

Common Error Messages and Potential Issues

Error messages can often be confusing and not point to the REAL problem. Here is the start to a running list of error messages, I have run across and what exactly they may mean.

Error:

Traceback (most recent call last):

File "/usr/local/bin/SNPweights2.1/calc_snpwt.py", line 188, in <module>
calculate_snpwt()

File "/usr/local/bin/SNPweights2.1/calc_snpwt.py", line 150, in calculate_snpwt
avg_allele_count.append(float(k)/float(n))

ZeroDivisionError: float division by zero

Potential Issue/Resolution:

It is possible that a marker used in the analysis is missing genotypes for all samples.

Error:

Traceback (most recent call last):

File "../src/run_pipeline.1.2.py", line 165, in <module>
k,v = line.split(':')

ValueError: need more than 1 value to unpack

Potential Issue/Resolution:

There are blank lines at the tail of the EIG par files.