

Task 1.1

Use the exhaustive search inference algorithm to find the best scoring model.

```
log posterior (marginal) likelihood $mLL: -239.9944
Error probabilities alpha and beta: 0.15 0.07
network structure regularization parameter $lambda (default: 0): 0
Prior weight $delta for assigning E-genes to virtual S-gene 'null' (default
: 1): 1
67 selected E-genes:
--> rel : 30 attached E-genes
--> key : 30 attached E-genes
--> tak : 9 attached E-genes
--> mkk4hep : 28 attached E-genes
--> null : 1 attached E-genes
```

Task 1.2

To which S genes are the E genes most likely connected to?

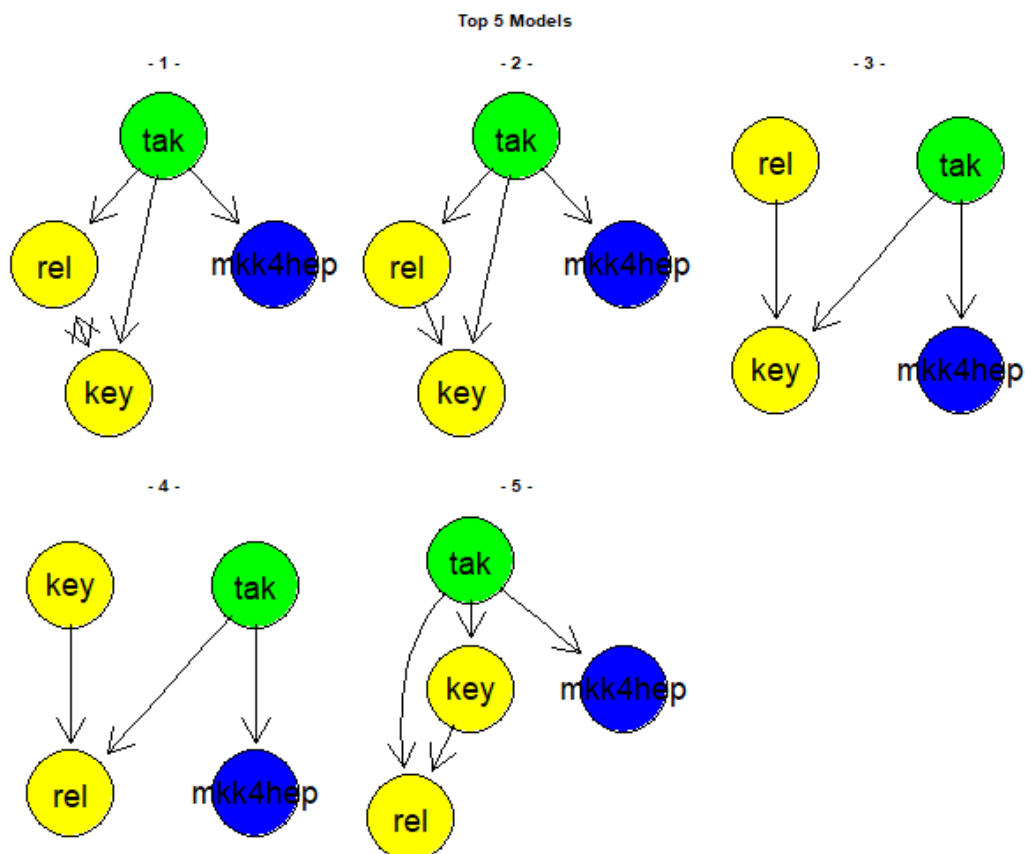
AttA	rel
CG8177	rel
KrT95D	tak
CG6725	mkk4hep
RhoL	mkk4hep
CG1141	mkk4hep
puc	mkk4hep
CG5775	mkk4hep
wun	mkk4hep
CG10076	rel
CG5835	mkk4hep
CG1225	rel
CG5346	mkk4hep
Su(dx)	tak
CG8008	rel
CecA1	rel
CecA2	rel
CecB	rel
CecC	rel
Gli	mkk4hep
Dro	rel
Mtk	rel
EG:95B7.1	mkk4hep
Nhe3	mkk4hep
CG11709	rel
CG12703	tak
CG13780	mkk4hep
CG13117	mkk4hep
CG11066	mkk4hep
CG15900	mkk4hep
CG8046	rel
CG8805	mkk4hep
CG3884	mkk4hep
CG6701	rel
CG12505	rel
CG18372	rel
CG10794	rel
CG15678	rel
CG4859	mkk4hep
CG13893	mkk4hep
CG18214	tak
CG9208	mkk4hep

