Preliminary comb experiment

# Experiment Description

1. I ran a total of 6 gphocs experiments. The experiments ran 5 million iterations. The experiments are -
   1. Dataset **M3.15.migAC\_0\_4**. Hypotheses -
      1. **AB\_C\_\_C->A**
      2. **BC\_A\_\_C->A**
      3. **AC\_B\_\_C->A**
   2. Dataset **M3.15.migAC\_0\_0**. Hypotheses -
      1. **AB\_C**
      2. **BC\_A**
      3. **AC\_B**
2. Using results from gphocs, I ran model-compare on AB\_C, BC\_A & AC\_B and on AB\_C\_\_C->A & BC\_A\_\_C->A
   1. Configuration files are located in */home/rvisbord/experiments/comb/M3.15.migAC\_0\_[0/4]/${hypothesis}*

# Gphocs

## Results

### Summary\*

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Hypothesis | theta\_A | theta\_B | theta\_C | theta\_XY’ | theta\_root | tau\_XY’ | tau\_root | Data-ld-ln | Gene-ld-ln | Full-ld-ln |
| AB\_C | 9.5 | 11.5 | 9.5 | 8.8 | 10.1 | 1.6 | 3.0 | -1359 | 145575 | -2863691 |
| BC\_A | 10.6 | 11.6 | 7.1 | 2.1 | 10.1 | 2.32 | 2.32 | -1359 | 145575 | -2863664 |
| AC\_B | 10.5 | 11.2 | 7.2 | 1.7 | 10.0 | 2.26 | 2.26 | -1359 | 145520 | -2863600 |
| AB\_C\_\_C->A |  |  |  |  |  |  |  |  |  |  |
| BC\_A\_\_C->A |  |  |  |  |  |  |  |  |  |  |
| AC\_B\_\_C->A |  |  |  |  |  |  |  |  |  |  |

\* - Results are in “eye-average” over the last 10 results

### Interpretation

Weird stuff:

* Both the true hypothesis (AB\_C) and the wrong ones (BC\_A & AC\_B) have the same data+gene+full likelihoods
* BC\_A & AC\_B have different theta\_XY though they are symmetrical

Good stuff:

* For BC\_A & AC\_B
  + they have almost the same trace (since they are symmetrical)
  + tau\_XY & tau\_root are equal (as expected)
* For AB\_C, values are very close to ‘truth’

### Raw results –

#### Original files:

/home/rvisbord/experiments/comb/M3.15.migAC\_0\_[0/4]/${hypothesis}/trace.tsv

#### Snippet:

AC\_B

Sample theta\_A theta\_B theta\_C theta\_AC theta\_root tau\_AC tau\_root Data-ld-ln Full-ld-ln Gene-ld-ln

4999995 10.39634 11.24638 7.16221 1.68289 10.08330 2.27428 2.27452 -1359.039678 -2863600.189069 145520.833627

4999996 10.34917 11.19536 7.12971 1.77245 10.03756 2.26396 2.26420 -1358.908352 -2863738.301458 145921.597384

4999997 10.68635 11.19536 7.12971 1.80724 10.03756 2.26396 2.26420 -1358.925909 -2863772.669893 145920.851376

4999998 10.68635 11.19536 7.47499 1.87144 10.03756 2.26396 2.26420 -1359.003123 -2863783.671594 145777.425589

4999999 10.21614 11.51500 7.45582 1.76935 10.14816 2.25816 2.25839 -1359.050238 -2863744.304768 145643.828281

BC\_A

Sample theta\_A theta\_B theta\_C theta\_BC theta\_root tau\_BC tau\_root Data-ld-ln Full-ld-ln Gene-ld-ln

4999995 10.65729 11.70889 7.16504 2.12546 10.14681 2.32425 2.32654 -1359.044552 -2863664.741501 145575.636555

4999996 10.61946 11.66732 7.36585 2.19020 10.11079 2.31600 2.31828 -1358.995852 -2863670.085667 145678.382191

4999997 10.65460 11.88088 7.06992 2.12139 10.14425 2.32367 2.32596 -1359.045128 -2863789.986374 145699.729725

4999998 10.64199 11.25901 7.06156 2.00413 10.13224 2.32092 2.32320 -1359.110683 -2863855.987895 145634.620906

4999999 10.67683 11.29586 7.08467 2.06405 10.16541 2.32852 2.33081 -1359.102381 -2863896.928962 145692.166110

AB\_C

Sample theta\_A theta\_B theta\_C theta\_AB theta\_root tau\_AB tau\_root Data-ld-ln Full-ld-ln Gene-ld-ln

4999995 9.49329 11.71581 9.46280 8.88409 10.19555 1.64334 3.02913 -1359.204874 -2863691.699557 145281.950625

4999996 9.85363 12.14321 9.69041 8.84994 10.15636 1.62726 3.01748 -1359.069844 -2863678.725911 145539.038495

4999997 9.70770 11.70090 9.68201 8.84227 10.14756 1.63625 3.01331 -1359.073895 -2863662.316527 145514.527069

4999998 9.42307 11.66589 9.65304 8.81581 10.11720 1.62322 2.97973 -1358.916581 -2863596.761425 145763.599184

4999999 9.42307 12.08332 9.88139 8.81581 10.11720 1.63279 3.00718 -1359.141781 -2863694.387519 145410.826323

# Mcref

## Results

### Summary\*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Hypothesis | Reference | Hm mean | Hm bootstrap | Rbf mean | Rbf bootstrap |
| AB\_C | Root comb | 2864116 | 13.8 | -47505 | 50 |
| BC\_A | Root comb | 2864182 | 16 | -61491 | 91 |
| AC\_B | Root comb | 2864151 | 6.8 | -61501 | 131 |
| AB\_C\_\_C->A |  |  |  |  |  |
| BC\_A\_\_C->A |  |  |  |  |  |
| AC\_B\_\_C->A |  |  |  |  |  |

## Interpretation

* Using either metric (hm or rbf), **we expect the better hypothesis to have a smaller value**. This being the case, we note that Rbf is horribly wrong about the correct model. Hm is correct, but its bootstrap is very weak, suggesting a non-significant result

### Raw results –

*cd /home/rvisbord/dev/modelcompare/experiments/comb/M3.15.migAC\_0\_0 && cat AB\_C/results/1494101193.9951937/summary.txt && echo && cat AC\_B/results/1494185574.5172143/summary.txt && echo && cat BC\_A/results/1494188028.6657648/summary.txt*

Summary:

Simulation: BC\_A

Comb: root | Comb Leaves: A,B,C | Populations: | Migration Bands:

hm\_data\_likelihood: {'ln\_mean': 2864182.8433766379, 'bootstrap': 16.194011154792808}

rbf\_ratio: {'ln\_mean': -61491.872659856475, 'bootstrap': 91.731035092537084}

Summary:

Simulation: AC\_B

Comb: root | Comb Leaves: A,B,C | Populations: | Migration Bands:

hm\_data\_likelihood: {'bootstrap': 6.8886662448515068, 'ln\_mean': 2864151.7907585669}

rbf\_ratio: {'bootstrap': 131.13229424652025, 'ln\_mean': -61501.157342367449}

Summary:

Simulation: AB\_C

Comb: root | Comb Leaves: A,B,C | Populations: | Migration Bands:

hm\_data\_likelihood: {'bootstrap': 13.855344828999932, 'ln\_mean': 2864116.9354259325}

rbf\_ratio: {'bootstrap': 50.256581039701224, 'ln\_mean': -47505.953562562121}