

Webinar #6 CompBioMed: Innovations on medical student training

5 December 2018



The webinar will start at 3pm CET



Speaker: **Prof. Andrea Townsend-Nicholson** (UCL)

Moderator: Ben Czaja (UvA)







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Welcome!



Speaker: Prof. Andrea Townsend-Nicholson (UCL) Moderator: Ben Czaja (UvA)





Poll time!

Poll number 1



Personalised Medicine

Taking advantage of supercomputers and the post-genomic era of biomedical science



Personalised Medicine

Virtual Human



Metagenomics and Microbiomes

What are they?



"Metagenomics is the study of genetic material recovered directly from environmental samples."

Wikipedia

Microbiota – community of microbes (found in or on multicellular organisms)

Microbiome – genetic material within a microbiota

From Skin to Metagenomics: You and Your Microbiome

Identifying microbes on human skin based on the sequences of their genetic material

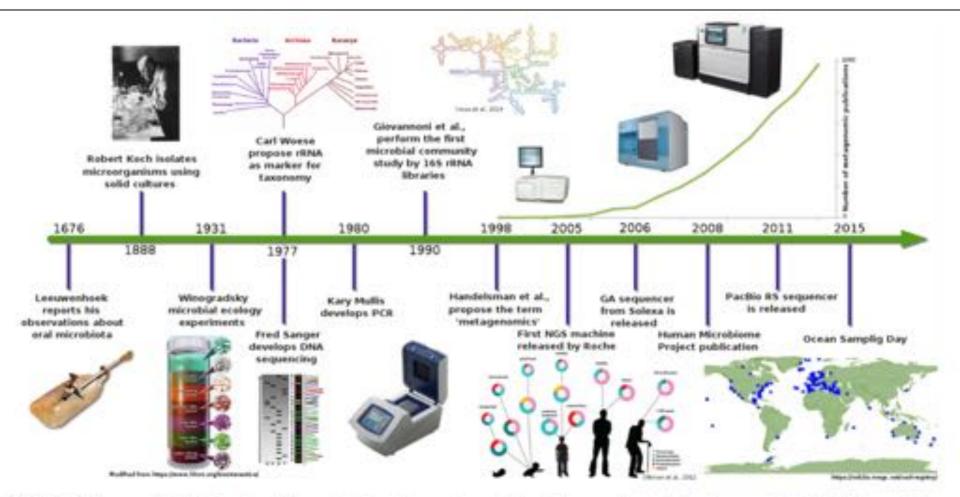
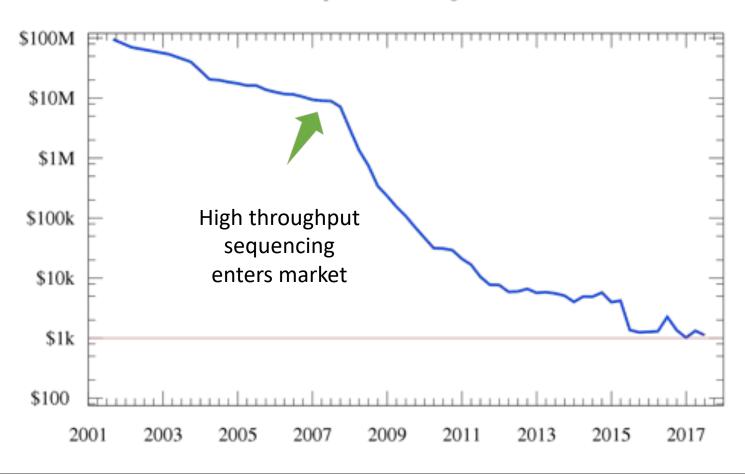