CG4437	rel
CG6449	mkk4hep
CG14567	rel
CG7629	rel
CG7142	rel
CG7956	tak
CG3348	tak
GH13327	rel
HL1913.	rel
LD32282	tak
Rel	rel
loco	tak
CG7816	rel
CG7778	rel
CG14704	rel
shn	rel
CG13503	mkk4hep
Rac2	mkk4hep
Fim	mkk4hep
AnnIX	mkk4hep
lama	tak
CG17723	mkk4hep
CG11798	rel
Jra	mkk4hep
CG4057	mkk4hep
CG11141	null

Task 1.3

How do the top 5 exhaustive models differ?

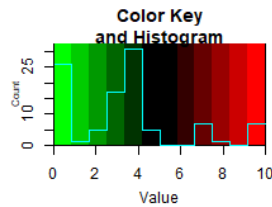
Model 1,2 and 5 are nearly similar but the double edges between key and rel are in 2 and 5 are only single edges. Model 3,4 are also equal with changed positions of rel and key.



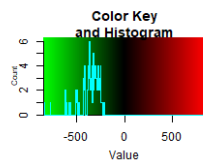
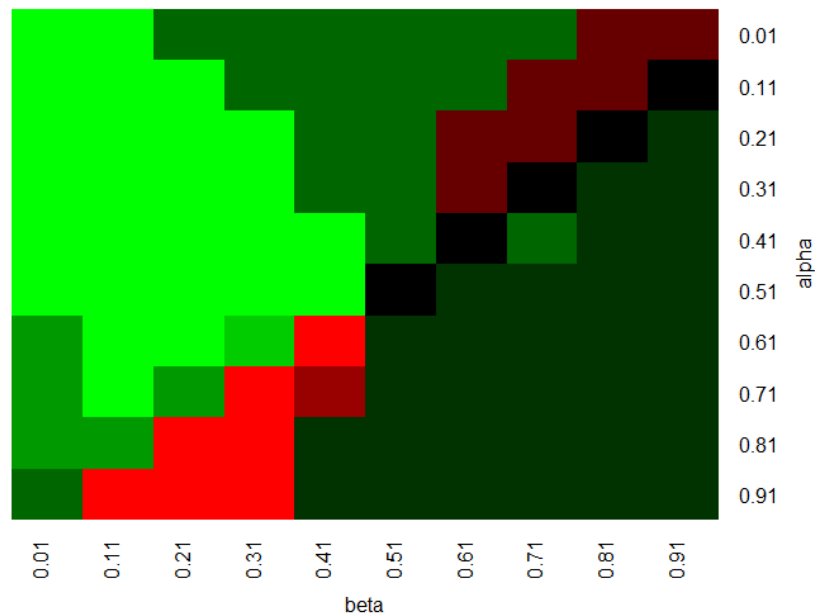
Task 1.4

Evaluate stability for different choices of alpha, beta.

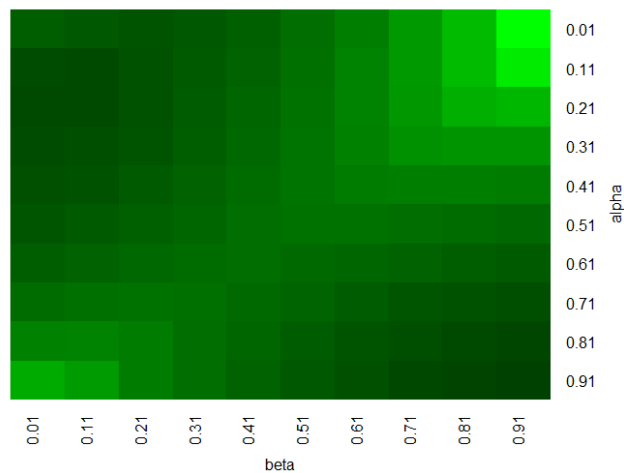
We test different choices for the alpha and beta error and count the differences to the model (alpha and beta: 0.15 0.07) with the calculated errors. The number of changes increase with the difference in the alpha and beta errors. The error rates allow a bigger verity in the model.



