Contig Generation Experiment

March 6, 2013

Different contig sizes

Run on x200

Contig length 100

```
#!/usr/bin/env bash
#SBATCH -A b2010008
#SBATCH -p node
#SBATCH -t 4:00:00

# This script generates contigs to be used for classification
# evaluation. The output is saved in order to be reused for all
# experiments.

#DATA_PATH=$HOME"/glob/data"
DATA_PATH=$HOME"/repos/DATA"

#RESULTS_PATH=$HOME"/glob/results/2013-01-18"
RESULTS_PATH=$HOME"/repos/DATA/contigs"

echo "Generate contigs" >&2
time ../programs/generate_contigs.py $DATA_PATH"/
   parsed_gen_2_2_complete_old.txt" -o $RESULTS_PATH"/
   contigs_2_2_old_100_100.fna" -d $DATA_PATH"/
   reference_genomes_ncbi" -c 100 -p "genomes" --contig_min_length
   100 --contig_max_length 100
```

Contig length 1000

```
#!/usr/bin/env bash
#SBATCH -A b2010008
#SBATCH -p node
#SBATCH -t 4:00:00

# This script generates contigs to be used for classification
# evaluation. The output is saved in order to be reused for all
# experiments.

#DATA_PATH=$HOME"/glob/data"
DATA_PATH=$HOME"/repos/DATA"

#RESULTS_PATH=$HOME"/glob/results/2013-01-18"
RESULTS_PATH=$HOME"/repos/DATA/contigs"

echo "Generate contigs" >&2
time ../programs/generate_contigs.py $DATA_PATH"/
    parsed_gen_2_2_complete_old.txt" -o $RESULTS_PATH"/
    contigs_2_2_old_100_1000.fna" -d $DATA_PATH"/
    reference_genomes_ncbi" -c 100 -p "genomes" --contig_min_length
    1000 --contig_max_length 1000
```

Contig length of 10000

```
#!/usr/bin/env bash
#SBATCH -A b2010008
#SBATCH -p node
#SBATCH -t 4:00:00

# This script generates contigs to be used for classification
# evaluation. The output is saved in order to be reused for all
# experiments.

#DATA_PATH=$HOME"/glob/data"
DATA_PATH=$HOME"/repos/DATA"

#RESULTS_PATH=$HOME"/glob/results/2013-01-18"
RESULTS_PATH=$HOME"/repos/DATA/contigs"

echo "Generate contigs" >&2
time ../programs/generate_contigs.py $DATA_PATH"/
    parsed_gen_2_2_complete_old.txt" -o $RESULTS_PATH"/
```

```
contigs_2_2_old_100_10000.fna" -d $DATA_PATH"/
reference_genomes_ncbi" -c 100 -p "genomes" --contig_min_length
10000 --contig_max_length 10000
```