



H3ABioNet

Pan African Bioinformatics Network for H3Africa

16SrRNA Intermediate Bioinformatics Online Course: Int_BT_2019

Module 3:

Sample collection, extraction and library prep for 16S NGS analyses

Part 3.5

It's not all about the 16S rRNA gene



H3ABioNet

Pan African Bioinformatics Network for H3Africa



16SrRNA Intermediate Bioinformatics Online Course:

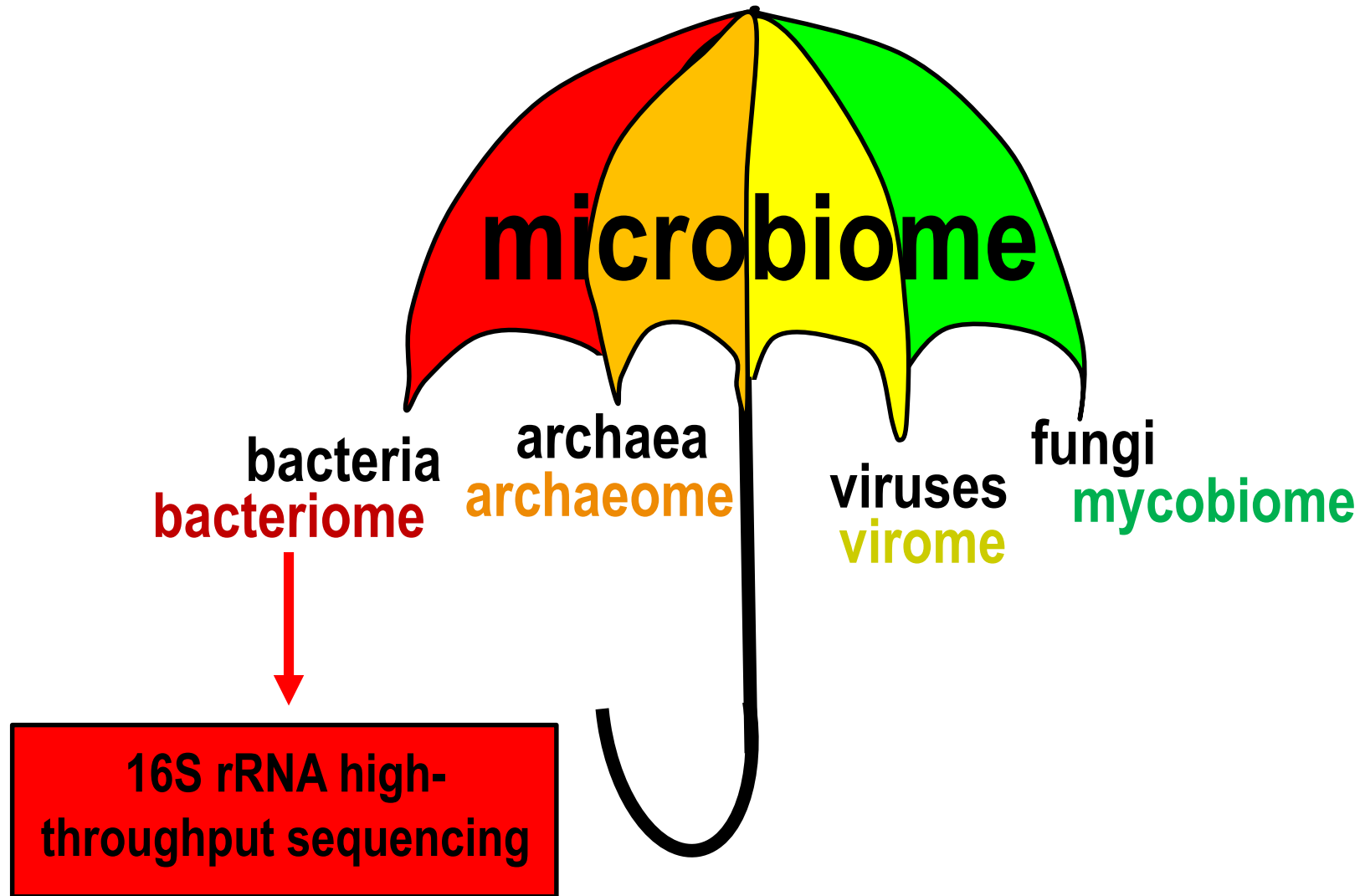
Int_BT_2019

Shantelle Claassen-Weitz

It's not all about the 16S rRNA gene



It's not all about the 16S rRNA gene



Review

The Multibiome: The Intestinal Ecosystem's Influence on Immune Homeostasis, Health, and Disease



Heather A Filyk, Lisa C Osborne *

Department of Microbiology & Immunology, Life Sciences Institute, University of British Columbia, Vancouver, BC, Canada

ARTICLE INFO

Article history:

Received 9 August 2016

Received in revised form 5 October 2016

Accepted 5 October 2016

Available online 6 October 2016

Keywords:

Microbiome

Mucosal immunology