of Changes in Models



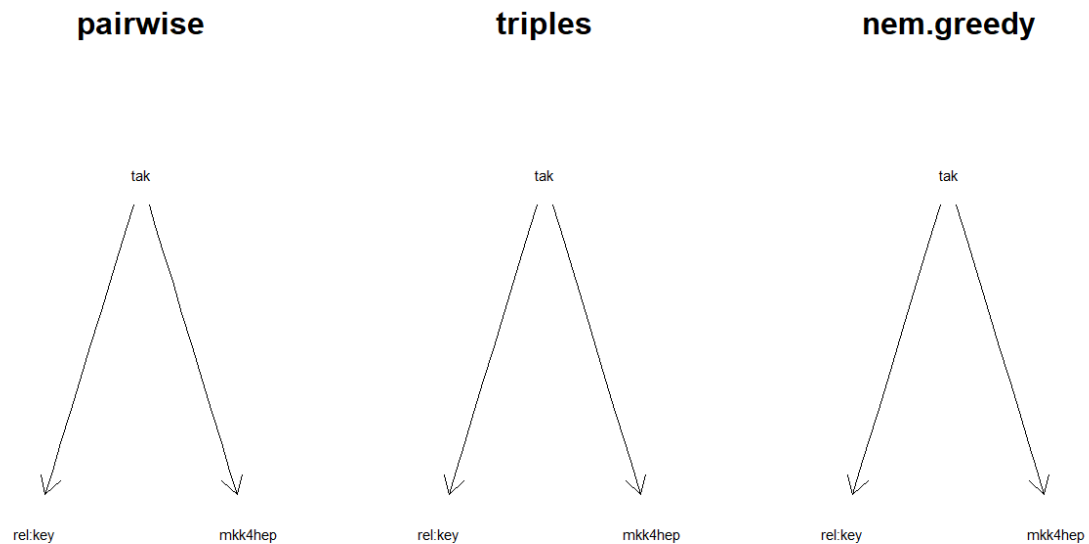
mLL of the best Models



In the histogram, there of the mLL are better scores darker. Thus, medium changes in alpha and beta error will lead to a model with a lower probability while big changes in both will lead to the original quality.

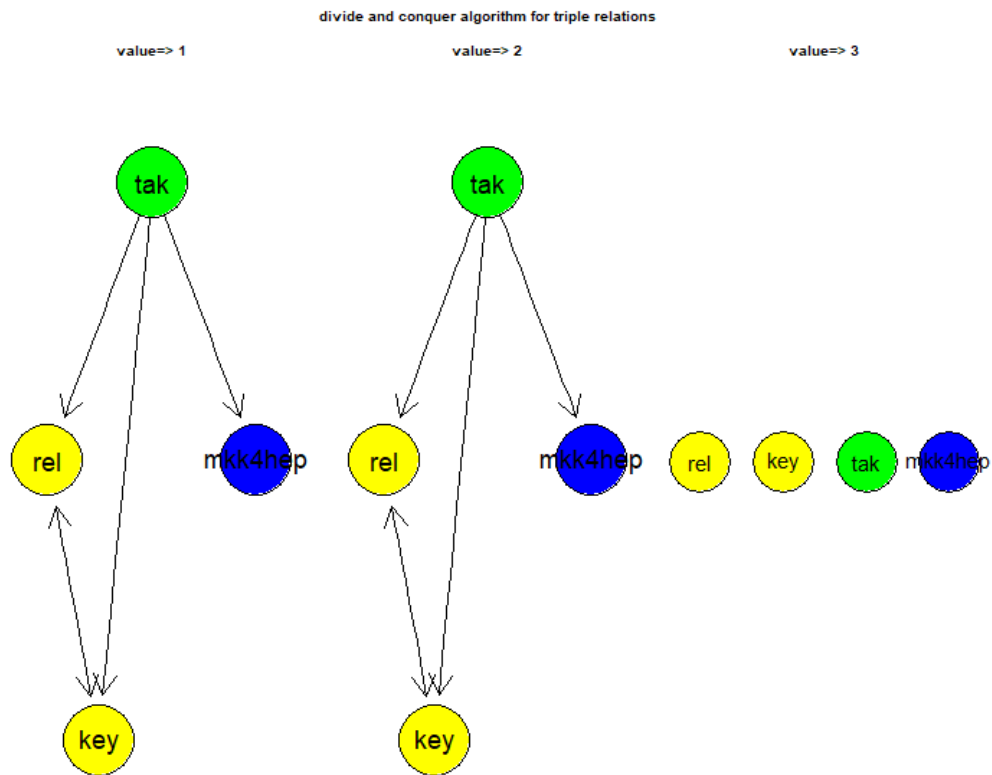
Task 2.1

The four algorithms end up with the same graph. The exhaustive search, triples, nem.greedy have the same mLL of -239.5778 the pairwise has a mLL of only -256. The selected genes are equal.

