

# Poretools qualdist 0.6.1a1

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Get the qual score composition of a set of FAST5 files

### Quick Start

- To use **Poretools qualdist 0.6.1a1**, import your data in FAST5
- **Resources:** <https://poretools.readthedocs.io/en/latest/>

### Test Data



Test data for this app appears directly in the Discovery Environment in the Data window under *Community Data* -> *iplantcollaborative* -> *example\_data* -> *poretools*

### Input File(s)

Use the following files from the directory above as test input:

- nanopore2\_R9\_MinKNOW\_0.51\_Ecoli\_K12\_MG1655\_lambda\_1004\_1\_ch106\_read73\_strand.fast5
- nanopore2\_R9\_MinKNOW\_0.51\_Ecoli\_K12\_MG1655\_lambda\_1004\_1\_ch112\_read42883\_strand.fast5
- nanopore2\_R9\_MinKNOW\_0.51\_Ecoli\_K12\_MG1655\_lambda\_2258\_1\_ch118\_read1032\_strand.fast5

### Parameters Used in App

When the app is run in the Discovery Environment, use the following parameters with the above input file(s) to get the output provided in the next section below.

- Use these parameters within the DE app interface:
  - Set the output file name to '**qualdist\_output.txt**'
  - Leave all other parameters as default

### Output File(s)

Expect **qualdist\_output.txt** as output.

### Tool Source for App

- <https://poretools.readthedocs.io/en/latest/>