Autoimmune disease

Inflammatory bowel disease

Helminth immunotherapy

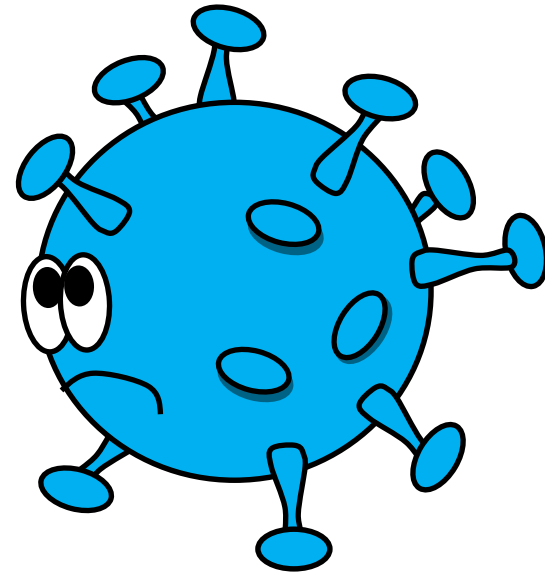
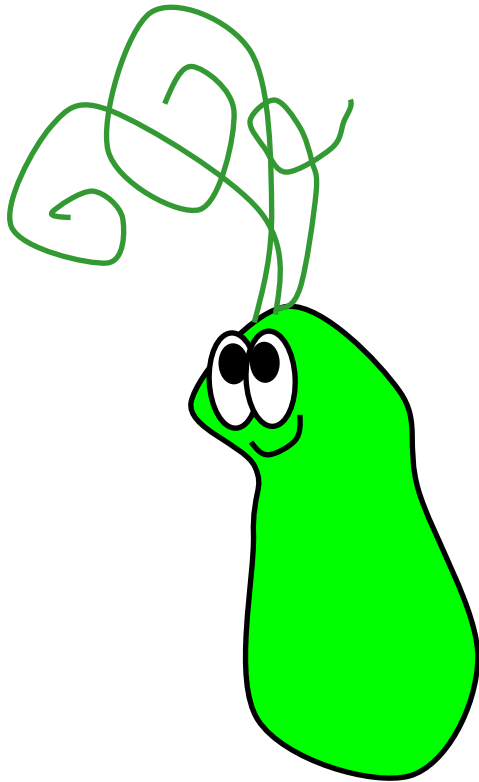
ABSTRACT

Mammalian evolution has occurred in the presence of mutualistic, commensal, and pathogenic micro- and macro-organisms for millennia. The presence of these organisms during mammalian evolution has allowed for intimate crosstalk between these colonizing species and the host immune system. In this review, we introduce the concept of the 'multibiome' to holistically refer to the biodiverse collection of bacteria, viruses, fungi and multicellular helminthic worms colonizing the mammalian intestine. Furthermore, we discuss new insights into multibiome-host interactions in the context of host-protective immunity and immune-mediated diseases, including inflammatory bowel disease and multiple sclerosis. Finally, we provide reasons to account for the multibiome in experimental design, analysis and in therapeutic applications.