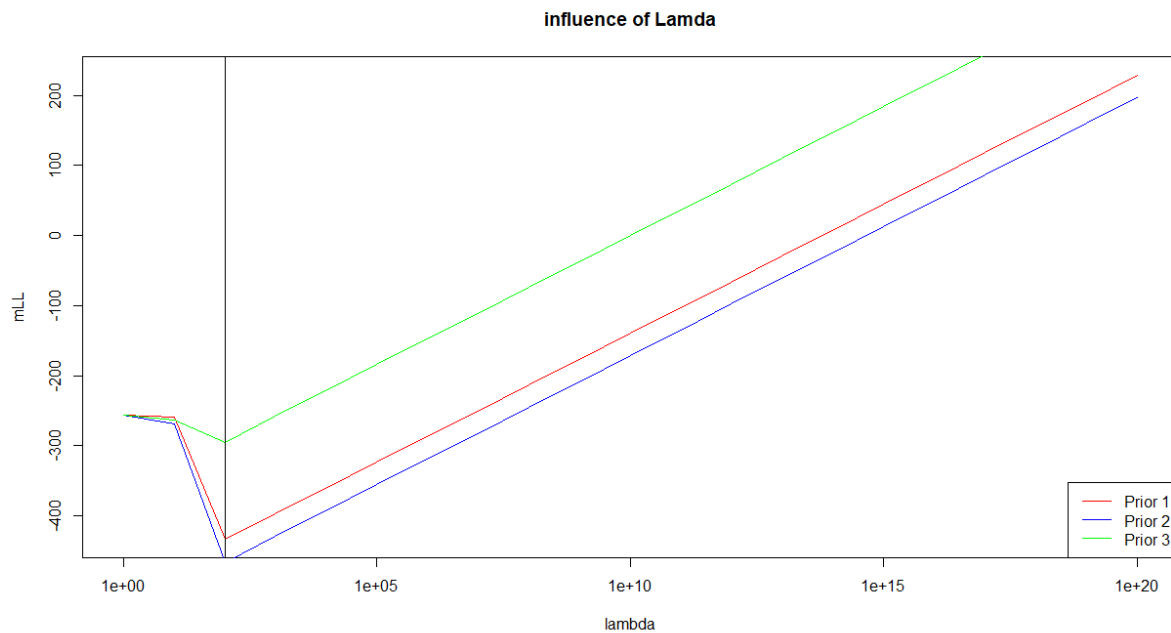


Task 2.2

For cutoff values 1,2 the model is still the same as in the tasks before. For a cutoff of at least 3 edges the graph will be fully separated.



