



The bioinformatics tutorials will give an introduction on how to use EU-SOL bioinformatics resources and how to exploit the tomato genome data. There will be four sessions with walk-through introductions and the opportunity for a guided hands-on training afterwards.

BreeDB: Mining the seeds of EU-SOL

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. This site is roughly divided into two sections. Data obtained from the tomato core collection and data obtained on experimental populations. A diverse set of tools is available to mine the diverse sets of data. In the tutorial we will focus on the question of how to mine this data, and in special, it will focus on the tools that allows exploration the genetic diversity within the tomato core collection.

The tutorial will include explanations on how to explore the phenotypic data that was obtained by screening of the group of Dani Zamir and by the companies within EU-SOL, and how to explore the genotypic data that was obtained by Keygene NV. We will show the tools that will allow the study of the genetic structure of the core collection and the tools that allows integration of genotype and phenotypic information on the tomato core collection. Finally, we will show the tool that allows users to take the step from the genetic, or QTL interval with a positive association to the corresponding region on the tomato genome sequence. Finally, we will show how to obtain the seeds of the germplasm that is of interest for your research / breeding goals.

Browsing the tomato genome

In this session we will show how the tomato genome data can be accessed through the generic genome browser. We will describe the various annotations that are visualized in the browser and show you how to find your favorite gene and obtain detailed information about it. We will also take a peek at the potato genome browser and briefly look at the similarities and differences between these two browsers.

Contribute your knowledge for a better Tomato

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 we provide the BOGAS interface that offers preprocessed data, and access to tools to allow experts to correct the predictions. During the workshop, we will demonstrate the possibilities BOGAS offers, including the usage of tools like JalView and GenomeView.

Comparative genomics resources for solanaceae

In this session we will introduce online resources and tools for comparative genomics in solanaceae. Starting from a solanaceae model such as tomato we will show 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.

Please register via Email and tell us if you can bring your own computer or if we should provide one for you.