

HaploPhyle: Graphical Haplotype Network in the Light of External Data

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.

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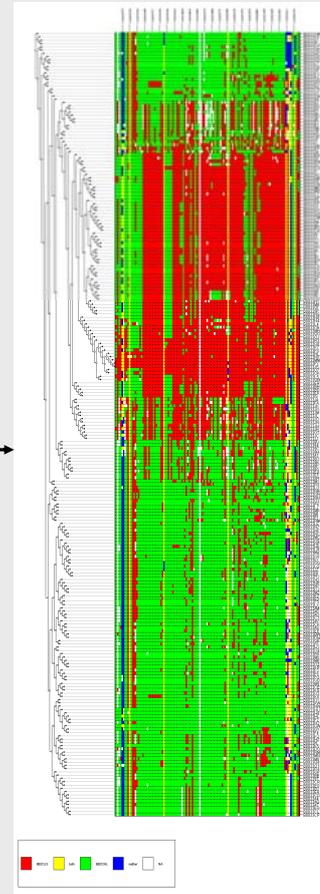
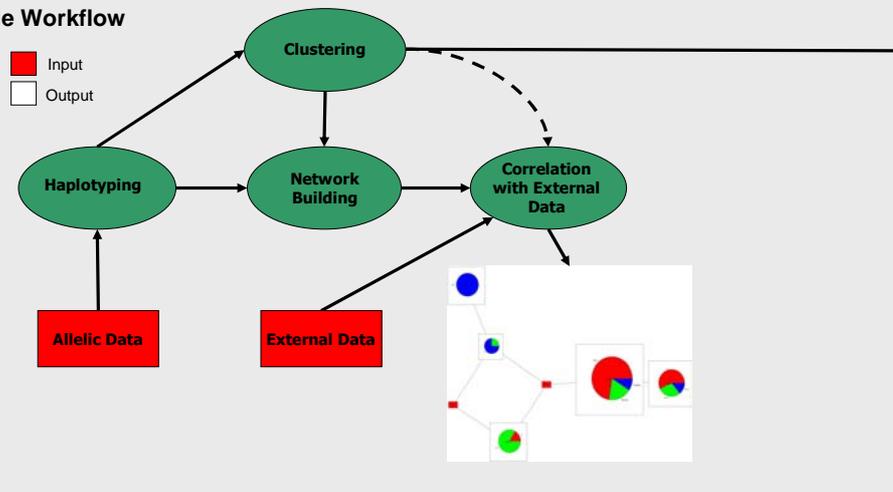
Objective 1: Haplotyping

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.

HaploPhyle Workflow



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 germplasm 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 germplasm 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.

Welcome on HaploPhyle

General | Haplotyping | Network Construction | External Data Correlation

General Settings

All in one Step by step

Allelic Data File: C:\Program Files\Gevall | Parcourir...

Starting Point: Haplotyping

Submit | Reset

References :

- [1] Saisho D and Purugganan MD. 2007. Molecular phylogeography of domesticated Barley traces expansion of agriculture in the Old World. *Genetics*, 177:1765-1776
- [2] Bandelt H-J, Forster P, Sykes BC and Richards MB. 1995. Mitochondrial portraits of human populations using median networks. *Genetics* 141: 743-753
- [3] Bandelt H-J, Forster P and Röhl A. 1999. Median-Joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 17: 37-48

