

"Training Course on the use of the HARNESSTOM Tomato database for breeders and scientists"

A training course on the use of the largest tomato database for breeders and scenters is organized by the <u>EU-funded HARNESSTOM project</u>. The workshop will take place the 21st of November at the FUNDACION GRUPO CAJAMAR partner facilities in Cajamar Innova, Ed. Bristol, Plaza San Sebastián, 8 – 1°, 04003 Almería

HarnesstomDB Datathon is a 1-day workshop aiming at introducing the <u>HarnesstomDB</u>, a comprehensive publicly available open-source multi-omics database for facilitating the use of the potential of tomato germplasm collections for breeding and research.

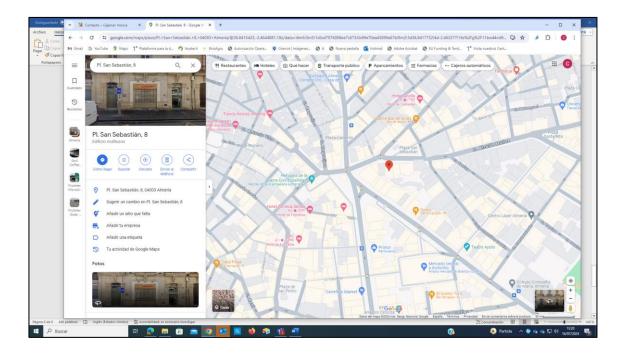
The hands-on course focuses on tools, resources and submission of (meta)data. During the course we will use a combination of theoretical and practical sessions to provide all participants with the knowledge, skills and confidence to work with HanesstomDB.

The outline and information about the course are found below including place, location. Teachers, program and how to register:

Workshop organizers: Dr. Clara Pons (cpons@upvnet.upv.es), Eng. David Pierre (david.pierre@toulouse-inp.fr), or Dr. Antonio Granell (agranell@ibmcp.upv.es).

Type of course: in person Language: English and Spanish Duration: From 8:30 to 14:30

Place: Cajamar Innova, Ed. Bristol, Plaza San Sebastián, 8 – 1º, 04003 Almería







Application: Please fill out this online registration form to apply for the Hands-on training course. Registration closes on 31/10/2024. https://forms.gle/hyq9GTJ9LGmuQpQF7

The course is available to any applicant who meets the requirements and have been selected via the selection process. Selected applicants will be notified by e-mail on 4/11/2024

Registration fees: Participation in the training school is free

Intended Audience: The course is directed at individuals having a minimum basic understanding on plant biology, genetics and breeding. A preference will be given to scientist and technical staff from seed companies: A baseline level of the understanding of concepts such as genetic resources, genome, genotype, molecular markers, mapping populations, experimental design, phenotype, QTL and GWAS and genetic variants are pre-requisite; A basic knowledge of Excel)

Material needed: Participants must bring their own laptop computer. Exercises will be performed on a remote server.

Material provided: We will provide experimental datasets for use during the course, as this helps to keep the workshop moving. There will be time, however, to discuss your own datasets and how you might work with them outside of the workshop.

Program:

SESSION 1	
8:30-8:45	Introduction to the course and introductions round
8:45-9:15	HarnesstomDB overview
9:15-9:45	HarnesstomDB: registration, terms and conditions, privacy.
	Hands-on
9:45-10:15	HarnesstomDB (meta)data submission.
10:30-11:00	Coffee break
SESSION 2	
11:00-13:00	HarnesstomDB entities: definitions, details and relationships
13:00-14:30	HarnesstomDB: searching, downloading and visualization tools.
	Introduction and hands-on





