HANDOUT II.2: Interpreting F Statistics

• Two subpopulations: $s = 1, 2$

• Two alleles A and a with frequencies p_s and $q_s = 1 - p_s$ in subpopulation s

• f_s = inbreeding coefficient in subpopulation s

• genotype frequencies in subpopulation s:

$$P_{AA,s} = p_s^2 + f_s p_s q_s$$
$$P_{Aa,s} = \left(1 - f_s\right) 2 p_s q_s = H_s \text{ ("observed" diversity in subpop } s\text{)}$$
$$P_{aa,s} = q_s^2 + f p_s q_s$$

• Consider 6 distinct scenarios, all with $\bar{p} = \left(p_1 + p_2\right)/2 = 0.5$:

subpop 1	subpop 2	F_{IS}	F_{ST}	F_{IT}
$p_1 = 0.5$ $f_1 = 0$	$p_2 = 0.5$ $f_2 = 0$	0	0	0
$p_1 = 0$ $f_1 = 0$	$p_2 = 1$ $f_2 = 0$	0	1	1
$p_1 = 0.2$ $f_1 = 0$	$p_2 = 0.8$ $f_2 = 0$	0	0.36	0.36
$p_1 = 0.2$ $f_1 = 0.1$	$p_2 = 0.8$ $f_2 = 0.1$	0.1	0.36	0.424
$p_1 = 0.2$ $f_1 = 0$	$p_2 = 0.8$ $f_2 = 0.2$	0.1	0.36	0.424
$p_1 = 0.2$ $f_1 = 0.2$	$p_2 = 0.8$ $f_2 = 0$	0.1	0.36	0.424