



**11/28/2023**  
**4-5 PM**  
**MARLEY 230**

*Refreshments provided in  
Marley Lobby 3:30-4pm*

*Live broadcast available on Zoom:*  
<https://arizona.zoom.us/j/83044711714>

*Password: spls23*

*Host: Marc Orbach, Ph.D*

## DR. SIMON ROUX

### VIRAL ECOGENOMICS: CAN MULTI'OMICS HELP US UNDERSTAND THE ROLE OF VIRUSES IN MICROBIOMES ?

**Abstract:** Microbes are recognized as key players across ecosystems, driving nutrient and energy transfers, and directly influencing human health and disease. They do so under strong constraints exerted by viruses, which shape microbial communities' structure and can reprogram host cell metabolism during infection. The world's oceans, for example, harbor an estimated 1030 virus particles, with an estimated 1 cell out of 3 infected at any given time. Understanding the full range of virus-host interactions and their associated ecological and evolutionary drivers is thus critical to fully comprehend microbiome dynamics.

While technical challenges initially limited our ability to even catalog the global virosphere, in the last few years alone, metagenomic approaches increased viral genome databases by > 200 times, and enabled comparative genomics studies which already revealed thousands of novel candidate viral genera. While still incomplete and unevenly representing the whole viral diversity, this comprehensive catalog of uncultivated virus genomes represents an invaluable resource to evaluate ecological and evolutionary patterns in the viral world.

Here I will present our latest work in the field of viral ecogenomics, including (i) new approaches to maximize the recovery and annotation of viral genomes from metagenomes and make these available to the broader community of researchers, (ii) analysis of virus-host dynamics across seasons in a natural soil ecosystem based on paired metagenomes and metatranscriptomes, and (iii) comprehensive characterization of CRISPR spacer repertoires in nature. Eventually, we envision that a full viral ecogenomics toolkit will empower researchers to characterize viral communities and virus-host interactions with an unprecedented level of details and resolution, enabling us to revisit long-standing biological questions and possibly inspiring new technologies for microbiome manipulation.