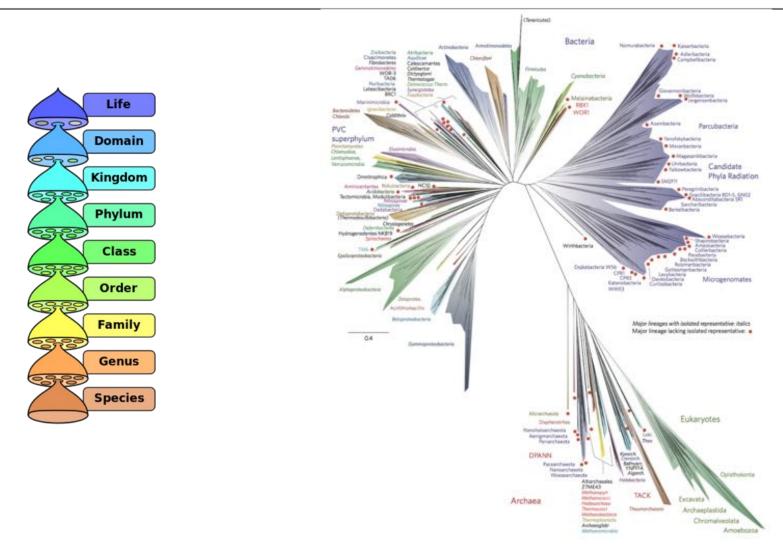
FIGURE 1 | Metagenomics timeline and milestones. Timeline showing advances in microbial communities studies from Leeuwenhoek to NGS (Ottman et al., 2012; Yarza et al., 2014).



Cost to sequence a human genome (USD)



Wikipedia



Wikipedia

Hug, et al. Nat Microbiol. 2016 Apr 11;1:16048. doi: 10.1038/nmicrobiol.2016.48.



Skin Microbiomes

How do we characterize them?

Purify
Amplify
Marker gene sequencing
DNA sequence analysis



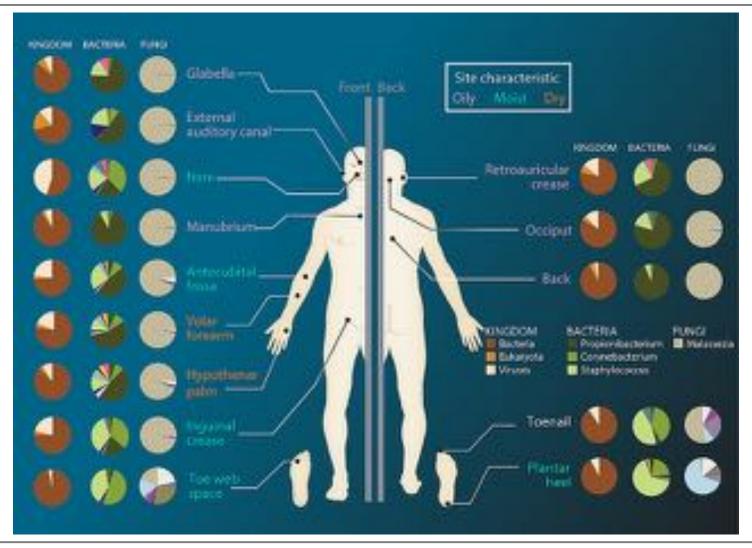
Microbiomes

Purify





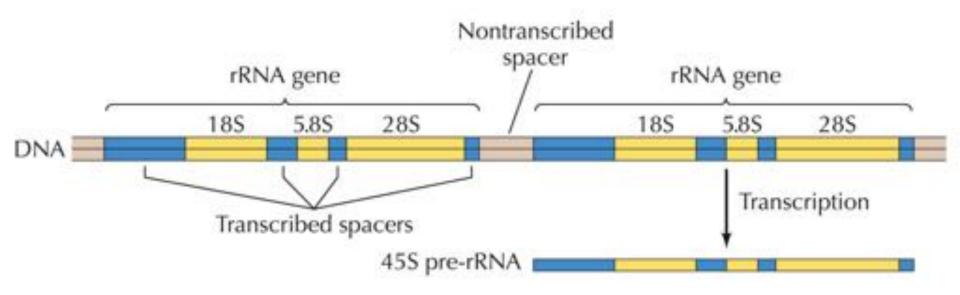




National Human Genome Research Institute (NHGRI)



Small subunit (SSU rRNA)		Large subunit (LSU rRNA)		Туре
30S (16S: 1542 nt)	50S (5S: 120 nt, 23S: 2906 nt)	70S	prokaryotic	
nt ^[4])	406 (185 :	60S (5S: 121 nt,[1] 5.8S: 156 nt,[2] 28S: 5070 nt[3])	808	eukaryotic
	406 (18S:	60S (5S: 121 nt,[1] 5.8S: 156 nt,[2] 28S: 5070 nt[3])	80S	eukaryotic

