

Debarcer: De-Barcoding and Error Correction

Paul Krzyzanowski
Ontario Institute for Cancer Research
Toronto, Ontario, Canada
paul.krzyzanowski@oicr.on.ca

April 7, 2016

1 Location

You can download the latest version of Debarcer from GitHub:

<https://github.com/oicr-gsi/debarcer/releases>

Once the archive has been extracted to a suitable directory, you will need to copy the `config_files/debarcer.dotfile` to `~/debarcer` as this configuration file is used throughout the pipeline.

The directory containing `runDebarcer.sh` must be in your PATH

2 Using Debarcer

2.1 Requirements

- Ensure you have 16G memory available
- Note that a bam file for the current alignment will be generated in your work directory
- Currently, you need to have access to 'qsub' through SGE or OGS

2.2 Running the package

Once `runDebarcer.sh` is in your \$PATH, either manually or using modules, you can run it as follows:

```
$ runDebarcer.sh -r -f [FASTQFILE] -n [SAMPLENAME] -o [OUTPUTDIR]
```

Using modules is handy for running via qsub:

```
qsub -N "Debarcer" -b y -cwd -l h_vmem=16g "module load debarcer/dev; \  
runDebarcer.sh -r -f [FASTQFILE] -n [SAMPLENAME] -o [OUTPUTDIR]"
```

There is a small test set of data included with the distribution:

```
runDebarcer.sh -r -f [DebarcerRoot]/demodata/Sample_Test.R1.fastq.gz -n Sample_Test -o ./testresults
```

This should take a few minutes to run.

2.3 Automating Analyses

To help automate this whole process, there is a script in the debarcer 'tools' directory that will create a results hierarchy based on a directory of fastq files and write the appropriate run scripts:

```
mkdir -p ResultsRoot\fastqs
cd ResultsRoot\fastqs
find [location of the the fastq files] -name "*fastq.gz" -exec ln -s {} \;
cd ..
svn export file:///u/pkrzyzanowski/svn/repo/projects/EAC/ \
molecular_barcoding/trunk/debarcer/tools/populateWorkDirectory.pl
# Make any necessary changes to populateWorkDirectory.pl
perl populateWorkDirectory.pl ./fastqs
# Setup any debarcer.conf files in the results directories, if needed
./relaunchAllDebarcers.sh
```

3 Output

The output contains several different types of files.

Package results files with a tar command that wraps up the files found by:

```
find . -name *.pdf -o -name "*bamPositionComposition*" -o \
-name "*UID*" -o -name "*SummaryStatistics.txt" -o -name "*log"
```

i.e.

```
tar cvfz results_file_name.tar.gz `[find command goes in backticks]`
```

4 Miscellaneous

Requirements: Consensus calling script needs at least 16G memory.

4.1 Revisions

- 0.3.0: April 7, 2016.
- 0.2.0: July 27, 2015. Svn Revision: 347.