© 2016 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Filyk and Osborne. (2016) *Front Microbiol.* doi: 10.3389/fmicb.2016.00459

It's not all about the 16S rRNA gene



Filyk and Osborne. (2016) *Front Microbiol.* doi: 10.3389/fmicb.2016.00459

Handley *Genome Medicine* (2016) 8:32
DOI 10.1186/s13073-016-0287-y

Genome Medicine

COMMENT

Open Access

The virome: a missing component of biological interaction networks in health and disease



Scott A. Handley

Handley *Genome Medicine* (2016) 8:32
DOI 10.1186/s13073-016-0287-y

Genome Medicine

Trends in Microbiology

CellPress

Review

The Bacterial Microbiome and Virome Milestones of Infant Development

Efrem S. Lim,¹ David Wang,¹ and Lori R. Holtz^{2,*}

Handley *Genome Medicine* (2016) 8:32
DOI 10.1186/s13073-016-0287-y

Genome Medicine

Trends in Microbiology

CellPress

Journal of Medical Virology 88:1467–1472 (2016)

Beyond the Gut Bacterial Microbiota: The Gut Virome

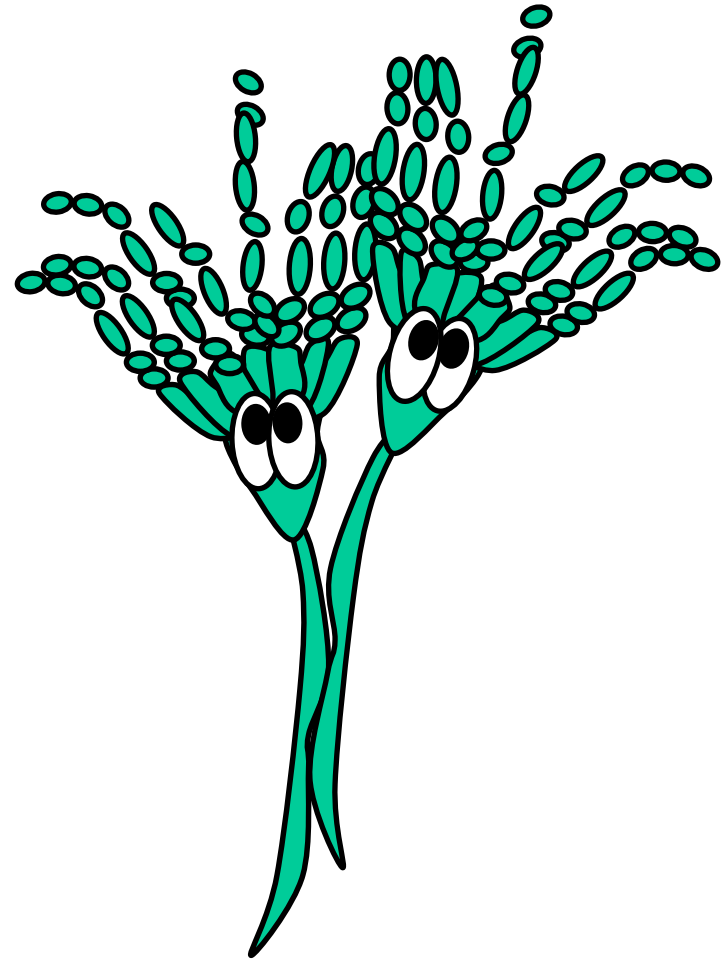
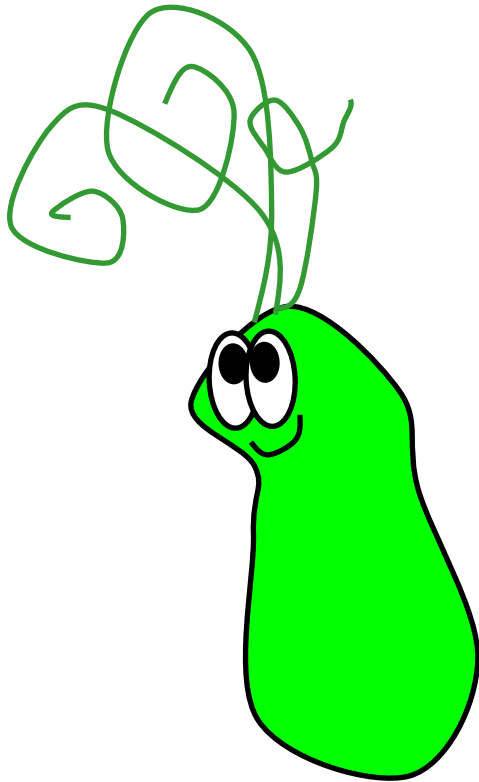
Paola Columpsi,¹ Paolo Sacchi,¹ Valentina Zuccaro,¹ Serena Cima,¹ Cristina Sarda,¹
Marcello Mariani,¹ Andrea Gori,² and Raffaele Bruno^{1,3*}

