Rationale
Altogether analyzing haplotype networks and relating them to geographic patterns allows development of phylogeographic analyses and has a great power for resolving crop domestication and understanding further crop adaptation [1]. This project intends to provide the community with a pipeline of analysis of genotyping data (sequences or SNP) which will include haplotype definition, haplotype grouping, haplotype network analysis and connexion with external data such as geographic origin or genetic group assessment.

Objective 1: Haplotyping
We use existing softwares: Gevat, PHASE (In progress), haplotyper (In progress). Users have the possibility to select which software they want to use and set the different parameters the selected software allows.

Objective 2: Haplotype Visualization
Users may wish to visualize at once the haplotypes, and enhance differences between haplotypes, by choosing some accessions as references. We created an R function which draw the haplotypes according to a tree. Users can set one color for each referent haplotypes, color for common alleles and color for new alleles. Missing data always appear in white. For a better visualization, haplotypes order is fixed by a tree. This representation allows users to visualize at once gene integration between two populations.

Objective 3: Network Building
We created a Jar file implementing the minimum spanning network algorithm. We plan to add soon the Reduced Median Network and Median Joining Network developed by Bandelt et al. [2,3]. In the future, more algorithms will be added enabling more choices to the users. Nodes sizes will be proportional to the numbers of germplasms sharing an haplotype and edges length will be proportional to the difference between haplotypes.

Objective 4: Correlation with External Data
Nodes of the network will be represented by pie-charts taking into consideration the repartition of external information (set by the user) among germplasms owning this haplotype. We can also add the graphical representation of the haplotype as explained in objective 2.

Objective 5: Creation of a Web Interface
The pipeline is available through a user friendly Web interface allowing users to set parameters for each step. The output image can be downloaded or visualized directly in the Web browser. User can zoom out and zoom in the image to have a general view of the network or to see more precisely a part of it.

References: