

Supplementary Digital Content

Expansion of Equation 8

Example CPRA calculation

Expansion of Equation 8

$P_{Negative\ XM} = [(1 - \sum A)(1 - \sum B)(1 - \sum C)(1 - \sum DR)(1 - \sum DQ)]^2$	Eq 8
$= [(1 - \sum B - \sum A + \sum AB)(1 - \sum C)(1 - \sum DR)(1 - \sum DQ)]^2$	
$= [(1 - \sum B - \sum A + \sum AB - \sum C + \sum BC + \sum AC - \sum ABC)(1 - \sum DR)(1 - \sum DQ)]^2$	
$= [(1 - \sum B - \sum A + \sum AB - \sum C + \sum BC + \sum AC - \sum ABC - \sum DR + \sum BDR + \sum ADR - \sum ABDR + \sum CDR - \sum BCDR - \sum ACDR + \sum ABCDR)(1 - \sum DQ)]^2$	
$= [(1 - \sum B - \sum A + \sum AB - \sum C + \sum BC + \sum AC - \sum ABC - \sum DR + \sum BDR + \sum ADR - \sum ABDR + \sum CDR - \sum BCDR - \sum ACDR + \sum ABCDR - \sum DQ + \sum BDQ + \sum ADQ - \sum ABDQ + \sum CDQ - \sum BCDQ - \sum ACDQ + \sum ABCDQ + \sum DRDQ - \sum BDRDQ - \sum ADRDQ + \sum ABDRDQ - \sum CDRDQ + \sum BCDRDQ + \sum ACDRDQ - \sum ABCDRDQ)]^2$	Eq 9

The haplotype frequencies for each of the gene combinations (i.e. one, two, three, four and five gene haplotype frequencies) can then be put into order and then grouped (Eq 10). The group of terms for the one, two, three, four and five gene haplotype frequencies are abbreviated S_1 to S_5 .

$= [1 - \sum A - \sum B - \sum C - \sum DR - \sum DQ + \sum AB + \sum AC + \sum ADR + \sum ADQ + \sum BC + \sum BDR + \sum BDQ + \sum CDR + \sum CDQ + \sum DRDQ - \sum ABC - \sum ABDR - \sum ABDQ - \sum ACDR - \sum ACDQ - \sum ADRDQ - \sum BCDR - \sum BCDQ - \sum BDRDQ - \sum CDRDQ + \sum ABCDR + \sum ABCDQ + \sum ABDRDQ + \sum ACDRDQ + \sum BCDRDQ - \sum ABCDRDQ]^2$	
$= [1 - (\sum A \sum B \sum C \sum DR \sum DQ) + (\sum AB \sum AC \sum ADR \sum ADQ \sum BDR \sum BDQ \sum CDR \sum CDQ \sum DRDQ) - (\sum ABC \sum ABDR \sum ABDQ \sum ACDR \sum ACDQ \sum ADRDQ \sum BCDR \sum BCDQ \sum BDRDQ \sum CDRDQ) + (\sum ABCDR \sum ABCDQ \sum ABDRDQ \sum ACDRDQ \sum BCDRDQ) - (\sum ABCDRDQ)]^2$	
$P_{Negative\ XM} = [1 - \sum S_1 + \sum S_2 - \sum S_3 + \sum S_4 - \sum S_5]^2$	Eq 10

Example CPRA calculation

For transplant candidate XY with unacceptable HLA-antigens: A1, B7, C3, DQ4, DR5:

1) First, we find the equivalent antigens:

A1 is equivalent to itself

B7 is equivalent to itself and B703

C3 is equivalent to itself and C9, C10

DQ5 is equivalent to itself and DQ1

DR4 is equivalent to itself

2) Next, we identify the haplotype frequencies for the antigens for the one, two, three, four and five gene combinations

One gene:

Antigen	Caucasian	African Am	Latino Am	Asian Am
A1	0.16	0.053058	0.058164	0.040948
B7	0.133833	0.083333	0.063069	0.040948
C3	0.052333	0.032974	0.064471	0.086207
C9	0.037333	0.01289	0.020322	0.038793
C10	0.052833	0.044964	0.058164	0.086207
DQ1	0.058167	0.064149	0.039944	0.047414
DQ5	0.139	0.169664	0.119832	0.202586
DR4	0.173333	0.056954	0.225298	0.133621

Two genes (antigen letters omitted):

