

## How to calibrate a DNA microarray

**Source code:** calibrate.cpp

Compile the source code with the following one-line command:

```
g++ calibrate.cpp -o calibrate
```

**Input files:** average.txt

**Set R2 cutoff:** 0.98

**Set model:** -freund F or -langmuir L or -linear LN or all

**Output file:** > calibrated\_probes.txt

*Instructions:*

Type the following line command:

```
./calibrate < average.txt -R2 0.98 -freund F -langmuir L > calibrated_probes.txt
```

### Interpreting the output file (calibrated\_probes.txt).

Note: the program picks the best model and ignores the other models.

Column 1: Probe\_identification

Column 2: First coefficient

Column 3: Second coefficient

Column 4: R<sup>2</sup> of the selected model

Column 5: Letter representing model selected: F for freud, L for Langmuir, LN for linear.