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ECCB 2016 MAIN CONFERENCE GENOME

HT05 – PANGENOME-BASED COMPUTATIONAL METAGENOMIC PROFILING ENABLES STRAIN-LEVEL CULTURE-FREE EPIDEMIOLOGY AND POPULATION GENOMICS STUDIES

Theater (plenary hall) **September 5, 2016** **2:40 pm - 3:00 pm**

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HIGHLIGHT TALK – THEME: GENOME

ABSTRACT

Microbial species comprise strains with largely different set of genes and functional potential. Identifying microbial strains and characterizing their genes is thus essential for pathogen discovery, epidemiology and population genomics. Here we present a novel computational strain-level metagenomic profiling tool, called PanPhlAn, for identifying the gene composition and in-vivo transcriptional activity of individual strains from metagenomic and metatranscriptomic samples. PanPhlAn enables both the identification of known organisms and the characterization of previously unseen strains. Applied to the 2011 German E. coli outbreak, we demonstrate the ability of PanPhlAn to recognize outbreak strains and identify their associated virulence and resistance factors. Based on almost two thousand samples, PanPhlAn produced the largest strain-level, culture-free population genomic study of human-associated microbial species. In a large cohort of preterm infants, PanPhlAn enabled the identification of disease-associated strain-level genetic biomarkers. PanPhlAn is available at http://segatalab.cibio.unitn.it/tools/panphlan (http://segatalab.cibio.unitn.it/tools/panphlan).

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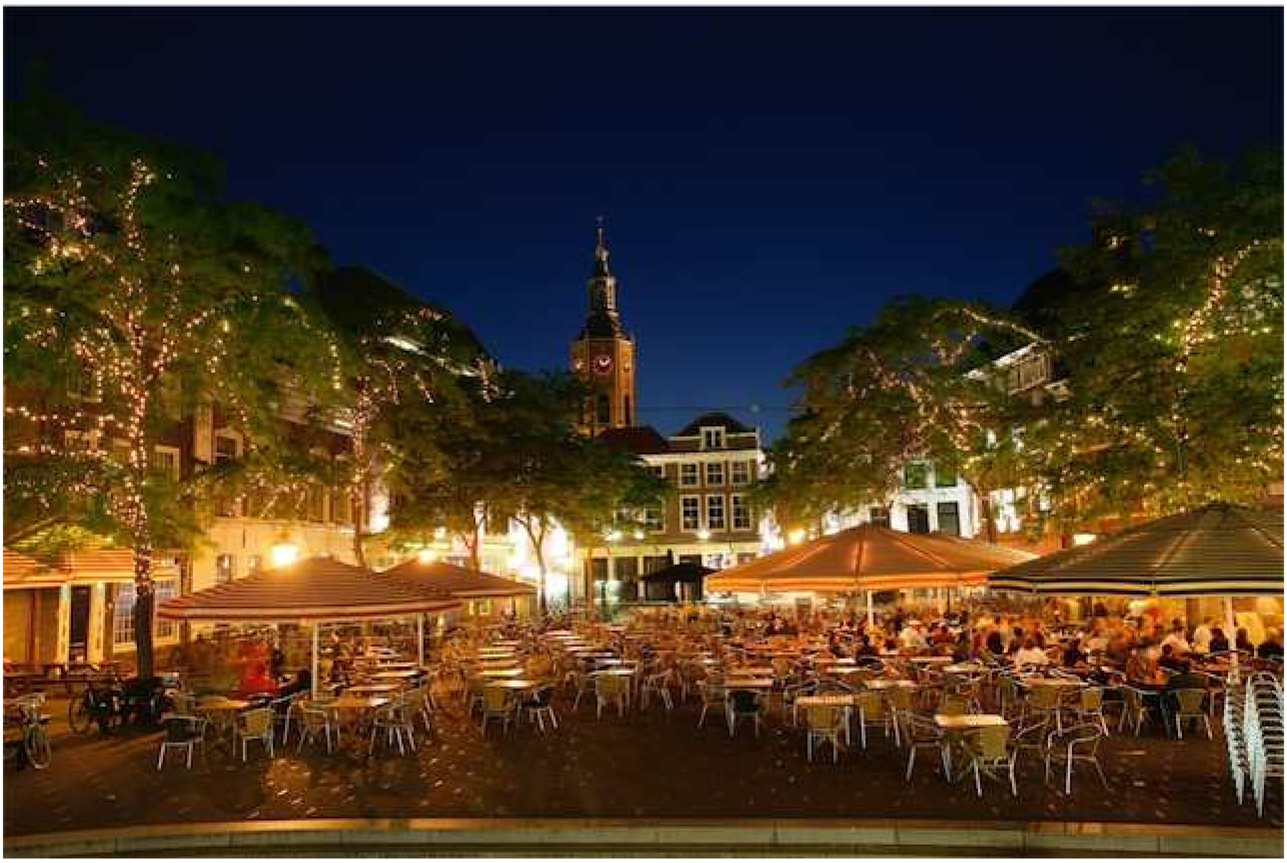
INVITATION

We cordially invite you to visit European Conference on Computational Biology 2016 which will be hosted by the Dutch Royal city of peace and justice. The Hague is ready to welcome you and offer you the perfect balance of science and pleasure.



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