¹Department of Infectious Diseases, Fondazione IRCCS Policlinico San Matteo, Pavia, Italy

²Clinic of Infectious Diseases, San Gerardo Hospital, University of Milano-Bicocca, Monza, Italy

³Department of Clinical, Surgical, Diagnostic and Pediatric Science, University of Pavia, Pavia, Italy

It's not all about the 16S rRNA gene



Filyk and Osborne. (2016) *Front Microbiol.* doi: 10.3389/fmicb.2016.00459

The Scientist » February 2016 Issue » Features

The Mycobiome

The largely overlooked resident fungal community plays a critical role in human health and disease.

By Mahmoud Ghannoum | February 1, 2016



3.3K



41



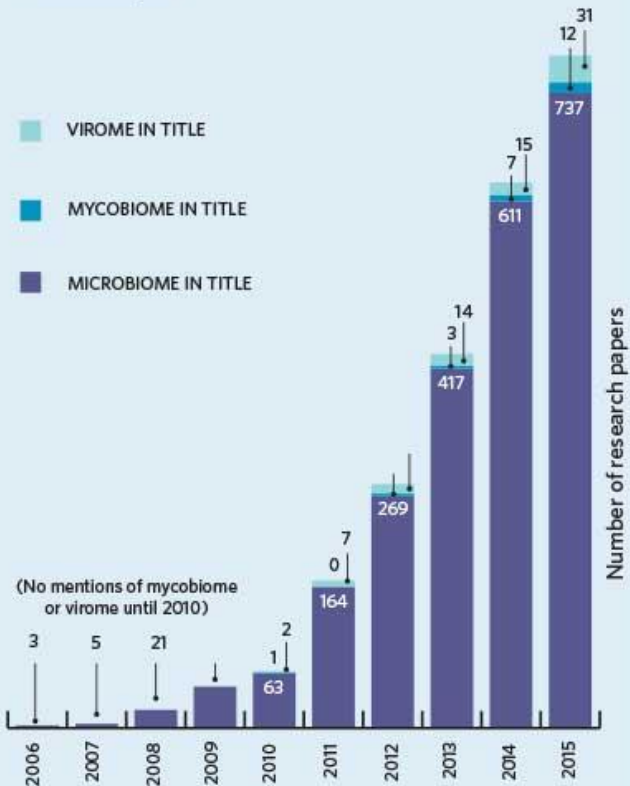
832



© VEM/SCIENCE SOURCE

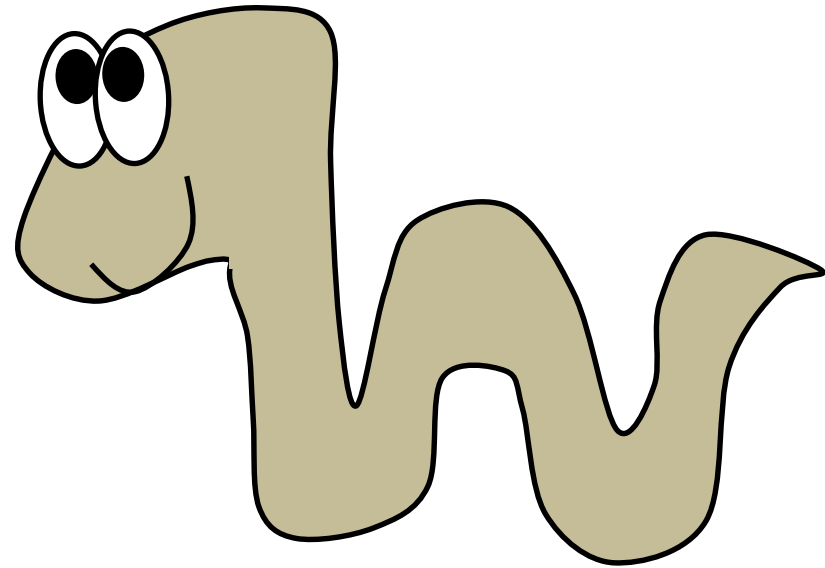
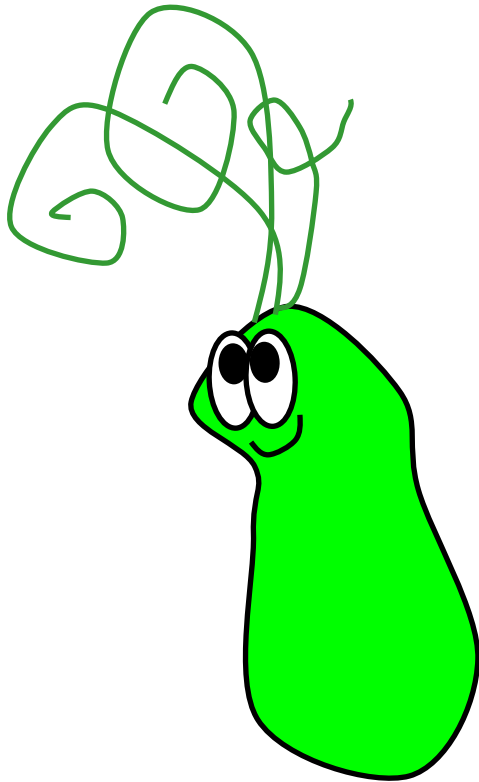
RESEARCHING THE HUMAN MICROBIOME

Prior to 2010, there were no mentions of the mycobiome or the virome in the literature. Even in the last five years, research on the human microbiome has been dominated by surveys and studies of bacterial species.



