

Populations 1.2.31

Population genetic software (individuals or populations distances, phylogenetic trees)

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- Distances between individuals (15 different [methods](#))
- Distances between populations (15 [methods](#))
- Bootstraps on loci OR individuals
- Phylogenetic trees (individuals or populations), using Neighbor Joining or UPGMA (PHYLIP tree format)
- Allelic diversity
- Converts data files from Genepop to different formats (Genepop, Genetix, Msat, Populations...)

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Authors

Olivier Langella

all systems

download populations

Ubuntu packages

If you are using Ubuntu, you can find "populations" and "treeplot" packages here : <https://launchpad.net/~olivier-langella/+archive>

Please modify your source list entries to add the repository that corresponds to your Ubuntu version ([Adding Repositories in Ubuntu how to](#))

Distances

- [DAS, shared allele distance](#) (Chakraborty et Jin., 1993)
- [Nei, minimum genetic distance](#), Dm (Nei, 1987)
- [Nei, standard genetic distance](#), Ds (Nei, 1987)
- [Cavalli-Sforza and Edwards](#), Dc (1967)
- [Nei et al's](#), DA (1983)
- [Latter](#), Fst (1972)
- [Prevosti et al.'s](#), Cp (1975)
- [Roger's](#), Dr (1972)
- [Reynolds J. unweighted](#), Dru (1983)
- [Reynolds J. weighted](#), Drw (1983)
- [Reynolds J. least squares](#), Drl (1983)
- Microsatellites distances
- Goldstein et al., dmu2 (1995a)
- Average Square Distance (ASD , Goldstein, Slatkin 1995)
- Shriver et al's, Dsw (1995)
- Lev A. Zhivotovsky, DR (1999)

Formats

- [input](#)
- [output](#)

input files

"Populations" accepts file from other population genetic softwares:

- [Genepop](#)
- [Génétix](#)

and it has its own format:

"Populations" format allows to use unlimited number of alleles, of haploids, diploids or nploids. The format is close to Genepop but alleles at a given locus are separated by ":". Thus, man can code alleles with all ASCII characters.

Diploid population example:

"Grape populations in southern France"

ADHLocus1

ADH#2

ADHthree

ADH-4

ADH-5

Pop Montpellier

Montpellier1 , 02:01 03:03 01:02 03:02 10:11

Montpellier2 , 02:02 03:01 01:02 03:03 11:11

Montpellier3 , 01:02 04:01 02:02 01:02 10:10

Montpellier4 , 01:03 02:02 01:01 02:02 10:11

Montpellier5 , 02:03 02:04 01:01 01:02 10:10

POP Gigondas

Gigondas1 , 01:02 02:02 02:01 04:05 08:07

Gigondas2 , 01:02 02:01 02:01 04:05 03:07

Gigondas3 , 02:01 02:03 01:01 05:05 04:02

Gigondas4 , 02:01 03:03 03:01 03:03 06:03

Gigondas5 , 01:01 02:01 03:01 05:05 08:07

Haploid example :

"Grape populations in southern France"

ADHLocus1

ADH#2

ADHthree

ADH-4

ADH-5

Pop Montpellier

Montpellier1 , 02 03 01 03 10

Montpellier2 , 02 03 01 03 11

Montpellier3 , 01 04 02 01 10

Montpellier4 , 01 02 01 02 10

Montpellier5 , 02 02 01 01 10

POP Gigondas

Gigondas1 , 01 02 02 04 08

Gigondas2 , 01 02 02 04 03

Gigondas3 , 02 02 01 05 04

Gigondas4 , 02 03 03 03 06

Gigondas5 , 01 02 03 05 08

example of haploid, using any ASCII character: no space in allele names:

"Grape populations in southern France"

ADHLocus1

ADH#2

ADHthree

ADH-4

ADH-5

Pop Montpellier

Montpellier1 , all2 03 01 03 10

Montpellier2 , all2 03 01 03 11

Montpellier3 , all1 04 02 01 miss

Montpellier4 , all1 02 01 02 10

Montpellier5 , all2 02 01 01 10

POP Gigondas

Gigondas1 , all1 02 02 04 08

Gigondas2 , all1 02 02 04 miss

Gigondas3 , all2 02 01 05 04

Gigondas4 , all2 03 03 03 06

Gigondas5 , all1 02 03 05 08

Structured population

To code metapopulations, you can choose either "Genepop" or "Populations" format. You only need to give the name of population after the keyword "POP " (separator = "/")

example:

exemple de populations structurées

locus1

locus2

locus3

POP Rennes/immeuble_sud/pop_3emeetage

ind1, (description des individus)

ind2, ...

ind3, ...

ind4, ...

