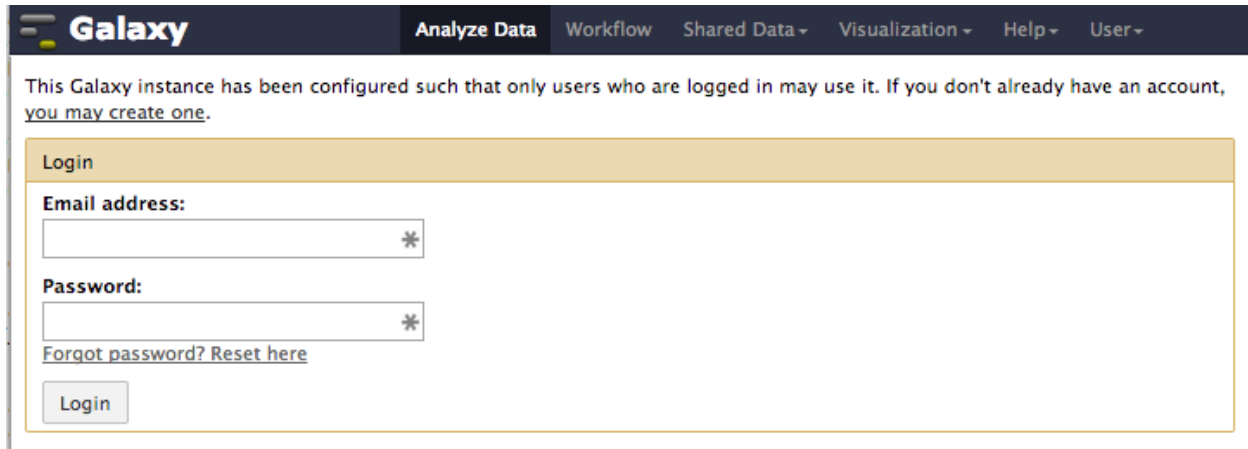


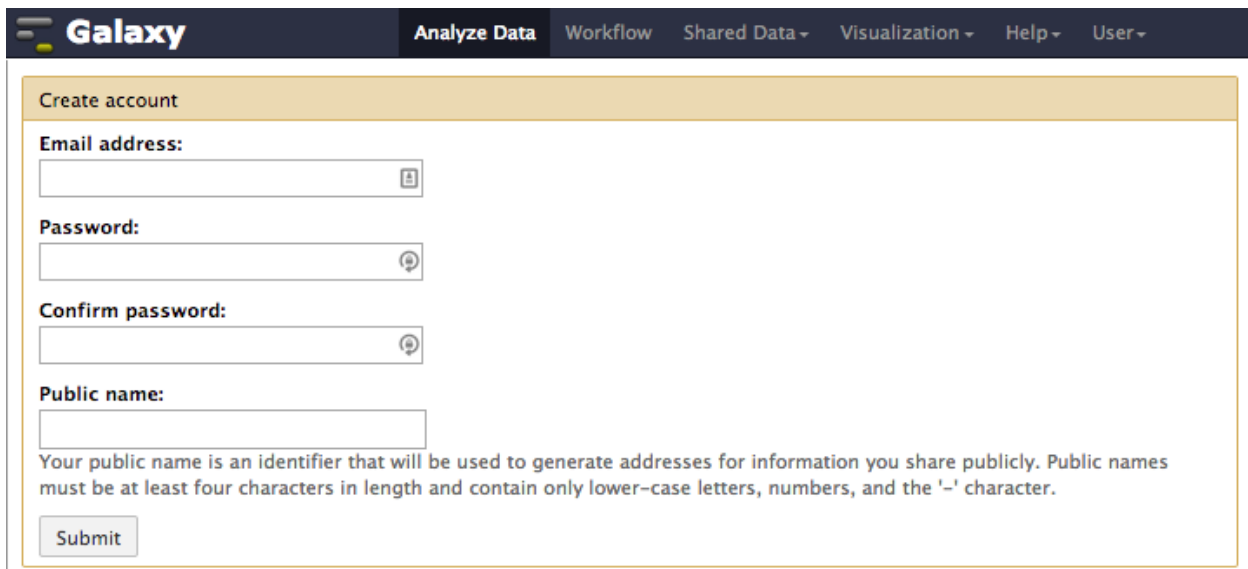
## Getting Started with TargetOrtho:

TargetOrtho is available at: <http://ec2-23-20-137-161.compute-1.amazonaws.com>.

1. Create a user account on the Hobert lab Galaxy instance.



The screenshot shows the Galaxy web interface. At the top, there is a dark navigation bar with the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and User. Below the navigation bar, a message states: "This Galaxy instance has been configured such that only users who are logged in may use it. If you don't already have an account, you may create one." The main content area is titled "Login" and contains a form with the following elements: "Email address:" with a text input field and a "\*" icon; "Password:" with a text input field and a "\*" icon; a link "Forgot password? Reset here"; and a "Login" button.



