



## CopyNumberNoise Documentation

**Description:** Measures noise, calculates QC metrics on copy number data.

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### Summary

This module measures the amount of signal and noise in copy number data. The signal is measured by the standard deviation of arm-level medians. The noise is calculated as the median of the absolute difference of log-2 copy ratios for adjacent probes. A noise threshold value of 0.63 was selected based on looking at the distribution of the noise value from thousands of samples, and selecting a value that separated the main distribution from the outliers. If the noise level is above the noise threshold, the copy number calls are considered unusually noisy, and will probably lead to hyper-segmentation results after segmentation.

### Parameters

Name	Description
input file	The file containing the quality scores computed by the CopyNumberInference module.
output file	The name of the output file. Default: <input.file_basename>.noise.txt

### Output Files

1. <output file>

A file containing the measured signal and noise level along with the recommended noise level threshold.

### Platform Dependencies

**Module type:** SNP Analysis

**CPU type:** any

**OS:** any

**Language:** Python

# GenePattern

## GenePattern Module Version Notes

Date	Version	Description
11/04/12	1	Initial version.