**nMAP**

A novel microarray data analysis program (nMAP) is a free script for SNP genotype determination without normalization. This program is available for CEL file data generated using the Affymetrix Genome-Wide Human SNP Array 6.0 platform.

**Requirement**

・python3

・The data of 95% confidence interval for Strength and Log Ratio (These data for 866,970 SNPs are uploaded separately by chromosome.)

**Usage**

python3 nMAP\_genotype\_determination.py <input file> <output file> <minimum cluster size>

**Test sample and Result**

We prepared the test sample (nMAP\_test\_sample.txt). When the minimum cluster size is set as 20 and 160, the genotype result and summary files are uploaded.

・result\_20.txt

・result\_160.txt

・Summury\_Of\_Genotype\_Determination\_Minimum\_Cluster\_Size\_20.txt

・Summury\_Of\_Genotype\_Determination\_Minimum\_Cluster\_Size\_160.txt

**Reference**

**Contact**

Kayoko Yagasaki: k-yagasaki@umin.ac.jp