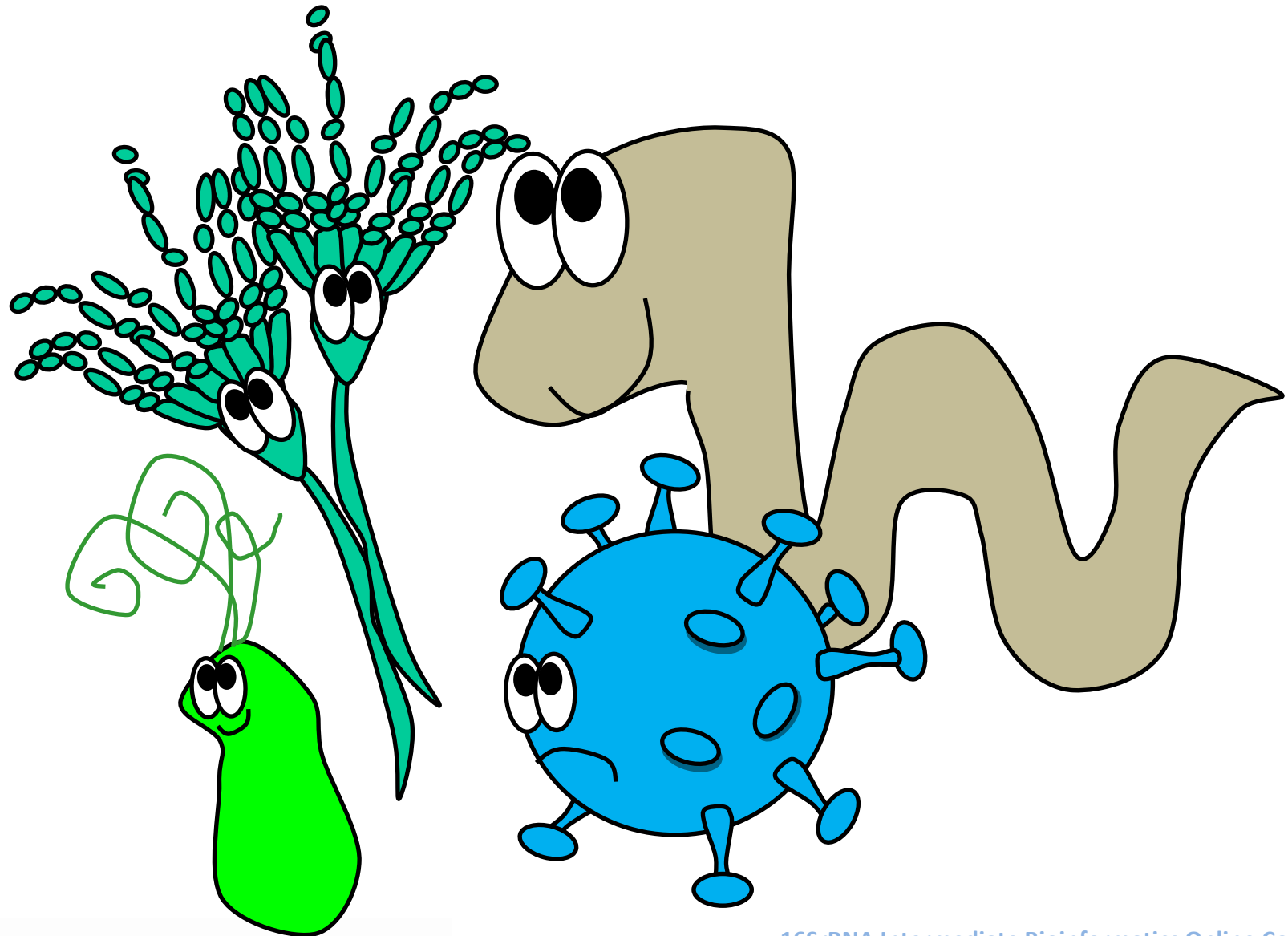
Data collected from ISI Web of Science on December 21, 2015

It's not all about the 16S rRNA gene

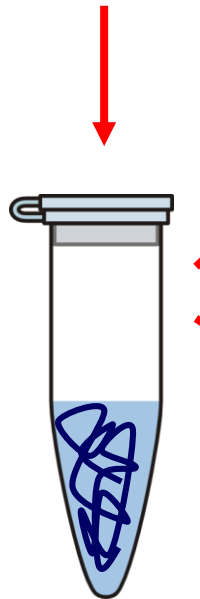
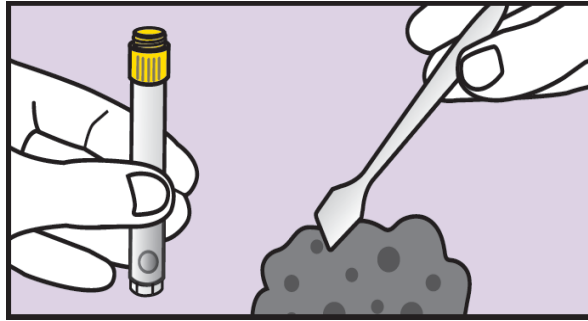


