

VABILO

Nacionalni inštitut za biologijo Vas vabi, da se udeležite seminarja
**»Metagenomic sequencing reveals the viral landscape in
human stool and wastewater samples«,**

ki ga bo predstavila

dr. Sara Javornik Cregeen

vodja skupine za Bioinformatiko,

**Alkek Center for Metagenomics and Microbiome Research
Assistant Professor, Department of Molecular Virology and Microbiology,
Baylor College of Medicine**



Seminar bo v četrtek, 26. oktobra 2023, ob 15. uri

v Biološkem središču v Ljubljani, Večna pot 111, v predavalnici B4 in v okolju Webex:

<https://nib-si.webex.com/nib-si/j.php?MTID=m947ca8a139621e5a20a5a9e0bfec451e>

Meeting number: 869 2560 2351, Password: sU2R6eYNK9m (78276396 from video systems)

Povzetek:

“The Center for Metagenomics and Microbiome Research (CMMR) at Baylor College of Medicine specializes in providing sequencing and analytical solutions to big data driven questions in infectious disease and human health. The CMMR has recently made advances in using metagenomics approaches to track viruses of pandemic potential in wastewater¹ and understanding the human virome in early life². 1) Analysis of wastewater may help us understand the health of populations, yet most current approaches overlook the activity of many human viruses and preclude a deeper understanding of human virome community dynamics. Over a period of 6 months, 363 wastewater samples from ten distinct sites in two major Texas cities were collected and comprehensive sequencing-based analysis of the virome was performed. Over 450 distinct pathogenic viruses from 28 viral families were observed, most of which have never been detected in such samples. Sequencing data was correlated to clinical data sets, outlining the public health utility of this approach. In this work the virome of human wastewater is revealed and its potential to improve our understanding of outbreaks, transmission, and its effects on overall population health discussed. 2) Humans are colonized with commensal bacteria soon after birth, however, less is known about phage communities in early human development. Whole genome shotgun data from the TEDDY study, composed of 12,262 longitudinal samples from 887 children in 4 countries, was analyzed to assess phage and bacterial dynamics simultaneously. Each child was observed to be colonized by hundreds of different phages during the early years, and phages were more transitory than bacteria. Clear trends of ecological succession amongst phages were observed and correlated well with putative host bacteria. This work contributes to improved understanding of phage-bacterial relationships and helps reveal new means by which to shape and modulate the microbiome and its constituents to improve health and reduce disease.”

Vljudno vabljeni! Seminar bo potekal v angleškem jeziku.

You are cordially invited to attend this lecture, which will be held in English.

Dodatne informacije: dr. Maruša Verbič Koprivšek, marusa.verbickoprivsek@nib.si.