# PPP Core Functions
## (VCF-based file Functions)

### VCF-Filter
- Comprehensive Filtering
- Produces VCFs or BEDs

### VCF-Calc
- Basic Statistic Calculator
- Produces STAT Files

### VCF-Split
- Splits Single VCF w/ BED or STAT File
- Creates Loci-VCFs

### VCF-Phase
- Phase VCFs using Beagle or SHAPEIT
- Creates Phased-VCFs

### Four-Gamete Test (FGT)
- Locate sub-regions that pass the FGT
- Creates FGT-compatible VCFs

# PPP BED/STAT Functions

### STAT-Sampler
- Samples STAT files
- Random & Uniform Sampling

### BED Modification Suite
- Edit and filter BED files
- Produces updated BED files

### Loci Filter
- Filters loci (rather than sites)
- Produces filtered BED or STAT files

# PPP Conversion Functions

### VCF to IM Format
- Convert multiple VCFs to single IM formatted file

### Conversion Suite
- Basic conversions between formats
- Connects to most PPP analyses

# PPP Analysis Functions

### IMa3
- Estimate the rooted phylogeny for multiple populations
- Integrate over all possible Isolation-with-Migration models

### Admixture
- Estimate individual ancestries

### Admixture statistics
- Estimate $f_3$, $f_4$, D, & $f_4$-ratio
- Assign populations using a model file

### Linkage Disequalibrium (LD)
- Calculate various LD statistics using PLINK