The screenshot shows the Galaxy web interface for creating a new account. At the top, there is a dark navigation bar with the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and User. Below the navigation bar, the main content area is titled "Create account" and contains a form with the following elements: "Email address:" with a text input field and a lock icon; "Password:" with a text input field and a lock icon; "Confirm password:" with a text input field and a lock icon; "Public name:" with a text input field; a message: "Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least four characters in length and contain only lower-case letters, numbers, and the '-' character."; and a "Submit" button.

## Browse example results and example input files:

See examples at:

<http://ec2-23-20-137-161.compute-1.amazonaws.com/u/laq2175/h/targetortho-examples>

## Galaxy History 'TargetOrtho examples'

### Dataset

1: MEME COE motif.txt	👁
2: VNC MN genes.txt	👁
3: TargetOrtho Results on data 1 and data 2 (html/text) [unc-3 whole genome with query list]	👁
4: MEME unc-3 daf-16 motifs.txt	👁
5: unc-3 daf-16 candidate genes.txt	👁
6: TargetOrtho Results on data 4 and data 5 (html/text) [unc-3 daf-16 CRM results with query list]	👁

To run TargetOrtho on example files

Galaxy Analyze Data Workflow **Shared Data** Visualization

### Data Library "TargetOrtho examples"

TargetOrtho example input files

<input type="checkbox"/> Name	
<input checked="" type="checkbox"/> MEME_COE_motif.txt	
<input type="checkbox"/> MEME_unc-3_daf-16_motifs.txt	None
<input checked="" type="checkbox"/> VNC_MN_genes.txt	None
<input type="checkbox"/> unc-3_daf-16_candidate_genes.txt	None

For selected datasets:

- Data Libraries
- Published Histories
- Published Workflows
- Published Visualizations
- Published Pages

Galaxy **Analyze Data** Workflow Shared Data Visualization Admin Help User Using 7%

Tools

search tools

Get Data

Motif Tools

TargetOrtho - transcription factor target gene prediction

MEME - Multiple Em for Motif Elicitation

FIMO - Find Individual Motif Occurrences

Sequence Logo generator for fasta (eg Clustal alignments)

Workflows

- All workflows

TargetOrtho (version 1.0.0)

job name: example\_job  
TF-1\_targets (no spaces allowed in job name)

add a log-odds motif file: 2: VNC\_MN\_genes.txt  
meme format (plain text) motif file, see example input below

add a query list of genes (optional): Selection is Optional  
gene public name (wormbase/wormmart) or FBgn (Flybase) in plain text format

only report query list results (faster):

reference genome: C. elegans

mode: use default settings

Execute

History

Unnamed history  
766 bytes

- 2: VNC\_MN\_genes.txt
- 1: MEME\_COE\_motif.txt

Results appear in your history

Galaxy **Analyze Data** Workflow Shared Data Visualization Admin Help User Using 7%

Tools

search tools

Get Data

Motif Tools

TargetOrtho - transcription factor target gene prediction

MEME - Multiple Em for Motif Elicitation

FIMO - Find Individual Motif Occurrences

Sequence Logo generator for fasta (eg Clustal alignments)

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add a query list of genes (optional): 2: VNC\_MN\_genes.txt  
gene public name (wormbase/wormmart) or FBgn (Flybase) in plain text format

only report query list results (faster):

History

Unnamed history  
766 bytes

- 3: TargetOrtho Results on data 2 and data 1 (html/text)
- 2: VNC\_MN\_genes.txt
- 1: MEME\_COE\_motif.txt

To run TargetOrtho on your own files:

**Galaxy** Analyze Data Workflow Shared Data Visualization Admin Help User

Tools

search tools

**Get Data**

- Upload File from your computer**
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX table browser
- EBI SRA ENA SRA
- Get Microbial Data
- BioMart Central server
- BioMart Test server
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server
- Flymine test server
- modENCODE modMine server

**Upload File (version 1.1.3)**

**File Format:**  
Auto-detect  
Which format? See help below

**File:**  
Choose File No file chosen  
TIP: Due to browser limitations, uploading files larger than 2GB is guaranteed to fail. To upload large files, use the URL method (below) or FTP (if enabled by the site administrator).

**URL/Text:**

Here you may specify a list of URLs (one per line) or paste the contents of a file.

**Convert spaces to tabs:**  
 Yes  
Use this option if you are entering intervals by hand.

**Genome:**  
unspecified (?)

**Execute**

**To generate your own motif files:**

Use: <http://meme.nbcrl.net/meme/cgi-bin/meme.cgi>