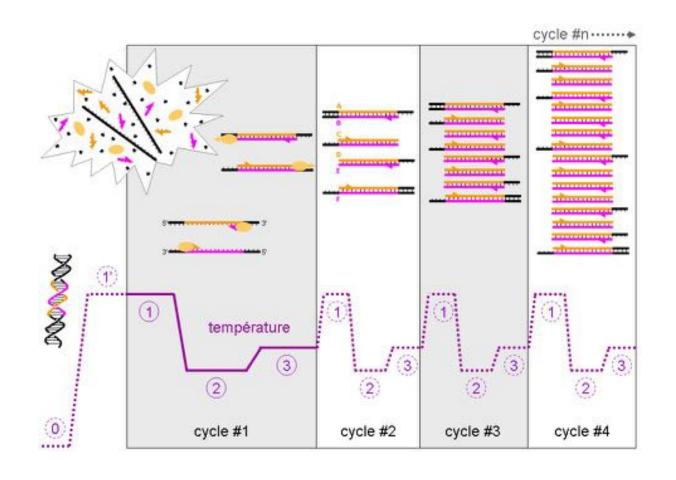




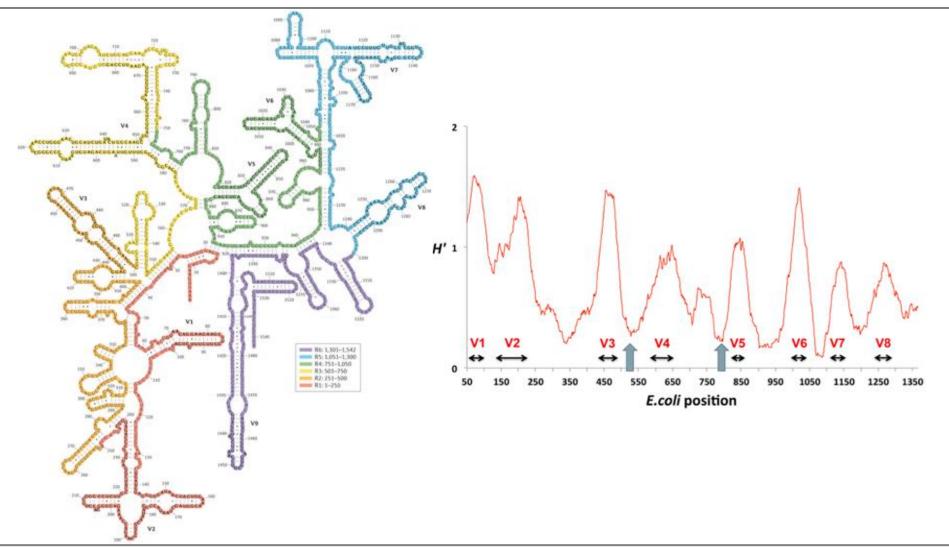
Microbiomes

Amplify









Yarza, et al, Nature Reviews Microbiology 12, 635–645 (2014) doi:10.1038/nrmicro3330