Antigen1	Antigen2	Caucasian	African Am	Latino Am	Asian Am
1	7	0.008671	0.003239	0.001549	0
1	3	0.00945	0.001413	0.001946	0
1	9	0.006483	0	0	0
1	10	0.010421	0.001924	0.000632	0
1	1	0.00899	0.004817	0.002285	0.00431
1	5	0.024729	0.006499	0.006666	0.008164
1	4	0.015052	0.004279	0.004544	0.002499
7	3	0.00686	0.00055	0.001236	0
7	9	0.00352	0.000357	0	0
7	10	0.005851	0.000775	0.000778	0
7	1	0.007395	0.008728	0.006613	0.00431
7	5	0.020255	0.006402	0.009057	0.012286
7	4	0.014449	0.004567	0.006335	0.003005
1	3	0.004282	0.002697	0.004187	0.0177
1	9	0.002412	0.000484	0.001653	0
1	10	0.002329	0.001243	0.000538	0
5	3	0.006418	0.002258	0.004855	0.007029
5	9	0.005133	0.00335	0.001397	0.010358
5	10	0.006171	0.007059	0	0.00786
4	3	0.009886	0.004946	0.025362	0.017241
4	9	0.006308	0.002204	0.004748	0.007871
4	10	0.009522	0.00502	0.027607	0.002781
4	1	0.009712	0	0	0
4	5	0.026079	0.000512	0.000402	0.00431

Three genes (antigen letters omitted):

Antigen1	Antigen2	Antigen3	Caucasian	African Am	Latino Am	Asian Am
1	7	3	0.000505	0	0.00035	0
1	7	9	0.000174	0	0	0
1	7	10	0	3.00E-04	0	0
1	7	1	0	3.00E-04	0	0
1	7	5	0.001812	0	0	0
1	7	4	0.001592	3.00E-04	0	0
1	1	3	0.000513	0	0	0
1	1	9	0.00062	0	0	0
1	1	10	0.000386	0	0	0
1	5	3	0.000829	0	0	0
1	5	10	0.001723	0.001333	0	0
1	4	3	0.001298	0	0	0
1	4	9	0.000953	0	0	0
1	4	10	0.001052	0	0	0
1	4	1	0.000939	0	0	0
1	4	5	0.004898	3.00E-04	0	0
7	1	3	0.000194	0	0.000385	0
7	1	10	0.000188	3.00E-04	0	0
7	5	3	0.001172	0	0	0.002155
7	5	9	0.000209	0	0	0
7	5	10	0.001327	0.000249	0	0
7	4	3	0.001478	0	0.000365	0
7	4	9	0.000631	0	0	0
7	4	10	0.000339	0	0.000353	0
7	4	1	0.00169	0	0	0
4	1	3	0.001619	0	0	0
4	1	9	5.00E-04	0	0	0

4	1	10	0.001117	0	0	0
4	5	3	0.00099	0.000191	0	0
4	5	9	8.00E-04	0	0	0.002155
4	5	10	0.000838	0	0	0

Four genes (antigen letters omitted):

Antigen1	Antigen2	Antigen3	Antigen4	Caucasian	African Am	Latino Am	Asian Am
1	7	5	3	0.000167	0	0	0
1	7	5	10	0	3.00E-04	0	0
1	7	4	5	0.00027	0	0	0
7	4	1	3	0.000215	0	0	0
7	4	1	10	0.000167	0	0	0
7	4	5	3	0.000212	0	0	0

There are no five gene frequencies

3) Next, we sum the frequencies for each of the one (S_1), two (S_2), three (S_3), and four (S_4) gene combinations above.

	Caucasian	African Am	Latino Am	Asian Am
S1	0.806832	0.517986	0.649264	0.676724
S2	0.230378	0.073323	0.11239	0.109724
S3	0.030386	0.003273	0.001453	0.00431
S4	0.001031	3.00E-04	0	0

4) Next, for each ethnic group we calculate $P_{Positive\ XM}$

	Caucasian	African Am	Latino Am	Asian Am
$P_{Positive\ XM}$	0.8446135	0.694894	0.786858	0.8162249

5) Next, we multiple $P_{Positive\ XM}$ by the national ethnic frequency for each group and sum

	Caucasian	African Am	Latino Am	Asian Am	
$P_{Positive\ XM}$	0.8446135	0.694894	0.786858	0.8162249	
<i>Frequency</i>	0.687	0.147	0.143	0.023	
<i>Product</i>	0. 580	0.102	0.1125	0.01877	0.81369