Filyk and Osborne. (2016) *Front Microbiol.* doi: 10.3389/fmicb.2016.00459

It's not all about the 16S rRNA gene

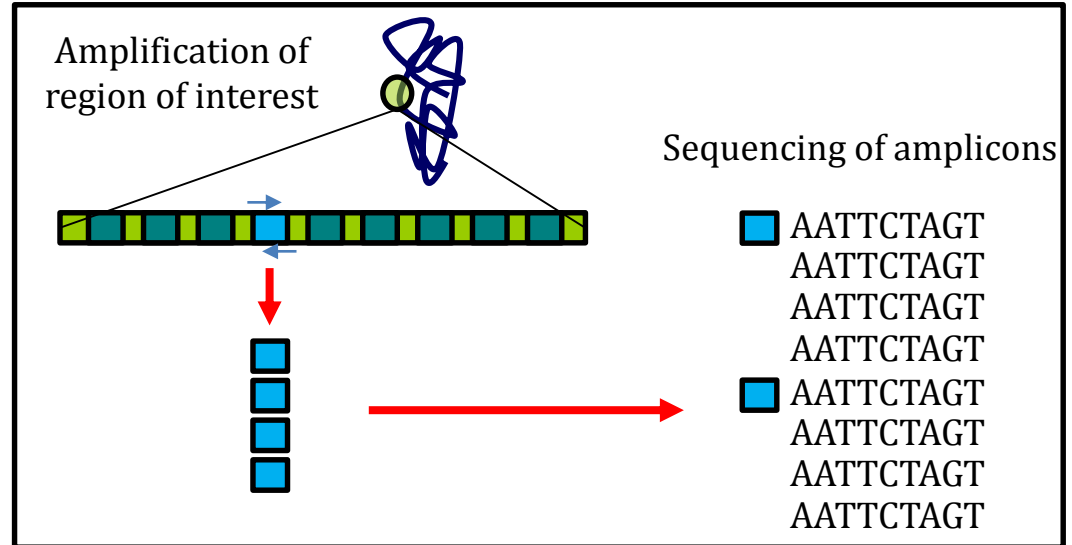


It's not all about the 16S rRNA gene

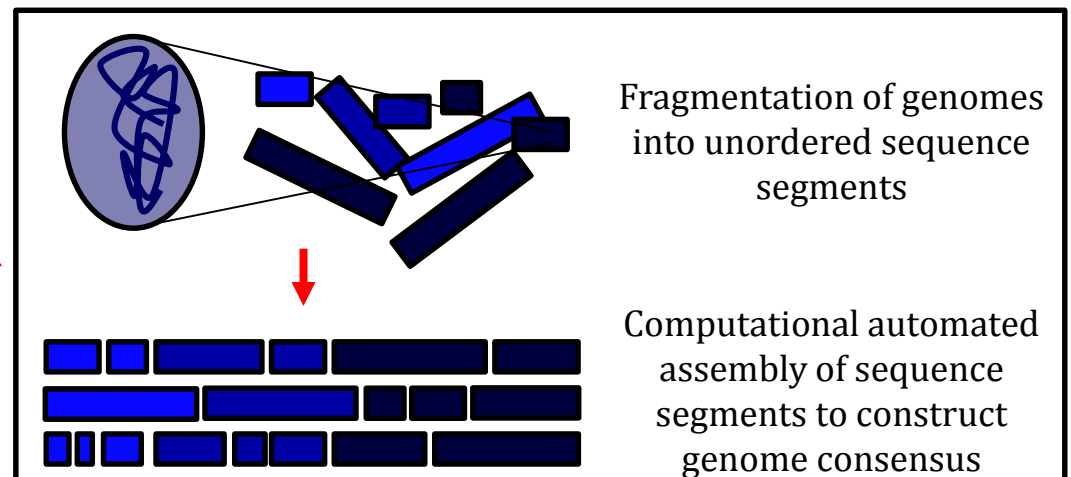


Nucleic acid

16S rRNA sequencing



Shotgun metagenomics sequencing



16SrRNA Intermediate Bioinformatics Online Course:

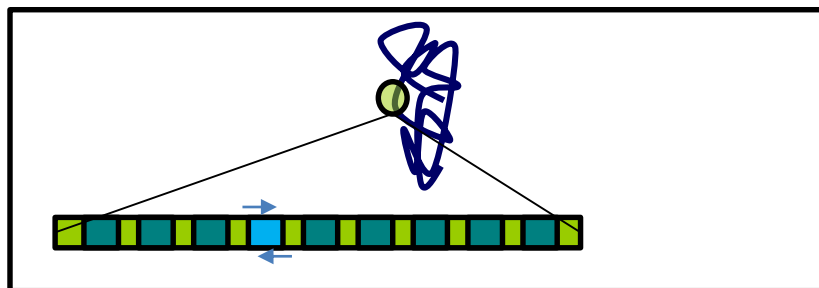
Int_BT_2019

Shantelle Claassen-Weitz



It's not all about the 16S rRNA gene

16S rRNA sequencing



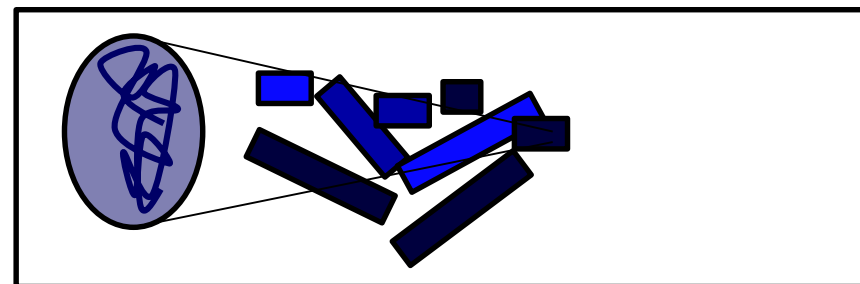
Benefits:

1. cost effective
2. data analysis can be performed by established pipelines
3. a large body of archived data is available for reference.

Limitations:

1. sequences only a single region of the bacterial genome
2. classifications often lack accuracy at the species level
3. specific genes are not directly sequenced, but rather predicted based on the OTUs

Shotgun metagenomics sequencing



Benefits:

1. sequence broad regions of the genome
2. identifies approximately twice as many species
3. identify organisms in additional kingdoms including viruses, fungi and protozoa
4. increased prediction of genes and functional pathways

Limitations

1. expensive
2. computationally intensive

Ranjan et al. (2016).
Biochem Biophys Res Commun. 469(4): 967–977.

It's not all about the 16S rRNA gene

In summary:

- The microbiome does not only refer to our bacterial communities.
- In addition to bacteria, our bodies are also inhabited by other microscopic, and sometimes macroscopic organisms, such as archaea, viruses, fungi and multicellular parasitic worms. The collective term used for these organisms is multibiome.
- Although studies focusing on the virome and mycobiome are still new, a reports have been published on the importance of these organisms in health and disease states.
- One way of studying our microbiomes as a whole is to use shotgun sequencing, however, using this technology is still very expensive and computationally intensive.

Module 3:

Sample collection, extraction and library prep for 16S NGS analyses