POP Rennes/immeuble_sud/pop_2emeetage

ind1, (description des individus)

ind2, ...

ind3, ...

ind4, ...

Output files

Populations is able to produce various population genetic software formats:

[Genepop](#)

[Génétix](#)

Populations

Lea

[Immanc](#)

microsat

[Admix \(G. Bertorelle\)](#)

[Fstat \(Jerome Goudet\)](#)

Phylogenetic trees are coded using the "Phylip" format. " [Treeview](#)" can be used for Windows or Linux, and you can use ">Treeplot" to convert the phylip format into postscript, adobe illustrator, gif... with colors for each populations

Matrix distances files are "Excel (gnumeric compatible)", "Phylip", "xgobi", "NTsys" or any text editor compliant.

Command line

You can use "Populations" as a command line programm (very useful for batch treatment) to infer phylogenetic trees:

populations name_of_input_file -"arguments"

Available arguments:

-phylogeny ind ou pop (default) for phylogenetic trees based on individuals or populations

-dist method (default: Nei standard, Ds) you can choose among: DAS, Dm, Ds, Dc, Da, dmu2, Fst, Cp, Dr, ASD, Dsw, Dr, Dru, Drw, Drl. see distances for details.

-construct method (default: upgma) possibilities upgma or nj (Neighbor Joining)

-bootstrap_ind number to indicate the number of bootstraps to perform on individuals
-bootstrap_locus number to indicate the number of bootstraps to perform on loci
-output_name_of_treeview_file to indicate the name of the tree file (phylip tree format)

-level number , structured populations allows to choose the structuration factor (in the example: town level is 1, building level is 2...).

example:

```
populations toutc2.txt -phylogeny pop -dist Dm -bootstrap_locus 10000 -output  
toutc2_10000_Dm.tre
```

Commands can be write in a .bat file (for DOS) or a script file (for UNIX).

Bibliography

Bruce Ranala and Joanna L. Mountain. Detecting immigration by using multilocus genotypes. *Proc.Natl. Acad. Sci. USA*, 94:9197-9201, 13/6/1997.

David B. Goldstein, Andres Ruiz Linares, Luigi Luca Cavalli-Sforza and Marcus W. Feldman. An Evaluation of Genetic Distances for Use With Microsatellite Loci. *Genetics*, 139:463-471, 5/10/1994.

D. B. Goldstein and D. D. Pollock. Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. *Journal of Heredity*, 88(335-342):0022-1503, 31/3/1997.

Li Jin and Ranajit Chakraborty. Estimation of Genetic Distance and Coefficient of Gene Diversity from Single-Probe Multilocus DNA Fingerprinting Data. *Mol. Biol. Evol*, 11(1):120-127, 13/9/1993.

Mark D. Shriver, Li Jin, Eric Boerwinkle, Ranjan Deka, Robert E. Ferrel and Ranajit Chakraborty. A Novel Measure of Genetic Distance for Highly Polymorphic Tandem Repeat Loci. *Mol. Biol. Evol*, 12(5):914-920, 13/4/1995.

Montgomery Slatkin. A Measure of Population Subdivision on Microsatellite Allele Frequencies. *Genetics*, (139):457-462, 19/6/1994.

Naruya Saitou and Masatoshi Nei. The Neighbor-joining Method: A New Method for Reconstructing Phylogenetic Trees. *Mol. Biol. Evol*, 4(4):406-425, 18/2/1987.

Naoko Takezaki and Masatoshi Nei. Genetic Distances and Reconstruction of Phylogenetic Trees From Microsatellite DNA. *Genetics*, (144):189-399, 6/6/1996.

William J. Bruno, Nicholas D. Socci and Aaron L. Halpern. Weighted Neighbor Joining: A Likelihood-Based Approach to Distance-Based Phylogeny Reconstruction. *Mol. Biol. Evol*, 17(1):189-197, 11/10/1999.