



WP5

LiceBase Introductory Course

Part 3 Basic steps

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Outline

- Overview on LiceBase, getting help
- Terms and definitions
- Basic functions: using Tripal
- Basic functions: using GBrowse
- Basic functions: BLAST
- Advanced topics: BLAST, GO, KEGG, and friends
- Examples: searching genes by functional annotation
- Exercise: finding GO I's, reconstruct pathways
- Annotation guide: RNAi experiment
- Exercise: annotate an RNAi experiment
- Annotation guide, novel genes and gene function
- Q & A

LiceBase technology

- Genomics web-pages
- Genome Browser



Script: Tripal

- Log in with your credentials, see how site changes
- Overview of functions and links, please follow the presenter
 - Log out link
 - read documentation and blog entries
 - try site search with term "chitin"
 - buttons to main functions
 - link levels: main menu links, primary, secondary links
- Create a blog post, name it "course_<name>", blog posts are visible to everyone!

Script: Tripal

- Organisms, Analyses, Features
- Open Organism search -> salmon louse
- Resources sidebar: go through all the links to the right: Downloads, Ensembl, data types, GO browser
- Features -> explain search form, and sequence types
- search EMLSAG00000010208, explain different search options, ends with, etc.
- search annotation for 'chitin synthase' (case sensitive!)
- search form remembers your settings
- go to EMLSAG-10208 and walk through resource links
- open the precomputed blast results, can we determine a function? Open the alignment information.
- some annotations are only available for the proteins, go to EMLSAP-10208

Script: GBrowse

- Open GBrowse, note you are already logged in
- How to get help, open the built in documentation
- Genomic information is displayed as tracks
- Go to Select Tracks -> activate ensembl genes if not already on
- Explain how to choose tracks, how to get track information
- Tracks are organized into track groups
- GBrowse remembers your track settings
- -> Back to Browser

Script: GBrowse

- Tracks are configurable, -> show config tool
- Tracks can be moved around, images of gene models can be saved
- Tracks show additional information on mouse over and on click, demonstrate display options for gene tracks
- Zoom in to a region
- Use the search function: find EMLSAG00000010208 then find term 'rRNA' -> multi result views
- Careful, searches can take too long and expire
- activate additional tracks -> non-stranded RNA-seq coverage track -> stranded RNA-seq -> configure stranded track
- -> open track Transcripts + CPM -> on mouse over: display expression bar plot
- explore more gene tracks and export fasta file of a gene
- copy DNA sequence to clipboard

Script: Blast

- Open Blast page from frontpage
- Blast commands: blastn, blastp, blastx, tblastn, tblastx
- Blast databases (type of db must match program)
- Paste in DNA sequence and run blastn
- Look at the result page, follow link out to GBrowse
- Excercise: try hard to find your gene of interest
- Excercise: get a protein sequence (e.g. from genbank) and find it in the genome, which programs and database combinations can you apply?