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



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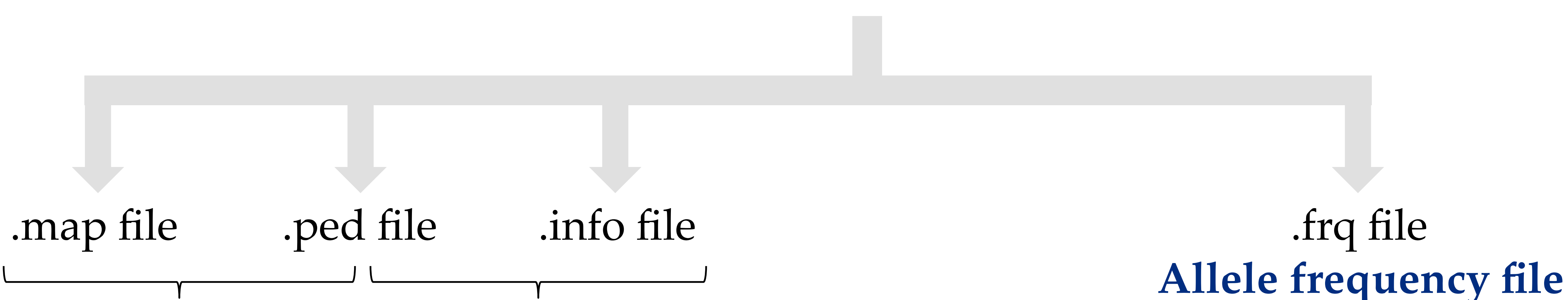
## Additional settings:

- 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	NB_1KG_	1KG_A1	ESP6500_EA	ESP6500_AA
					CHR	_FREQ	_A1_FREQ	_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<sup>#</sup>

- 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
- **Dec. 2017 update:** sync with HaploView + gene borders

## Perspectives (June 2018):

- Accelerate runtime speed
- Grant access to HLA alleles<sup>§</sup>
- Functional annotations

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