ANSC 446 Formula sheet for Exam 1

R = net replacement rate $= N_{t+1}/ N_t$
$N_t = R^t N_0$ = population size in generation t

Binomial probability: $Pr(i) = ((N!/(i!j!)) p^i q^j$
Where p = P(A) = probability of event A, q = P(B) = probability of event B, i = number of occurrences of event A, j = number of occurrences of event B

Multinomial probability: $Pr(i,j)=(N!/(i!j!k!))P^i H^j Q^k$

Independent events: P(A or B)= P(A)+P(B) –P(AB)
Mutually exclusive events: P(A or B) = P(A) + P(B)

Bayes' theorem: event A, outcome B; A^C is complement of A

$$P(A|B) = \frac{P(B|A)\,P(A)}{P(B|A)P(A) + P(B|A^C)P(A^C)}$$

Hardy Weinberg principle for two alleles A_1 with frequency p, and A_2 with frequency q, genotypes A_1A_1, A_1A_2, A_2A_2 have frequencies p^2, 2pq, q^2 respectively, and $p^2 + 2pq + q^2 = 1$

Testing for Hardy-Weinberg equilibrium:
O: Observed
E: Expected

$$\chi^2 = \sum_{i=1}^{k} \frac{(O-E)^2}{E}$$

Genotype frequencies for A_1A_1, A_1A_2, A_2A_2 are designated, respectively, P, H, and Q
Relationship between allele and genotype frequencies: $p = P + \frac{1}{2} H$ $q = Q + \frac{1}{2} H$

For multiple alleles, $p_i = P_{ii} + \frac{1}{2} \Sigma P_{ij}$ where $j \neq i$

Expected heterozygosity: $H_E = 1 - \Sigma p_i^2$
Estimated heterozygosity should be corrected for small sample sizes: multiply by 2N/(2N-1)

Maximum H_E = n-1 / n where n is no. alleles
Observed heterozygosity, $H_O = \Sigma N_{ij}/N$ where $i \neq j$

Possible pairwise comparisons: S(S-1)/2

Effective no. of alleles: $A_E = 1/(1-H)$

Bonferroni correction: 1/n where n is number of hypotheses tested.

p distance: s/n where s is segregating sites; n is sequence length

nucleotide diversity π-hat = $(N/(N-1))\Sigma(p_i p_j)\pi_{ij}$ where N is sample size; p is frequency and π is proportion of differences (draw unit square)

Heterozygosity estimates across alleles and loci:

$$\hat{H} = \frac{1}{Nm}\sum_{i=1}^{N}\sum_{j=1}^{m} H_{ij}$$

Allele frequency estimates (draw unit square):

(2) Codominance $\hat{q} = \frac{\frac{1}{2}N_{12} + N_{22}}{N}$

(3) Dominance $\hat{q} = \left(\frac{N_{22}}{N}\right)^{1/2}$

(4) Codominance, X-linked or haplo-diploid $\hat{q}_f = \frac{\frac{1}{2}N_{12} + N_{22}}{N_f}$

$\hat{q}_m = \frac{N_2}{N_m}$

Dominant series, 3 alleles:

$$\hat{p}_1 = 1 - \left(\frac{N_{22}+N_{23}+N_{33}}{N}\right)^{1/2}$$

$$\hat{p}_2 = \left(\frac{N_{22}+N_{23}+N_{33}}{N}\right)^{1/2} - \left(\frac{N_{33}}{N}\right)^{1/2}$$

$$\hat{p}_3 = \left(\frac{N_{33}}{N}\right)^{1/2}$$

Normal distribution: 68% within +/- 1sd of mean; 95% within +/- 1.96 sd of mean. sd = $\sqrt{V_x}$
V_x = variance = $(1/n-1)\Sigma(x_i - \bar{x})^2$

Are 2 allele frequencies different in 2 populations:

$$\chi^2 = \frac{2N\,V(\hat{p})}{\bar{p}\bar{q}}$$

$$V(\hat{p}) = \sum \frac{N_j}{N}\hat{p}_j^2 - \bar{p}^2$$

Nei's standard genetic distance, D = -ln (I) where I is genetic identity:

$$J_{xy} = \sum_{i=1}^{n} p_{i\cdot x} p_{i\cdot y}, \qquad J_x = \sum_{i=1}^{n} p_{i\cdot x}^2, \qquad J_y = \sum_{i=1}^{n} p_{i\cdot y}^2 \qquad I = \frac{J_{xy}}{(J_x J_y)^{1/2}}$$