

Interactive
Environments

BG & ER

What are IEs?

Demo

How?

Who?

Why?

Use Cases

Teaching
Research

Available IEs

IPython
RStudio

Thanks

Q&A

Galaxy Interactive Environments

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Interactive Environment (IEs)

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Q&A

- New way to interact with your data, without leaving Galaxy
- Flexible, efficient, extensible, and interactive
- Full spectrum of use; Teaching, Research, and Development

Your favourite Data Science tools...

IPython: Notebook ipython_galaxy_notebook

File Edit View Insert Cell Kernel Help



Welcome to the interactive Galaxy IPython Notebook.

You can access your data via the dataset number. For example, `handle = open(get(42), 'r')`. To save data, write your data to a file, and then call `put('filename.txt')`. The dataset will then be available in your galaxy history. Notebooks can be saved to Galaxy by clicking the large green button at the top right of the IPython interface.

More help and informations can be found on the project [website](#).

In [1]:

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... Inside of Galaxy

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The screenshot displays the Galaxy IPython Notebook interface. The main window is titled "IP[y]: Notebook ipython_galaxy_notebook" and features a standard menu bar (File, Edit, View, Insert, Cell, Kernel, Help) and a toolbar with various execution and navigation icons. A large green box contains the text: "Welcome to the interactive Galaxy IPython Notebook." Below this, a paragraph explains how to access data via dataset numbers, using an example: `handLe = open(get(42), 'r')`. It also mentions saving data to a file and finding more information on the project website. The input prompt "In [1]:" is visible at the bottom of the notebook area.

On the right side, the "History" panel shows a search bar and a list of datasets. The first entry is "Unnamed history" (1 shown, 2 hidden) with a size of 47 bytes. The second entry is "3: Pasted Entry" (4 lines, format: txt, database: 2), which is highlighted in green. Below the history list, there is a table of data:

| T | A |
|---|---|
| 1 | 2 |
| 3 | 4 |
| 5 | 6 |

IE Demonstration

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- We'll demonstrate some analysis ...
- `www.youtube.com/watch?v=UOFFkDuJxgk`

How does this magic work?

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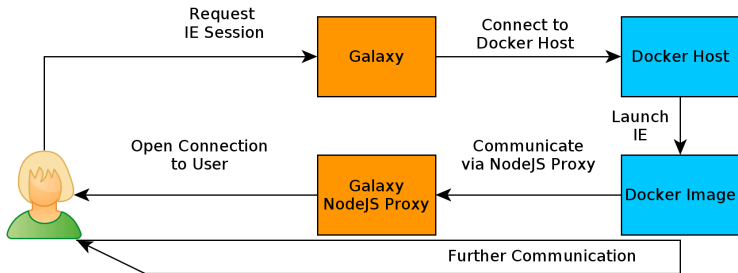
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Who should use IEs?

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Q&A

- Everyone!
- IPython/RStudio are great for bioinformaticians and Data Scientists
- The upcoming iobio visualization IEs are great for Life Scientists

Why use IEs instead of ... Galaxy Tools/Viz?

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Q&A

- Tools are not one-size-fits-all
- Visualisations are restrictive
- Complete freedom!

Why use IEs instead of ... “normal” service deployments?

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- IPython Notebooks are stored as history elements
- Notebooks are re-runnable, maintaining reproducibility
- API interactions required to access data are all 100% transparent
- Transparently integrates with standard Galaxy deployments and authentication schemes
- Notebooks are rendered into HTML for easy viewing/sharing, without launching an IE

Teaching

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- Ideal for teaching:
 - Researchers
 - Bioinformatics
 - Data Wrangling
 - and Scientific Programming
- Share notebooks with students inside of Galaxy
- Use “literate programming” in IPython to teach students how analyses work, line-by-line

Research

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Q&A

- Reproducible and transparent scripts
- Share “hotfix” scripts easily between bioinformaticians and researchers

Development

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Q&A

- Rapidly prototype new scripts and tools for your organisation
- Immediately test them on your large, real datasets
- Does an existing visualisation not meet your goals? Build a new one immediately in IPython/RStudio.

IEs

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Available Now

- IPython (included in Galaxy 15.05/Cloudman)
- RStudio (coming in Galaxy 15.07)

Coming Soon

- iobio BAM
- iobio VCF

In the Works

- Apache Zeppelin
- WebApollo
- Jupyter 3/4 (Python/R/Julia/Perl/Ruby)

IPython IE Features

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Q&A

- Baked in Bioblend access to Galaxy
- Easily get data from/put data into Galaxy
- Bash and R “magics”
- Pre-installed: numpy biopython scikit-learn pandas
scipy sklearn-pandas bioblend matplotlib patsy
pysam khmer dendropy ggplot mpld3 sympy rpy2

RStudio IE Features

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Q&A

- Easily get data from/put data into Galaxy
- R version 3.2.1
- Knitr/Sweave available
- R Packages: RCurl, XML, markdown, shiny, ggvis, dplyr, ggplot2, plyr, reshape2, devtools, RODBC, maps, pheatmap, readr, tidyr, dplyr, RJSONIO, shinyapps, knitr
- Bioconductor: edgeR, Rgraphviz, biomaRt, topGO, limma, DESeq2, cummeRbund, Biostrings, GenomicRanges, Rsamtools, affy

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A big thank you to:

- John Chilton for his help getting the IE codebase merged into Galaxy originally
- Enis Afgan for getting the IEs into Cloudman
- the Galaxy Team for supporting this exciting new feature we've developed.

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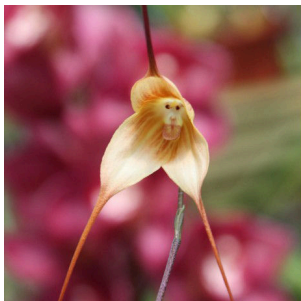
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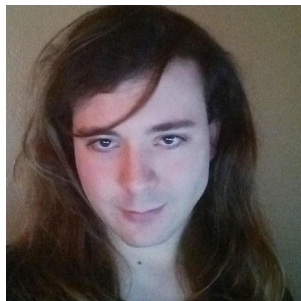
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Q&A



github.com/bgruening



github.com/erasche

- IPython <http://bit.ly/gxIEipython>
- RStudio <http://bit.ly/gxIERstudio>