

# New Tool Forms for Galaxy

Aysam Guerler

# Goal

- New input elements
- Unified design patterns
- Instant validation
- Instant form update
- Improved reliability on job submission

# New Galaxy Tool Form

Plot CuffDiff data with cummeRbund (Galaxy Tool Version 1.0.1)

Versions Options

Question? Search Share Download Requirements See in Tool Shed

Select backend database (sqlite)

7: http://gaius.bx.psu.edu

Plots

1: Plots

The width of the image

1280

The height of the image

960

Plot type

Boxplot

Replicates?

Yes No

Apply log10 transformation on FPKM values?

Yes No

+ Insert Plots

Execute


# New Element: Batch Mode submission

The diagram illustrates the process of submitting multiple datasets in batch mode. It shows two input fields. The top field contains a single dataset: "6: amino\_acid\_features.txt". A red curved arrow points from this field to the bottom field, which contains a list of multiple datasets: "82: Pasted Entry", "51: ToolTemplate on data 12", "11: Merge Columns on data 6", and "6: amino\_acid\_features.txt". A black callout box with the text "Multiple datasets" points to the list of datasets in the bottom field. Below the list, a small icon of a grid is followed by the text: "This is a batch mode input field. A separate job will be triggered for each dataset."

6: amino\_acid\_features.txt

Multiple datasets

82: Pasted Entry  
51: ToolTemplate on data 12  
11: Merge Columns on data 6  
6: amino\_acid\_features.txt

 This is a batch mode input field. A separate job will be triggered for each dataset.

# New Element: Slider

Floating regions of regions of sizes

101.09



# New Element: Color Selection

Title Color

Select a color

Theme Colors

Standard Colors

# New Element: Data Library Selector

Some library dataset

Select Library

Library 2



/sdafdasf/Pasted Entry



/dsafdsafdsaf/ToolTemplate on data 3

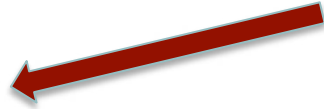


/sdafdasf/Pasted Entry

Pick some a library dataset

# Unified appearance: Selections

## Drill down 2




Select/Unselect all

- Heading 1
  - Option 1
  - Option 2
- Heading 2
  - Option 3
  - Option 4
- Option 5



# Unified appearance: All selections searchable

 Pick a genome

unspecified (?)

No selection

**unspecified (?)**

A. gambiae Feb. 2003 (IAGEC MOZ2/anoGam1) (anoGam1)

A. mellifera Jan. 2005 (Baylor 2.0/apiMel2) (apiMel2)

A. mellifera July 2004 (Baylor 1.2/apiMel1) (apiMel1)

Afrotheria Apr. 24. 2006 (UCSC Recon/afrOth13) (afrOth13)

Armadillo Jul. 2008 (Broad/dasNov2) (dasNov2)

Armadillo May 2005 (Broad/dasNov1) (dasNov1)

...





# Unified appearance: Repeat

1: Repeat 


**Standard columns**

Auswahl 2 


**Dataset**

   82: Pasted Entry 

**Column for x axis**


Column: 1 



# Unified appearance: Sections



A section 

**Some library dataset**

Select Library

Library 2 

 /sdafdasf/Pasted Entry 

-  /dsafdsafdsaf/ToolTemplate on data 3
-  /sdafdasf/Pasted Entry

Pick some a library dataset

# Improved Error Handling

↓ Please verify this parameter.

**Drill down**

- Heading 1
  - Option 1
  - Option 2
  - Heading 2
  - Option 5

- Instantly scrolls to the corresponding input element
- Highlights the error

# Upcoming: New Workflow Tool Form

The screenshot displays the Galaxy workflow editor interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The main workspace is a grid-based 'Workflow Canvas | Unnamed workflow'. On the left, a 'Tools' sidebar lists various tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', and 'NGS: QC and manipulation'. In the center, a tool form titled 'Add column' is being configured. It shows a dropdown menu with 'to Dataset' selected and an input field containing 'out\_file1'. Below this, a larger 'ToolTemplateSimple' configuration window is visible, listing tool options like 'Bam', 'Dataset', 'SeriesSeries', and 'fasta - Sequences'. The right-hand 'Details' panel shows the tool's configuration, including 'ToolTemplateSimple including all supported features of the new toolform (Galaxy Tool Version 1.0.0)', a 'Pick a genome' dropdown with 'A. mellifera Jan. 2005 (Baylor 2.0/apiMel2) (apiMel2)' selected, and sections for 'Bam', 'Dataset', 'Token', 'Standard columns', 'Extended columns', and 'Output format' (set to 'Tabular (extended 25 columns)').

# Upcoming: New Workflow Tool Form

The screenshot displays the Galaxy workflow editor interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The main workspace is titled 'Workflow Canvas | Unnamed workflow' and contains a grid with two tool forms:

- Add column**: A small form with a search field containing 'to Dataset' and a dropdown menu showing 'out\_file1'.
- ToolTemplateSimple**: A larger form with a search field containing 'Bam'. Below it, a list of series is shown: 'SeriesSeries', 'SeriesSeriesSeriesSeriesSeriesSeries 1 > Dataset', 'SeriesSeries', 'SeriesSeriesSeriesSeriesSeriesSeries 1 > Series 1 > Dataset', and 'fasta - Sequences'. The 'fasta - Sequences' series has three input fields: 'output (tabular)', 'trim\_fasta (fasta)', and 'trim\_qual'.

On the right side, the 'Details' panel for the selected tool shows configuration options:

- Standard columns**: A dropdown menu set to 'Auswahl 2'.
- Dataset**: 'Data input 'input' (tabular)'.
- Column for x axis**: An empty text input field.
- Column for y axis**: An empty text input field.
- Include comment column**: An empty text input field.
- Pick a genome**: A dropdown menu set to 'A. mellifera Jan. 2005 (Bayl...'.
- Include comment column**: Radio buttons for 'no' and 'yes', with 'yes' selected.
- Floating regions of regions of sizes**: A text input field with '88.04' and a slider control.
- Column with comment**: An empty text input field.
- Include comment column**: A dropdown menu set to 'yes'.
- Column with comment**: An empty text input field.
- Category**: A dropdown menu.

A red arrow points from the text 'Supports Dynamic Parameters' to the 'Pick a genome' dropdown menu in the details panel.

Supports Dynamic Parameters

**Thank you for your attention.**