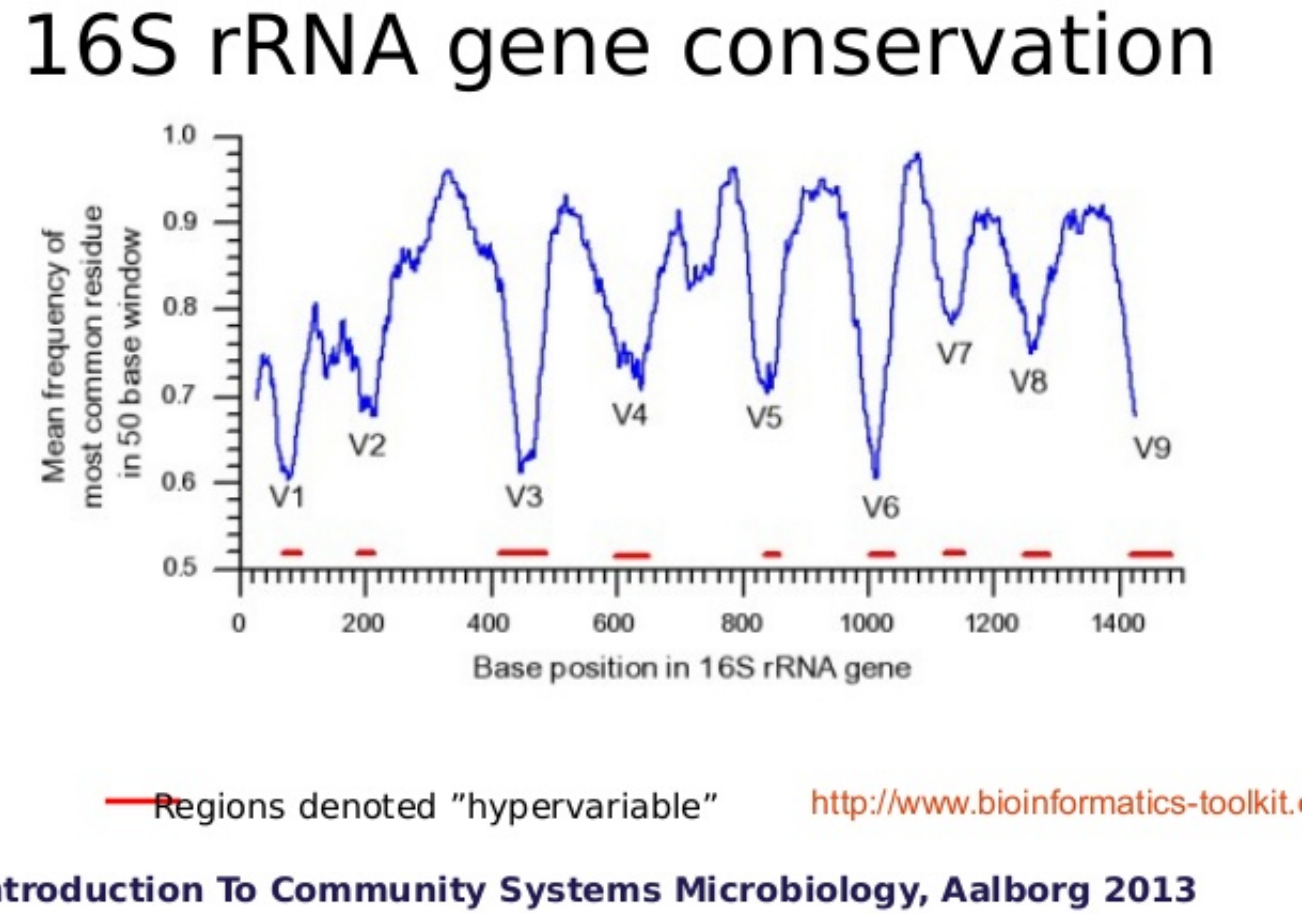
# Primers and history for 16S amplification

## The regions

Basically, there are 9 variable regions in the 16S rRNA, and the variablity inside this regions is a temporal map of the different phylogenies of bacteria types.

Here we can see in an image the regions distributed:




In marine studies, the usual hipervariable regions used have been between the V1 and the V4 (even though intial studies used clonning, getting the complete gene!).

Along the years of using this gene as a marker to establish the community structure, various attempts have been done in marine science. Let's see some of them.

## The primers

- **8F/1492R**: The initial one, used by covering the complete region, and resulting in an amplicon of almost 1485 bp. Right now, with the technologies that we use (and Illumina) this is far too big.
- **341F/907R**: This one was used for performing DDGEs .
- **8::12F/519R**: A length of 445.
- **515/806R**: EMP. Earth Microbiome Project.
- **358F/806RB**: These are the ones that were used in Blanes amplification. By Herleman and Appil et al.
- **515F/926R**: Parada et al. Used in Malaspina, and the ones developed by Furhman et al. They have Cyanobacteria bias, presenting sobreestimations of abundance.