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

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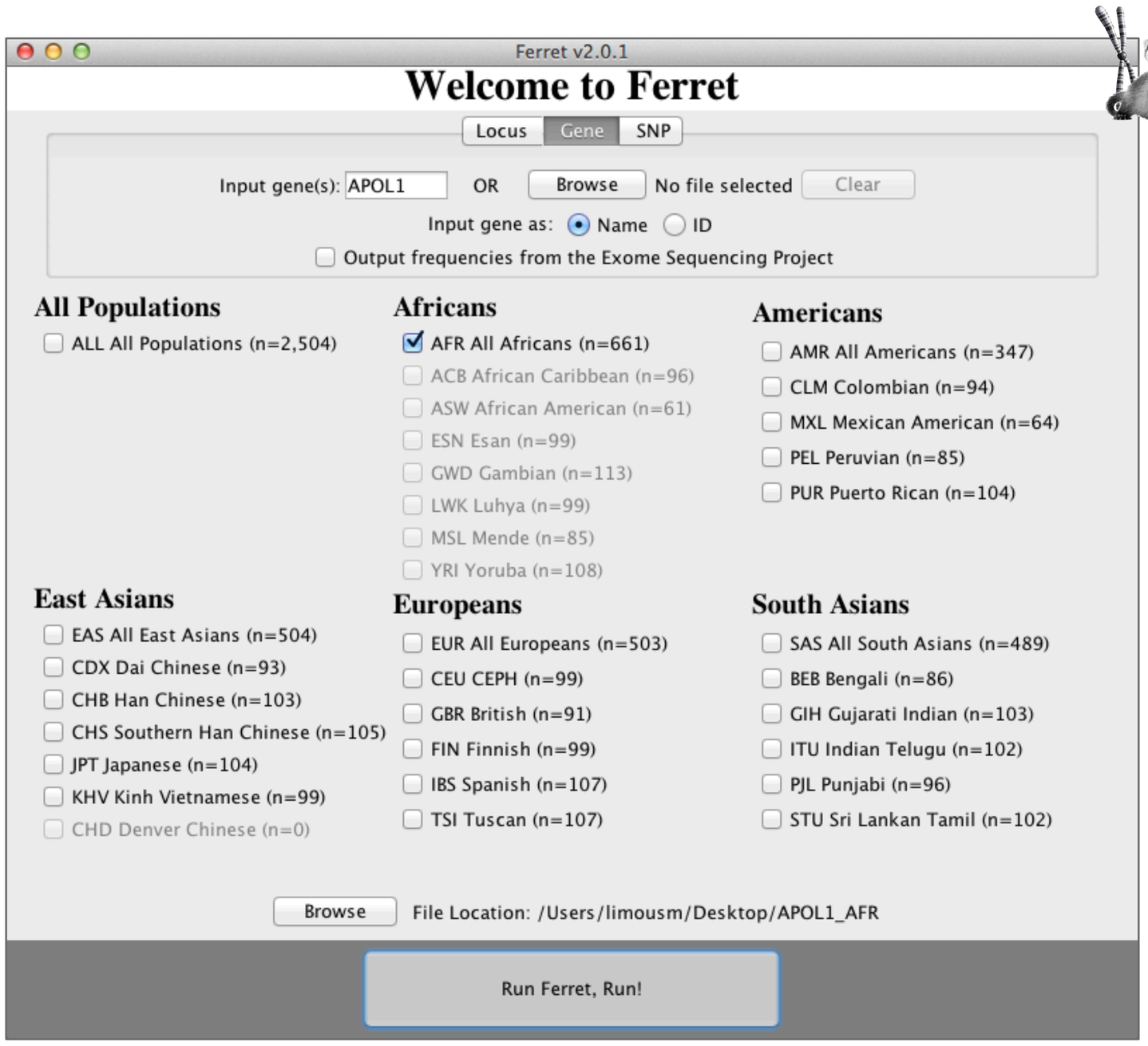

Retrieve 1000 Genomes Project data
(and optionally Exome Sequencing Project –ESP– data)

.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
22	rs6000220	36649966	C	T	1322	0.8517	0.883	0.8418
22	rs182609191	36650106	T	C	1322	1.0	0.9893	0.9986
22	chr22_36650116	36650116	TTAAAA	T	.	.	0.9999	0.9998
22	rs13057901	36650481	T	C	1322	0.8464	.	.
22	rs9610468	36650956	G	A	1322	0.9622	0.815	0.9217
22	indel_rs136158_AT/A	36656652	AT	A	1322	0.6354	.	.

Unique advantages of Ferret

- User-friendly interface
- Accepts input query as locus, gene(s), or SNP(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

Future prospects:
- Minor GUI improvements
- Add a plugin with HaploView

Publicly available at https://ccrod.cancer.gov/confluence/display/BCGC/FERRET+Software

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