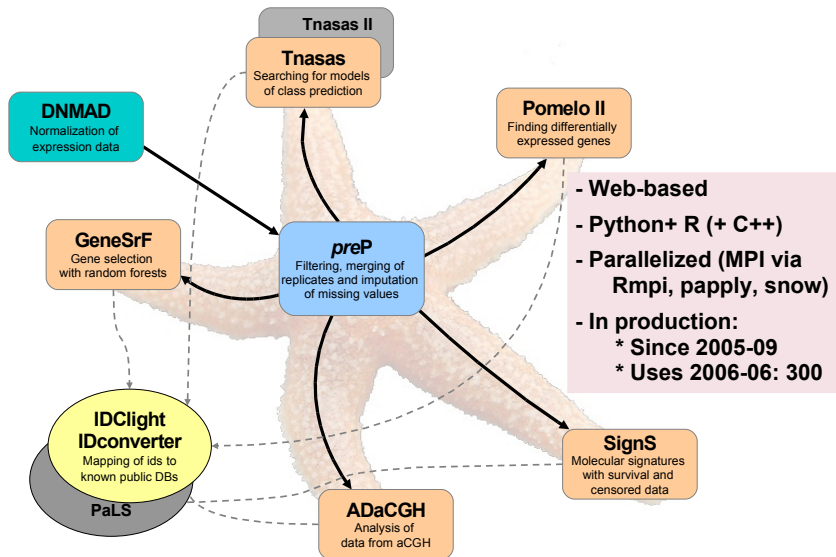
Asterias: an example of using R in a web-based bioinformatics suite of tools

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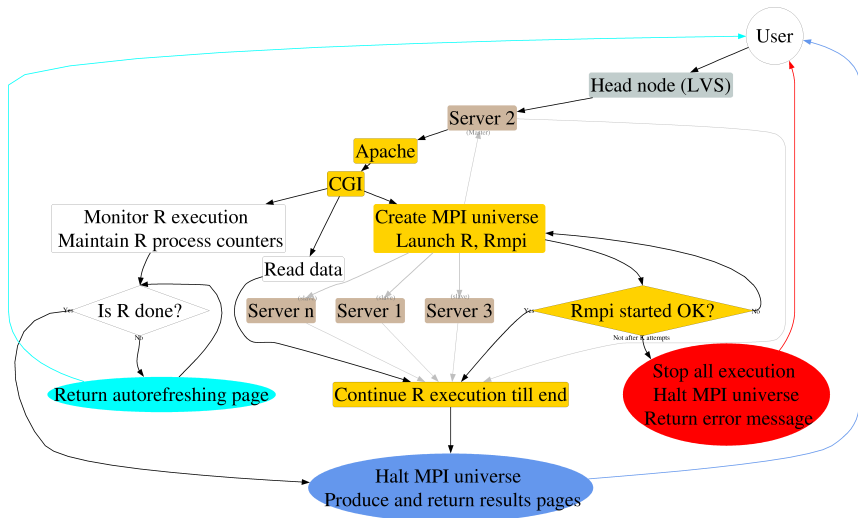
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useR! 2006

Asterias tools



How it works: overview



Exception and error handling

- CGI and Python pre-processing: catch all user errors
- R: Liberal use of `try`:
 - ▶ Orderly exit R (and Rmpi) (→ whole appl.)
 - ▶ Error message (function call), traceback, figure
 - ★ `caughtUserError`
 - ★ `caughtOurError`
 - ▶ (Few, if any, should ever be user errors: caught before by Python code)

Testing

- Whole system and regression testing: FunkLoad
 - <http://funkload.nuxeo.org/>
 - ▶ A suite per application/component
 - ▶ Allows simple stress-testing
- Hourly run one FunkLoad test
 - ▶ Test head node, servers, MPI
 - ▶ Send email if failure
- Other checks (head nodes, NFS servers, each node)

Availability

- Using it: <http://www.asterias.info>
- Project page: <http://bioinformatics.org/asterias>
- License: GNU GPL + Affero GPL.

Future

- Simple installation
- Use virtual servers (Linux VServer, Xen) for security and deployment ease
- Further parallelization work: UPC, MPI + OpenMP
- Use of Grid
- Allow deployment as web services