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

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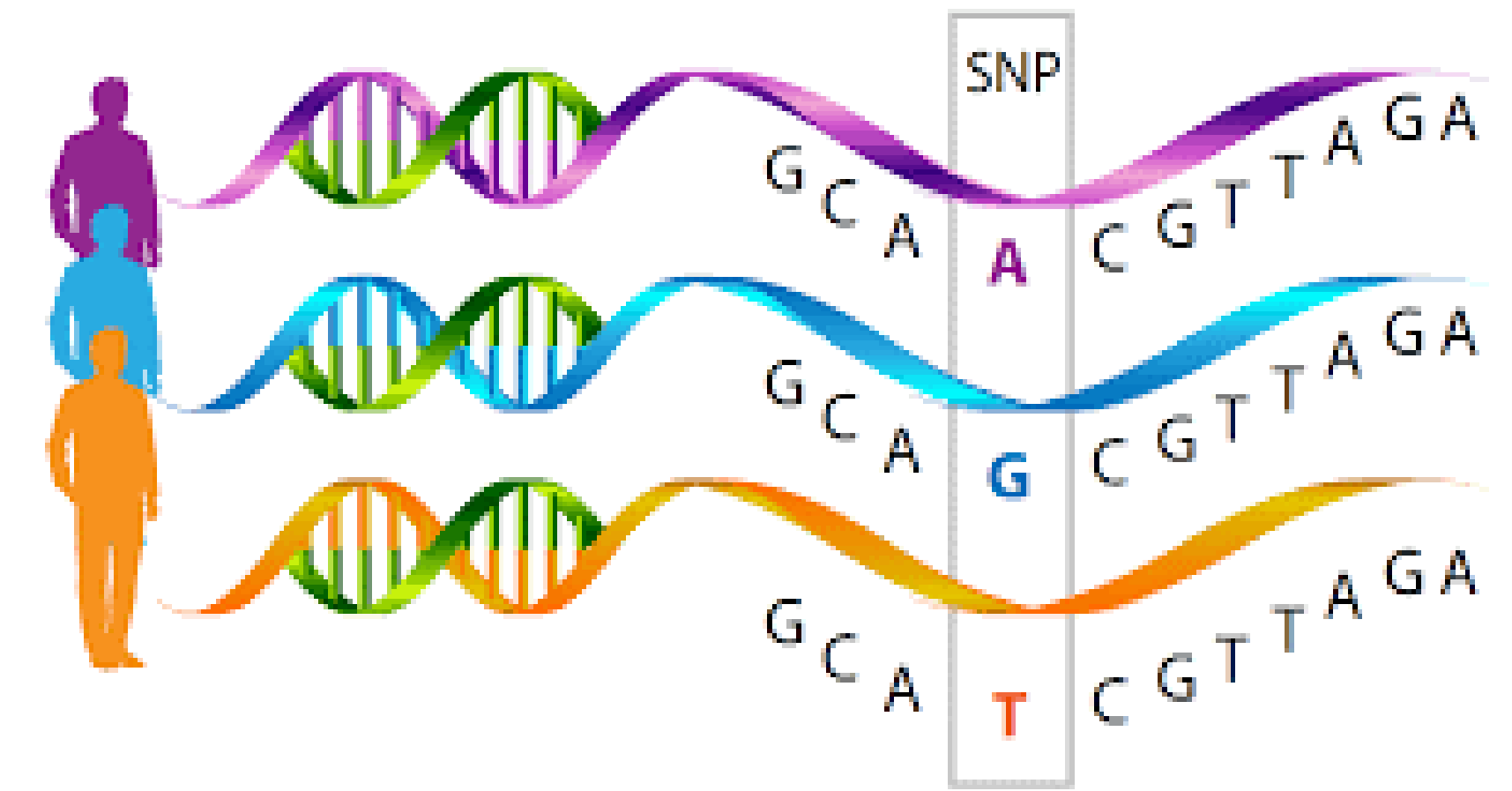
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About the 1000 Genomes Project*

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



Additional settings

Genome version
Output format
Frequency filter

Input flexibility

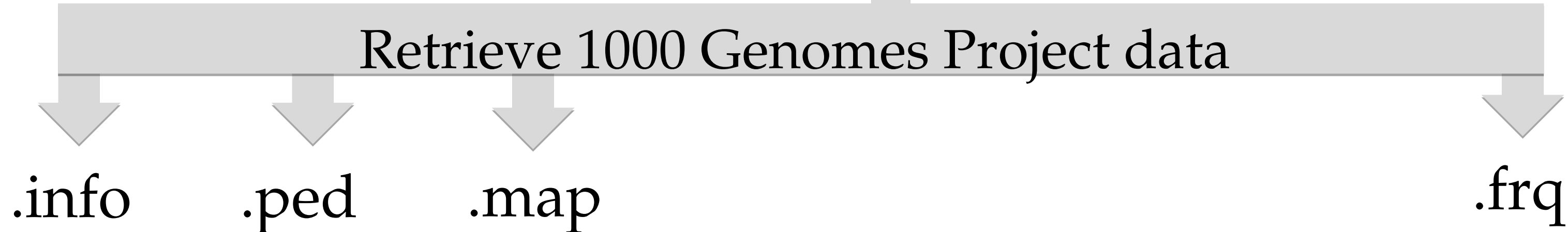
Locus position
Gene
Variant ID

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



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

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/>

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

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