

List contents of FAST5 file(s)

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This App runs hdf5lib 1.10.0

- See information about contents of FAST5 files. Can be used to determine whether the FAST5 file contains raw and/or sequence data


App Creator

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Quick Start

- Need FAST5 files about which you would like information
- **Resources:** <https://support.hdfgroup.org/HDF5/doc/RM/Tools.html#Tools-Ls>

Test Data

 Test data for this app appears directly in the Discovery Environment in the Data window under *Community Data* -> *iplantcollaborative* -> *example_data* -> *nanopolish* -> *extract*

Input File(s)

Use the LomanLabz_PC_Ecoli_K12_R7.3_2549_1_ch8_file30_strand.fast5 files from the nanopolish directory for an example run.

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 section below.

Leave all parameters as default.

Output File(s)

The app will produce a single output file that contains this information:

Analyses Group
Sequences Group
UniqueGlobalKey Group

From this you can tell that the FAST5 file contains sequences (and thus has been basecalled).

Tool Source for App

- <https://support.hdfgroup.org/HDF5/doc/RM/Tools.html#Tools-Ls>