

Installation instructions for tools used in largeSV_pipeline.sh on MacOSX
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BreakDancer

<https://github.com/genome/breakdancer>

Installed as outlined in INSTALL.md

Additional steps:

Added breakdancer/build/bin path to bash profile

Copy contents of perl/ into breakdancer/build/bin

Perl modules required, installed using cpanm and add module directory to PERL5LIB path in bash profile:

Statistics::Description

Bio::Perl

GD::Graphics::histogram

Crest

<http://www.stjude.com/research/site/lab/zhang>

Installed as outlined in README

Additional steps:

Added path to Crest directory to bash profile

Dependencies:

BLAT: <http://genomic-identity.wikidot.com/install-blat>

CAP3: <http://seq.cs.iastate.edu/cap3.html>

Perl modules required:

Bio::DB::Sam

Pindel

<http://gmt.genome.wustl.edu/packages/pindel/install.html>

Additional steps:

Issues with Mac version of gcc (error: fatal error omp.h not found). Updated gcc using macports (<http://www.ficksworkshop.com/blog/post/installing-gcc-on-mac>)

Error when attempting to run: dyld: Library not loaded: /path/to/location/lib/libhts.2.dylib

To fix: <https://github.com/genome/pindel/blob/master/FAQ>

```
cd pindel
```

```
git clone https://github.com/samtools/htslib into pindel directory
```

```
cd htslib
```

```
make
```

```
sudo make install
```

```
cd ..
```

```
./INSTALL htslib
```

Added path to pindel directory to bash profile

Delly

<https://github.com/dellytools/delly>

Install as outlined in README.md

Additional steps:

Error during install: gcc: error: unrecognized command line option '-rdynamic'
Due to MacOSx, to fix, edit line 31 in delly/src/bcftools/makefile:

```
DYNAMIC_FLAGS = -rdynamic
```

to:

```
DYNAMIC_FLAGS = -Wl,-export_dynamic
```

(as per: <https://sourceforge.net/p/samtools/mailman/message/34699333/>)

Error when attempting to run: dyld: Library not loaded: libboost_iostreams.dylib

To fix, added the following to bash profile:

```
export DYLD_FALLBACK_LIBRARY_PATH=/Path/To/delly/src/modular-bost/  
stage/lib:/Path/To/delly/src/htslib/:$DYLD_FALLBACK_LIBRARY_PATH
```

* note that due to system integrity protection (SIP) in Macs when invoking .sh scripts, all DYLD_* environment variables are purged. A work around was adding the above export in the .sh script.

Additional tools:

BWA: <https://github.com/lh3/bwa.git>

SeqKit: <http://bioinf.shenwei.me/seqkit/download/>

Picard: <http://broadinstitute.github.io/picard/>

BLAT suite: <https://genome.ucsc.edu/goldenpath/help/blatSpec.html>

bcftools: <https://samtools.github.io/bcftools/>