H3N2 kappa 0.1

indicator

58 : 88.463

169: 136.486

274: 89.047\*

542: 80.979\*

564: 163.317

571: 108.977\*

587: 144.063\*

590: 131.53

598: 56.698

613: 113.43

619: 154.412

632: 166.314

637: 128.549

692: 89.384

749: 89.323\*

774: 150.705

776: 140.913

88.5, 136.486, 89.047, 80.979, 163.317, 108.977, 144.063, 131.5, 56.698,

89.38, ...

In general, the MCMC mixing is adequate across replicates.

MCMC $I\_i$ is our main parameter of interest.

In each replicate, (802-17) nodes have ESS >1000).

In the first replicate (used for our analysis), 17 / 802 nodes have lower ESS, but still between 56 – 166.314 .

The estimated proportion is usually very similar across all runs…

Maybe summarize the range or boxplot… and cite github

Mu:

note: I tried to compute the Euclidean distance of the 2 dimensions:

/Users/charles/Documents/researchData/clustering/forManuscript-organized/h3n2/kappa0\_1/C3b-mds0\_1/EuclideanStat.log

537-2 126.162 (double) -> 1700

544-2 155.431 (double) -> 1601

574-1 94.772 ->106

598-1 191.765 ->915

598-2 186.637 (double)

748-1 189.851 ->770

Euclidean

Q. use combine?

The ESS of the Mu is also very good.

In each of the replicate, Among 803 nodes giving rise to 1606 parameters to be estimated, the vast majority of the ESS of $I\_i$ is high in all replicates (majority of them >1000).

5 of them are worse performing ones, but still with ESS between 94.8 – 189.9.

The main reason for this relatively lower ESS is because some of these nodes constantly flip about the horizontal line (y axis; origin of the 2nd dimension)

Because it occurs relatively less, ESS is less… but this is not a problem because the most important relationship to preserved is the relatively distance between one node to another… not whether it is diverging + or – by the same magnitude

ultimately causing also the second dimension of the antigenic location of a group of viruses to be affected

virusLocs:

low ESS , but all > 58.. only in the second dimension where occasional switching

from one side to another is difficult the either positive or negative is okay...

almost all > 100, many > 500.

serumLocs

in general mixes better than virusLocs, with some has ESS >60 antigenic dimension 2.. .same

Similar across runs

Other parameters, across all runs…

posterior: 719.982 - 1488.621

prior: 1112-2055

aglikelihoodtreecluster: 472.3 - 697

K: 439.9 - 1454

serum drift: 469.1 - 1140

probActiveNode: 838-2062

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H1N1:

kappa: 0.3

**posterior**: 1127 - 2030.663

prior: 1323 - 2251

aglikelihoodtreecluster: 1488-2074

K: 1280 - 2202

serum drift: 873 - 1174

probActiveNode: 1687 - 2251

indicators:

mostly > 10000, 2 of them = 110, 163

virusloc:

all > 100,

serum:

all > 100, quick glance majority > 1000

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For H1n1 kappa = 0.3,

Similar observations..

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