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► **To cite this version:**

S. Limou, A. Taverner, N. Vince, P.-A. Gourraud, C.-A. Winkler. Ferret: a user-friendly tool to extract data from the 1000 Genomes Project. EFI 2017, May 2017, Mannheim, Germany. inserm-02161754

HAL Id: inserm-02161754

<https://inserm.hal.science/inserm-02161754>

Submitted on 21 Jun 2019

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

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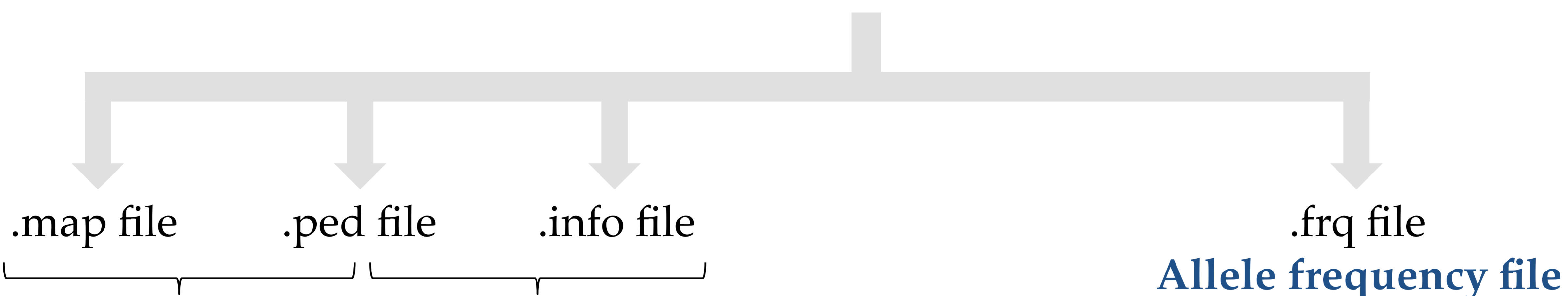
Additional settings:

- Genome version
- Output format
- Frequency filter

Input flexibility:

- Locus position
- Gene
- Variant ID

Retrieve 1000 Genomes Project data
(and optionally Exome Sequencing Project –ESP– data)



PLINK files

can be merged with user's dataset, etc.

HaploView files

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

CHR	VARIANT	POS	A1	A2	CHR	NB_1KG_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
- Accepts input query as locus, gene(s), or variant(s)
- Handles SNPs and indels
- Outputs suitable for well-known pre-existing tools
- Computes allelic frequency for SNPs, indels and CNVs
- Retrieves allelic frequency from ESP

Perspectives:

- Minor GUI improvements
- Grant access to HLA alleles^s

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