

## DEALING WITH DIFFERENT TOPOLOGIES (ML tree -Fig. 2- and Bayesian Inference -)

We employed the following commands to test the two topologies arisen by the two phylogenetic approaches and comprising the three sequences:

```
MrBayes > execute archivo.nex
```

```
MrBayes > constraint clustering = 20_HAV_Malaga 4_HAV_Malaga MF805872  
(identical to RIVM- HAV16- 090)
```

```
MrBayes> constraint noclustering negative = 20_HAV_Malaga 4_HAV_Malaga  
MF805872 (identical to RIVM- HAV16- 090)
```

**Hypothesis 1:** topology considering the clustering among 20 and 4 HAV Malaga strains with the original Dutch HAV strain RIVM-HAV16- 090

Run	Arithmetic mean	Harmonic mean
1	-3441.03	-3467.47
2	-3437.91	-3470.62
TOTAL	-3438.56	-3469.97

**Hypothesis 2:** topology considering an independent clustering among 20 and 4 HAV Malaga strains, and the original Dutch HAV strain RIVM-HAV16- 090

Run	Arithmetic mean	Harmonic mean
1	-3435.67	-3475.03
2	-3439.09	-3467.36
TOTAL	-3436.33	-3474.34

$2\log(B_{12}) = 2 * (-3469.97 - (-3474.34)) = 8.74$ , where  $B_{12}$  is the Bayes factor.  
According to the following table:

$2\log_e(B_{12})$	$B_{12}$	Evidence against $H_2$
0 to 2	1 to 3	Not worth more than a bare mention
2 to 6	3 to 20	Positive
6 to 10	20 to 150	Strong
> 10	> 150	Very strong

Interpretation of the Bayes factor ( $B_{12}$ ). Based on (Kass and Raftery, 1995).

Therefore, there is strong evidence against the second hypothesis (compared to  $H_1$ ), that is, against a separate branch among local strains (20 HAV Malaga and 4 HAV Malaga) and the Dutch strain.