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

S. Limou, A. Taverner, N. Vince, P.-A. Gourraud, C.-A. Winkler

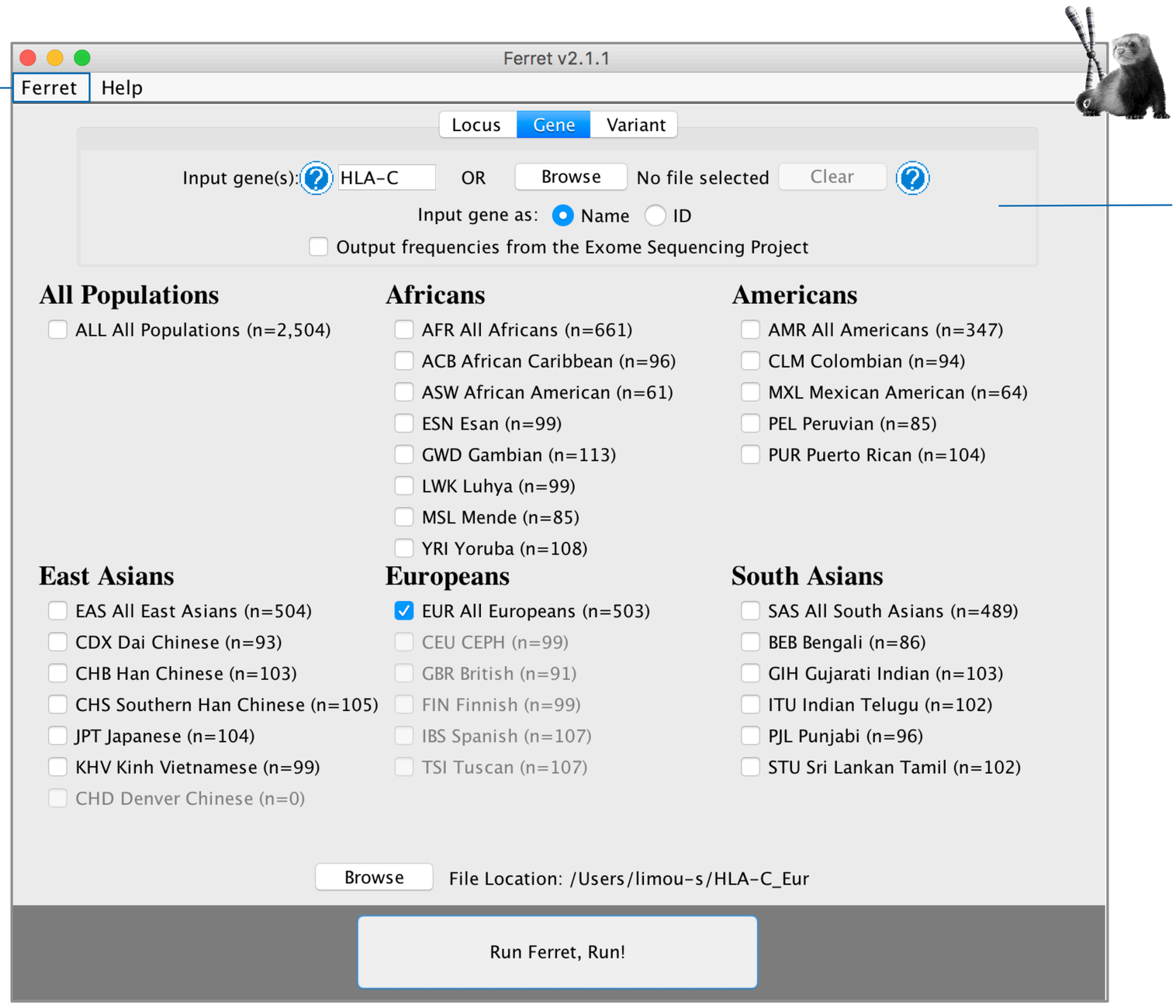
Ferret: a user-friendly tool to extract data from the 1000 Genomes Project

S. Limou[1-4], A. Taverner[4,5], N. Vince[1,2], PA. Gourraud[1,2], and CA. Winkler[4]

[1]Centre de Recherche en Transplantation et Immunologie (CRTI) UMR 1064, INSERM, Nantes, France
[2]Institut de Transplantation Urologie Néphrologie (ITUN), CHU Nantes, Nantes, France
[3]Ecole Centrale de Nantes, Nantes, France
[4]Basic Research Laboratory, NCI/NIH, Leidos Biomedical Research Inc., Frederick MD, USA
[5]Quantitative and Computational Biology program, Princeton University, Princeton NJ, USA

Contact:
ferret@nih.gov

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)

.map file .ped file .info file .frq file

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

HaploView files
data visualization, LD pattern, haplotypes, tagSNP design, 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
- 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[§]

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

[§]Gourraud *et al.* PLoS One 2014