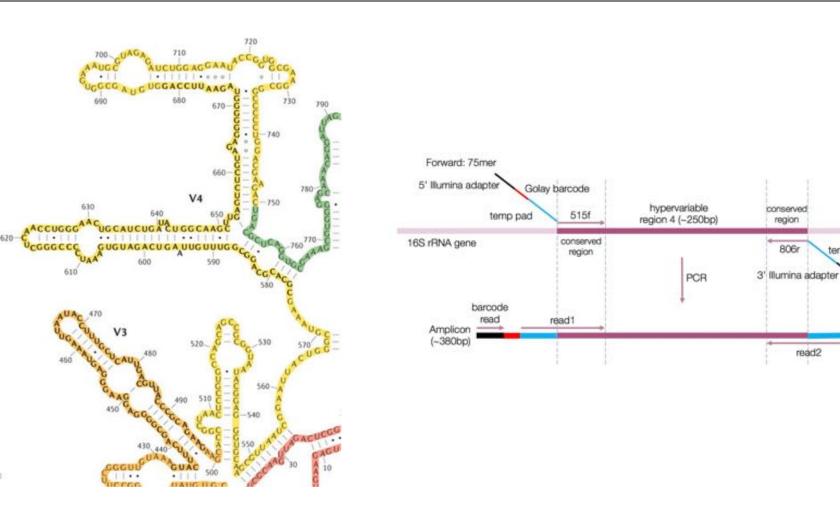
Microbiomes

Marker Gene Sequencing – 16S rRNA gene

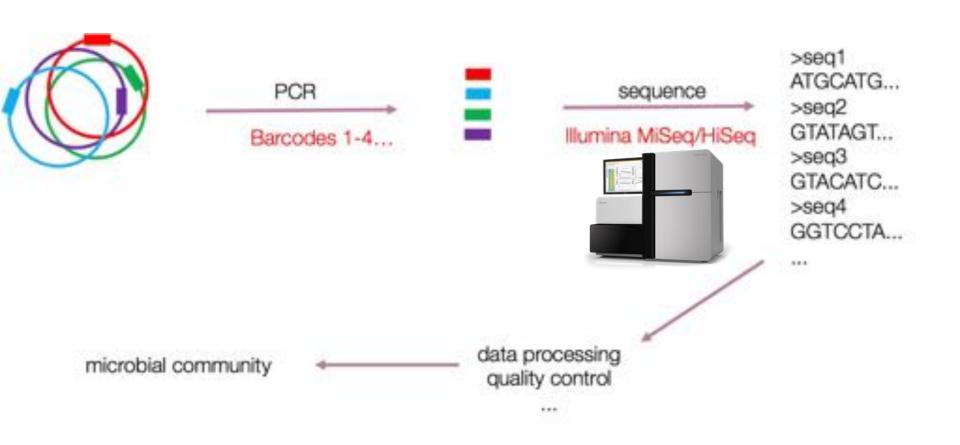
temp pad

Reverse: 56mer











Poll time!

Poll number 2



Innovations in HPC training for medical, sciences and engineering students

CompBioMed Education Aim

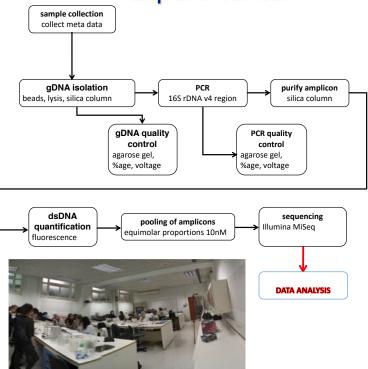
To bridge the computational-experimental divide by supporting and developing existing users

To create a new category of users of HPC ("future users") who will be fluent both computationally and experimentally

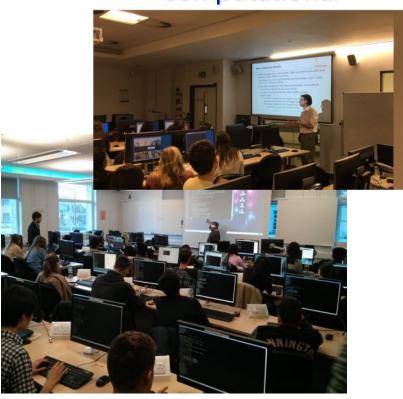
To provide 'tried and tested' educational templates and expertise for adoptions by other universities and institutions

From 2019, CompBioMed2 educational expertise will be adopted across the EU commencing with: University of Amsterdam/SURFsara, University of Sheffield, University of Oxford and the Universidad Pompeu Fabra/Barcelona Supercomputing Centre

Experimental



Computational



SSC: Student Selected Component (UCL Medical School)

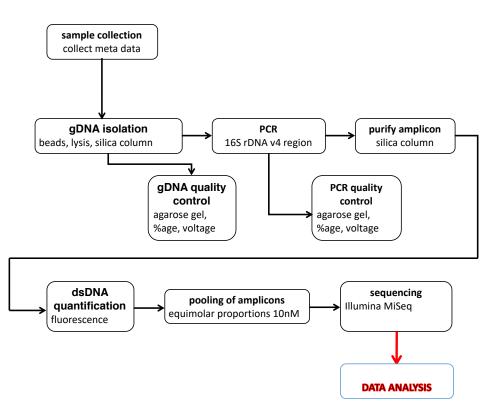
Year 1 - From Skin to Metagenomics: Exploring Your Microbiome

Running at UCL since September 2017

Professor Andrea Townsend-Nicholson



Experimental Workflow







Poll time!

