GWAS Interpretation
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From the class GWAS with data combined between last year and this year, we have the following data for the bitter phenotype with the most significantly correlated SNP (p=6e-5, N=58)

<table>
<thead>
<tr>
<th></th>
<th>CC</th>
<th>CG</th>
<th>GG</th>
<th>NULL</th>
</tr>
</thead>
<tbody>
<tr>
<td>bitter_no</td>
<td>9</td>
<td>4</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>bitter_yes</td>
<td>1</td>
<td>29</td>
<td>14</td>
<td>1</td>
</tr>
</tbody>
</table>

From the genotypes, we can construct the following contingency table:

<table>
<thead>
<tr>
<th>Can taste bitter?</th>
<th>Yes</th>
<th>No</th>
</tr>
</thead>
<tbody>
<tr>
<td>Allele Counts</td>
<td>C</td>
<td>31</td>
</tr>
<tr>
<td></td>
<td>G</td>
<td>57</td>
</tr>
</tbody>
</table>

From this contingency table, we can calculate an odds ratio and likelihood ratio.

Odds Ratio
Definition: odds ratio – a measure of effect size, describing the strength of association or non-independence between two binary data values.

In a case control study, this is the ratio between the fraction with the risk variant versus non-risk variant in the groups of affected versus the controls, i.e. expressed in terms of probabilities conditional on the affection status:

\[ OR = \frac{a \times d}{b \times c} \]

Therefore, the OR is:

\[ OR = \frac{31 \times 6}{22 \times 57} \]
\[ OR = 0.15 \]

Likelihood Ratio

Given a risk allele, what is the likelihood of having the disease?
LR = P(A | Trait) / P(A | No trait)
P(A | Trait) = P(Trait & A ) / P(Trait)

In our example:
P(G | bitter taste) = 57/(57 + 31)
P(G | No trait) = 6/(6+22)

LR = [57/(57 + 31)] / [6/(6+22)]
LR = 3.02

This is the likelihood of tasting bitter given a G allele. What does this mean in terms of GG and GC? You can use P(GG | Trait) / P(GG | No trait) and look at GG versus GC and CC using the genotypes table from last week.

Relative Risk

The relative risk (RR) is the probability that a member of an exposed group will develop a disease relative to the probability that a member of an unexposed group will develop that same disease. This calculation requires that we know something about the overall incidence of the trait.

R_{CC} = P(trait | CC)/population prevalence of trait
R_{CC} = P(affected | CC genotype)/population affected prevalence