



EU-SOL Bioinformatics Tutorials

EU-SOL has developed a number of bioinformatics tools that enable researchers to explore and analyse the rich variety of data that has been stored during the past five years. To facilitate continued use of these database in the post EU-SOL era tutorials have been developed.

BreeDB is the primary database resource for the EU-SOL genotyping and phenotyping data and is hosted at <https://www.eu-sol.wur.nl>. This database hosts data-sets collected within EU-SOL. In the tutorial we focus on the question of how to mine this data, and in special, it focuses on the tools that allows exploration the genetic diversity within the tomato core collection.

<http://www.eu-sol.net/science/bioinformatics/tutorials/breedb-tutorial/>

The **GBrowse** tutorial shows how the tomato genome data can be accessed through the generic genome browser. The various annotations that are visualized in the browser are described and it shows how to find a favourite gene and obtain detailed information about it.

<http://www.eu-sol.net/science/bioinformatics/tutorials/gbrowse-tutorial/>

The **PlantsDB** tutorial introduces online resources and tools for comparative genomics in Solanaceae. Starting from a solanaceae model such as tomato it shows how to find, browse and use associated data both in related species and non-model Solanaceae. These data involves orthologous/homologous gene models, multi-species gene families and synteny on the micro- and macro-level.

<http://www.eu-sol.net/science/bioinformatics/tutorials/plantsdb-tutorial/>

The **iTAG** annotation for Tomato, integrates protein homology, homology to other dicot genomes, EST and cDNAs, RNAseq reads from all 3 available technologies, ab initio methods from GeneID, Augustus and TwinScan and MS/MS data. This is the first time gene prediction has been done with such a diversity of data. iTAG aims at providing the best possible genome annotation. Still, errors can occur. For this purpose the **BOGAS** interface offers preprocessed data, and access to tools to allow experts to correct the predictions.

<http://www.eu-sol.net/science/bioinformatics/tutorials/bogas-tutorial/>

GenomeView is a stand-alone sequence browser specifically designed to visualize and manipulate a multitude of genomics data interactively. GenomeView enables users to dynamically browse high volumes of aligned short read data, with dynamic navigation and semantic zooming, from the whole genome level to the single nucleotide. At the same time, the tool enables visualization of whole genome alignments of dozens of genomes relative to a reference sequence. GenomeView is unique in its capability to interactively handle huge data sets consisting of dozens of aligned genomes, thousands of annotation features and millions of mapped short reads both as viewer and editor.

<http://www.eu-sol.net/science/bioinformatics/tutorials/genome-view-tutorial/>

And there is several others, all accessible through <http://www.eu-sol.net/science/bioinformatics/tutorials>

