ABSTRACT

The lack of cultivated reference strains for the majority of naturally occurring microorganisms has lead to the development of plurality and single-cell sequencing methods and the field of metagenomics, offering a glimpse into the taxonomic and functional diversity of this so-called ‘microbial dark matter’. An explosion of sequencing initiatives has followed, attempting to capture and extract biological meaning from MDM across a wide range of ecosystems, from deep-sea vents and polar seas to waste-water bioreactors and human beings. Current analytic approaches focus on taxonomic structure and metabolic potential through a combination of phylogenetic anchor screening of the small subunit ribosomal RNA gene (SSU or 16S rRNA) and general sequence searches using homology-based inference. Though much has been learned about microbial diversity and metabolic potential within natural and engineered ecosystems using these approaches, they are insufficient to resolve the ecological relationships that couple nutrient and energy flow between community members — ultimately translating into ecosystem functions and services. This shortcoming arises from a combination of data-intensive challenges presented by environmental sequence information that span processing, integration, and interpretation steps, and a general lack of robust statistical and analytical methods to directly address these problems.

My research addresses some of these shortcomings through the development of a modular analytical pipeline, MetaPathways, allowing for the large-scale and systematic processing and integration of many forms of environmental sequence information. MetaPathways is built to scale, comparing hundreds of metagenomic samples through the efficient use of data structures, grid compute models, and interactive data query. Moreover, it attempts to bring functional analysis back to the metabolic map through the creation of environmental pathway/genome databases (ePGDBs), adopting the Pathway Tools software for metabolic pathway prediction on the MetaCyc encyclopedia of genes and genomes. ePGDBs and the pathway-centric approach are validated to provide known and novel insights into community structure and function. Finally, novel methods for taxonomic and functional analysis supporting the pathway-centric model are derived and demonstrated that enhance Pathway Tools as a framework for engineering microbial communities and consortia.

BIOGRAPHICAL NOTES

Place of Birth:	Winnipeg, Manitoba
Academic Studies:	B. Sc., Computer Science, UBC, 2011

GRADUATE STUDIES

Field of Study: Bioinformatics

Courses		Instructors
CPSC 545	Algorithms in Bioinformatics	Dr. I. Meyer
CPSC 533C	Information Visualization	Dr. T. Munzner
BIOF 501A	Special Topics in Bioinformatics	Dr. R. Brinkman, Dr. F. Pio
BIOF 520	Problem-Based Learning In Bioinformatics	Dr. S. Jones
BIOF 548	Bioinformatics Directed Studies	Dr. K. Konwar, Dr. S. Hallam

AWARDS

UBC Four-year Doctoral Fellowship (2011)

SELECTED PUBLICATIONS

K. Leung, H. Zahn, T. Leaver, K. M. Konwar, **N. W. Hanson**, A. P. Pagé, C.-C. Lo, P. S. Chain, S. J. Hallam, C. L. Hansen, A programmable droplet-based microfluidic device applied to multiparameter analysis of single microbes and microbial communities. PNAS. 109, 7665–7670 (2012).

K. M. Konwar, **N. W. Hanson**, A. P. Pagé, S. J. Hallam, MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. BMC Bioinformatics 14, 202 (2013).

N. W. Hanson, K. M. Konwar, S.-J. Wu, S. J. Hallam, MetaPathways v2.0: A master-worker model for environmental Pathway/Genome Database construction on grids and clouds. IEEE Proceedings on Computational Intelligence in Bioinformatics and Computational Biology, 2014, 1–7 (2014).

N. W. Hanson, K. M. Konwar, A. K. Hawley, T. Altman, P. D. Karp, S. J. Hallam Metabolic pathways for the whole community. BMC Genomics 15, 619 (2014).

PRESENTATIONS

N. W. Hanson. Metabolic Interaction Networks for the Whole Community. Asia Pacific Bioinformatics Conference (APBC 2012), La Trobe University, Melbourne, Australia. January 17-19 2012.

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THE UNIVERSITY OF BRITISH COLUMBIA
Graduate and Postdoctoral Studies

PROGRAMME

The Final Oral Examination
For the Degree of

DOCTOR OF PHILOSOPHY
(Bioinformatics)

NIELS W. HANSON

B.Sc., Computer Science, UBC, 2011

Wednesday, April 1, 2015, 4:00 pm
Room 200, Graduate Student Centre
Latecomers will not be admitted

“MetaPathways: A Modular Pipeline for the Analysis of Environmental Sequence Information”

EXAMINING COMMITTEE

Chair:
  Dr. Pamela Hoodless (Medical Genetics)

Supervisory Committee:
  Dr. Steven J. Hallam (Microbiology & Immunology)
  Dr. Tamara Munzner (Computer Science)

University Examiners:
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  Dr. Rosemary Redfield (Zoology)

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