Population Genomics

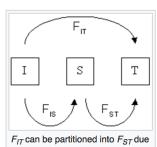**Prof. Roberto Fritsche-Neto**

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Baton Rouge, Jan 30th, 2023

Population parameters

- **Whole population**
- **Markers** (p, q, MAF, Ho, He, F, GD, PIC, EHW)

- **Genotypes** (Heterozygosity / Endogamy)

- **Population** (MAF, He, Ho, GD, PIC)

- **Variability** (Ne, Va, Vd)

$$p = \frac{H + 2D}{2(D + H + R)} \qquad Ho = \frac{H}{(D + H + R)} \qquad F = 1 - \frac{Ho}{2pq}$$

$$q = MAF = 1 - p \qquad He = 2pq$$

$$GD = 1 - \sum_{i=1}^{k} pi^2 \qquad PIC = 1 - \sum_{i=1}^{k} pi^2 - \sum_{i=1}^{k-1} \sum_{j=i+1}^{k} 2pi^2 pj^2$$

- **Subpopulations**
- The same parameters, plus

- **Fixed alleles**

- **Exclusive alleles**

F_{IT} can be partitioned into F_{ST} due to the Wahlund effect and F_{IS} due to inbreeding.

$$\chi^2_{calc} = \sum_{i=1}^{j} \left(\frac{Obs - Exp}{Exp} \right)$$

$$Ne = \frac{1}{2F} \qquad Va = 2pq \quad Vd = 4p^2 q^2$$

- **Inbreeding coefficient** of individual (**I**), subpopulation (**S**), and total (**T**) population

$$Fst = \frac{var(p)}{p(1 - p)} \qquad 1 - Fit = (1 - Fis)(1 - Fst)$$

	snp2	snp5	snp6	snp7	snp8	snp9	snp10
gid 1	1	1	1	1	0	0	0
gid 2	1	1	0	1	0	0	0
gid 4	2	0	0	2	0	0	0
gid 5	2	2	0	2	2	2	2
gid 6	2	2	2	0	2	2	2
gid 7	0	2	1	2	2	2	2
gid 8	0	1	1	1	2	2	2
gid 9	1	2	2	1	2	2	2
gid 10	2	1	2	2	2	1	1