Poll number 3



Computational Analyses

DNA Sequence Analysis

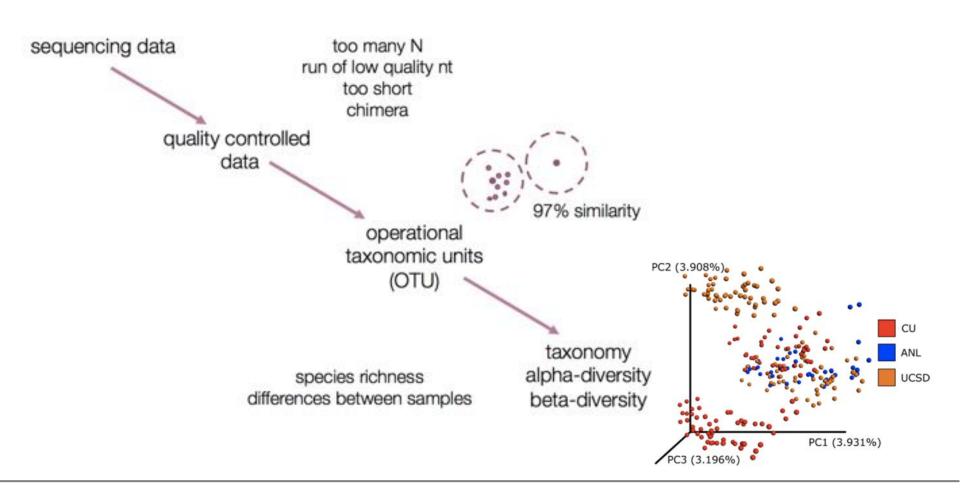


Computational Analyses

Porting Qiime to HPC architectures

Training novice users in command line
Introducing novice users to HPC

Data analysis and Qiime on HPC





Results

Which bacteria and archaea are present

Significant representation (millions of sequences, a billion prokaryotes)

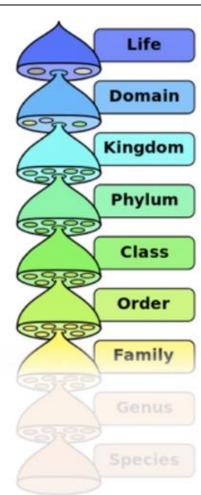
100% success rate (n=135)



Caveats

Single gene ≠ whole genome

Limited resolution to assign taxonomy ~250bp region of 16S rRNA





Poll time!

Poll number 4



CompBioMed2

From 2019, CompBioMed2 educational expertise will be adopted across the EU.

You and Your Microbiome will be taught at medical schools outside UCL, commencing with, but not restricted to:

University of Amsterdam/SURFsara
University of Sheffield
University of Oxford
Universidad Pompeu Fabra/Barcelona Supercomputing Centre



You and Your Microbiome

chez vous...?



You and Your Microbiome flat pack versions....

Medical School SSC-type modules (24 or 48 contact hours)
One week workshop



- Introduction to the module
- Protocol design
- Introduction to NGS (Next Generation Sequencing)
- Workshops in Computing and High Performance Computing
- Collection of skin microbiome samples
- DNA isolation, PCR amplification, sample purification
- NGS (Illumina) sequencing
- Analysis of sequence data using Qiime (command line)
- Comparison of data and summary of findings



Acknowledgments

UCL

EPCC

surfSARA

BSC

UvA



Q&A

To pose a question, you can write your question in the "Questions" tab



Thank you for participating!

...don't forget to fill in our feedback questionnaire...

Visit the CompBioMed website (www.compbiomed.eu/training)
for a full recording of this and other webinars,
to download the slides
and to keep updated on our upcoming trainings



