## Tutorial for Cortex and Bubbleparse

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#### 1 Introduction

This tutorial will show you how to download the Cortex and Bubbleparse sources, how to compile the code, and how to find the SNPs between two different accessions of *Arabidopsis thaliana*.

Because of memory and processing requirements, we recommend that this tutorial is carried out on a cluster instead of a desktop computer.

## 2 Download and compile sources

- 1. Download Cortex Con sources from https://sourceforge.net/projects/cortexassembler/files/cortex\_con/.
- 2. Download Bubbleparse sources from https://github.com/richardmleggett/bubbleparse.
- 3. Copy bubbleparse.c into the src/util directory of the Cortex sources.
- 4. To build Cortex, change into the cortex\_con build directory (the one containing Makefile and the src directories) and type:

```
make MAXK=31 cortex_bub
```

Or, if building on Mac OS X:

make MAXK=31 MAC=1 cortex\_bub

- 5. Assuming there are no compilation errors, a file called cortex\_con\_31 will appear in the cortex\_con/bin directory. You might like to copy this to another directory where you store tools.
- 6. Now to build Bubbleparse, type:

```
make MAXK=31 bubbleparse
```

Or, if building on Mac OS X:

make MAXK=31 MAC=1 bubbleparse

7. A file called bubbleparse\_31 will appear in the cortex\_con/bin directory.

## 3 Download Arabidopsis reads

- 1. For this tutorial, we will use the Col-0 and Tsu-1 accessions of Arabidopsis thaliana.
- 2. Create a data directory somewhere to store the reads and cortex files.
- Download two files of Col-0 reads from http://www.ebi.ac.uk/ena/data/view/ SRX000702. You will end up with two files called SRR013327.fastq and SRR013328.fastq.
- Download five files of Tsu-1 reads from http://www.ebi.ac.uk/ena/data/view/ SRX000704. You will end up with files called SRR013334.fastq, SRR013335.fastq, SRR013336.fastq, SRR013337.fastq, SRR013338.fastq.

## 4 Merge reads and make CTX files

1. Within the data directory, create a file of files for the Col-0 reads. Copy the following into a text file called col0reads.txt:

```
SRR013327.fastq 0
SRR013328.fastq 0
```

2. Now create a file of files for the Tsu-1 reads. Copy the following into a text file called tsu1reads.txt:

```
SRR013334.fastq 0
SRR013335.fastq 0
SRR013336.fastq 0
SRR013337.fastq 0
SRR013338.fastq 0
```

3. We'll now create a single Cortex CTX file which includes all the Col-0 reads. Use the following command line:

```
cortex_bub_31 -k 21 -n 24 -b 55 -t fastq -c 100 -s 1 -i colOreads.txt -o colO.ctx -l colO.log
```

To execute this command, Cortex will require approximately 32Gb of RAM, so you may need to specify this as a parameter to your cluster's job submission system. On our cluster, this command took around 90 minutes to complete. On successful completion, Cortex will write a CTX file called colo.ctx and a log file called colo.log.

4. Now for the Tsu-1 reads. Use the following command line:

```
cortex_bub_31 -k 21 -n 24 -b 75 -t fastq -c 100 -s 1 -i tsu1reads.txt -o tsu1.ctx -l tsu1.log
```

To execute this command, Cortex will require approximately 32Gb of RAM. On our cluster, it took around 2 hours to complete. On successful completion, Cortex will write a CTX file called tsu1.ctx and a log file called tsu1.log.

### 5 Find bubbles

1. Create a new file of files called colotsulfiles.txt containing the following text:

```
col0.ctx 0
tsu1.ctx 1
```

2. To run Cortex bubble finding, type the following:

To execute this command, Cortex will require approximately 48Gb of RAM. On our cluster, it took around 3 hours to complete.

 Cortex will write two files: col0tsu1output.fasta (containing contigs representing paths through bubbles) and col0tsu1output.coverage (containing the coverage of those paths).

### 6 Rank SNPs

1. We need to create an options file for bubbleparse. Create a new file called bpoptions.txt containing the following text:

```
EXPECTEDCOVERAGE "0,10,100,0"
EXPECTEDCOVERAGE "1,10,100,0"
MINIMUMCONTIGSIZE "100"
```

2. Now create a file of files called allfiles.txt containing ALL the input files, as follows:

```
SRR013327.fastq 0
SRR013328.fastq 0
SRR013334.fastq 1
SRR013335.fastq 1
SRR013336.fastq 1
SRR013337.fastq 1
SRR013338.fastq 1
```

3. Now to run bubbleparse, type:

This should create a ranked table called table.txt and the same data represented in comma separated format called table.csv.

#### 7 Further information

For further information, please refer to the Cortex and Bubbleparse manuals.

Please report any bugs or problems with the bubble finding options in Cortex, or with bubbleparse, to richard.leggett@tgac.ac.uk. General problems with Cortex should be referred to the appropriate authors.