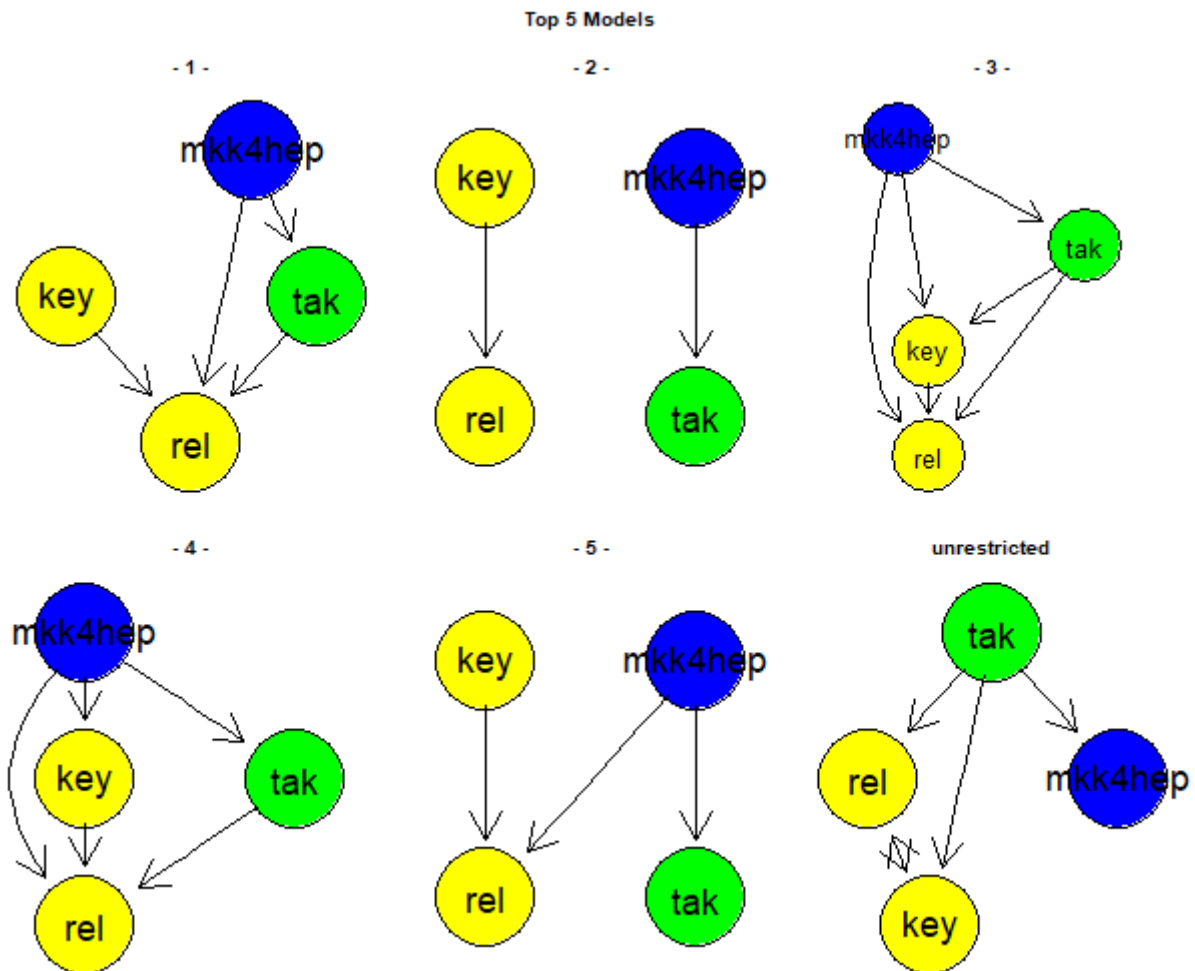
Task 3



A bigger lambda will decrease the mLL until a lambda of 100. It stepwise forces the graph to equal the prior. For lambda, bigger than 100 it seems that the mLL only depends on lambda and the data has not longer a influence to the model.

Task 4

We assume that the given directed edges contradict the edges in the opposite direction. There are 29 models which includes mkk4hep -> tak and key -> rel and excludes tak -> mkk4hep and rel -> key. We decide to just plot again the five best models.



The models look all different. But 1,3,4 are nearly equal and 2,5 similar. Model 1 is most like the unrestricted model.

Task 5

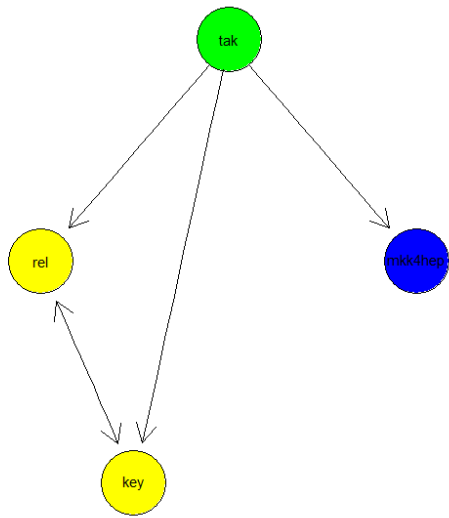
For the Bootstrapfunctions we use 1000 iterations and a threshold of 0.95.

edge_properbility

source	target	rel	key	tak	mkk4hep
rel	rel	0.000	0.997	0.017	0.001
key	key	0.988	0.000	0.017	0.001
tak	tak	0.957	0.965	0.000	0.982
mkk4hep	mkk4hep	0.029	0.038	0.059	0.000

The models are equal to the best exhaustive search model

own bootstrap model



buildin bootstrap model

