Ferret: a user-friendly tool to extract data from the 1000 Genomes Project

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Ferret: a user-friendly tool to extract data from the 1000 Genomes Project

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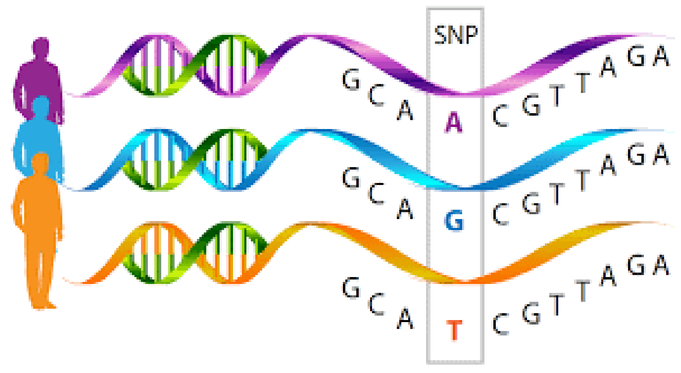
About the 1000 Genomes Project*

International consortium to establish the largest public catalogue of human genetic variations: >84M SNPs for 2504 individuals



HaploView files
data visualization, LD pattern, haplotypes, tagSNP design, etc.

PLINK files
can be merged with user's dataset, etc.

Allele frequency file

CHR	VARIANT	POS	A1	A2	NB_1KG_CHR	1KG_A1_FREQ	ESP6500_EA_A1_FREQ	ESP6500_AA_A1_FREQ
6	rs1065711	31236853	G	A	1006	0.1213	.	.
6	rs1049853	31236900	G	A	1006	0.8867	0.8726	0.9209
6	indel_rs41548117_TC/T	31237100	TC	T	1006	0.9553	0.9594	0.9183
6	rs41542414	31237766	A	T	1006	1	0.9995	0.9897
6	rs9264623	31237950	T	C	1006	0.2773	.	.
6	indel_rs9281300_C/CA	31239170	C	CA	1006	0.4195	0.535	0.4125

Unique advantages of Ferret#

- User-friendly interface
- Input flexibility
- Handles SNPs and indels
- Outputs suitable for pre-existing tools
- Computes allelic frequency
- Retrieves allelic frequency from ESP (Exome Sequencing Project)
- **Dec. 2017 update**: sync with HaploView + gene borders

Perspectives (Aug. 2018)

- Grant access to *HLA* alleles data§
- Functional annotations
- Bi-directional filter for frequencies
- Increase runtime speed

References

*The 1000 Genomes Project Nature 2015
#Limou *et al.* Bioinformatics 2016
§Gourraud *et al.* PLoS One 2014

Publicly available at http://limousophie35.github.io/Ferret/