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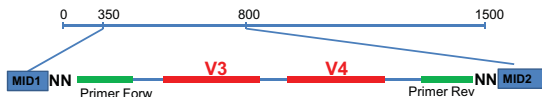
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From high throughput 454 GS FLX data analysis process of 16S RNA gene sequences using barcoding to bacterial community exploration

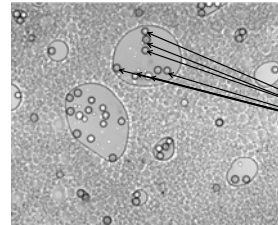
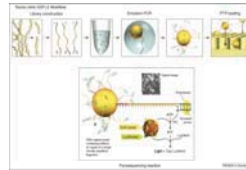
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The bacterial community of 97 cow rumen samples was explored using a 440 bp V3-V4 16S RNA amplicon. Each sample is barcoded using a couple of MIDs.



Since sequences might be randomly over represented within a run when sequencing is done using the Roche 454 pyrosequencing platform (Gomez-Alvarez et al. 2009), random nucleotide dimers were introduced in the sequence.



Eight beads instead of one

Pipeline

Rawdata : 889 029 reads



16Spyrocleaner (python)

- Length > 150 nt
- Sequence with one N are removed
- Homopolymere > 10 are removed

-19.7%

MOTHUR (<http://www.mothur.org>)

- Alignment (Silva base)
- Distance matrix
- Assigning sequences to OTU



NNpyrocleaner (python)

- Remove over represented sequences (-0.24%)

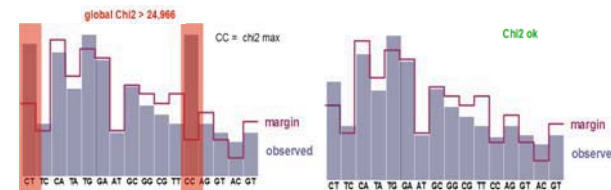
MOTHUR (<http://www.mothur.org>)

- Alignment
- Bad aligned seq were removed (-1%)
- Distance matrix
- Assigning sequences to OTU

706 155 reads
7249 reads/sample

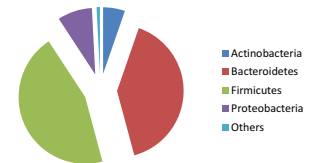
- Taxonomic assignment (bootstrap 60%)

- 868 OTU /sample (cutoff 0.1)
- Coverage of 95.9%
- Diversity indices



Taxonomy levels	Groups identified	% Affiliation
Phylum	15	100
Class	24	98
Order	51	95
Family	114	84
Genus	293	50

1.4% of reads not affiliated to any phylum were removed.

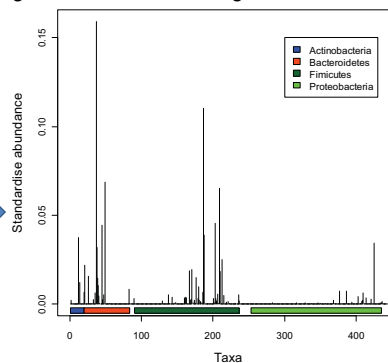


Mean distribution of major bacterial groups at the phylum level

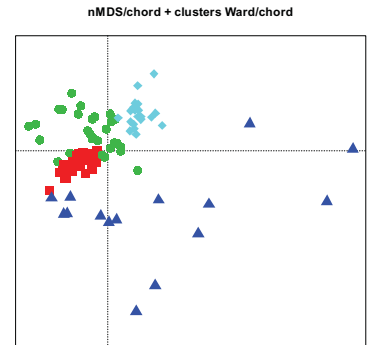
Analysis

From the 97 samples, we identified 430 different taxa leading to a taxonomic ecological matrix. The resulting data set can be used for ordination and clustering analysis (after normalisation) using R software.

X - matrix	Taxon 1	Taxon 2	Taxon 3	Taxon 7	Taxon 8	Taxon 9	...	Taxon 430
Ruminal fluid 1	0	0	0	0	57	0	...	0
Ruminal fluid 2	1	0	3	0	53	0	...	0
Ruminal fluid 3	0	0	0	0	4	0	...	0
Ruminal fluid 4	0	0	1	0	92	0	...	0
Ruminal fluid 5	0	0	1	0	25	0	...	0
Ruminal fluid 6	0	2	3	2	49	0	...	0
...
Ruminal fluid 97	0	0	4	0	75	1	...	0



Plot of the mean of the standardise abundance of each taxa upon the 97 samples



Ordination plot (nMDS) of the 97 samples and classification in 4 clusters