Consed/Phred/Phrap

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Install Phrap
Install Phred
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Installed on kremlin (Matz Lab), genomes (Jansen Lab), ceres (Wilke Lab), and phylocluster. Licensed only for academic use, meaning don't use it to process someone else's data. Just process your own.

To use consed/phred/phrap you need to put this in your ~/.bashrc:

```bash
CONSED_HOME=/share/apps/genome
PHRED_PARAMETER_FILE=$CONSED_HOME/lib/phredpar.dat

export CONSED_HOME
export PHRED_PARAMETER_FILE
PATH=$CONSED_HOME/bin:$PATH
export PATH
```

The path /share/apps/genome is a symlink to the current version which you can display with the command “ls -l /share/apps/genome”. If you use this path in the above variable settings, then you can be sure that you are always using the updated version of consed/phred/phrap. It is possible to use an older version, by providing the specific genome17 directory; however, this is not recommended as the upgrade notices typically say to immediately stop using older versions.

Docs are installed in /share/apps/genome/doc

To use the test files provided by consed (see the file README.txt in the $CONSED_HOME/doc) make a test copy with

```bash
cp -r /share/apps/genome17/test consed-test
```

It's been reported that (some?) ACE files may need to have an entry like this put at the end which points them to the right phd directory:

```bash
WA{
 phdBall newbler 080416:144002
  ../phdball_dir/phd.ball.1
}
```

Apparently this can be cut and paste as is, and just adjusted to have the right phd path.

BLOSUM50/62, PAM250, mat50, and mat70 files needed by swat (and others?) are installed in $CONSED_HOME/lib/swat.