Pathways Project: Annotation Workflow

Examine genomic neighborhood surrounding target gene in *D. melanogaster*

Identify genomic location of ortholog in target species

tblastn
Query: *D. melanogaster* protein
Database: target species assembly

Examine genomic neighborhood of putative ortholog in target species

Use synteny to gather additional evidence for the ortholog assignment

***blastp* (Protein BLAST)**
Query: Accession No. of protein sequence of putative ortholog in target species
Database: refseq_protein *Drosophila melanogaster*

Repeat *blastp* for genomic neighbors

Determine gene structure in *D. melanogaster*

Determine approximate location of coding exons (CDS's) in target species

***tblastn* (Align two or more sequences)**
Query: Each individual CDS of target gene in *D. melanogaster*
Subject: Accession No. of scaffold containing ortholog in target species

Narrow region of scaffold to search via "Subject subrange"

Refine coordinates of CDS's

Gene Predictions	Splice Sites	RNA-Seq	Comparative Genomics
Explain anomalies	Explain anomalies	Explain anomalies	Explain anomalies

Verify gene model

Custom Gene Model

GFF File
Transcript Sequence File
Peptide Sequence File

Dot plot
Protein alignment

Explain anomalies

Complete Pathways Project: Annotation Report

Submit to your instructor

Legend

D. melanogaster Genome Browser
Target Species Genome Browser
Genome Assembly BLAST
NCBI BLAST
Gene Record Finder
Gene Model Checker

Document
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Screenshot

Last Update: 03/09/2021