Luana Presta

Curriculum Vitae

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Personal Informations

Date of birth	April 11th 1985
Place of birth	Paola (CS)
Current State	PhD Candidate

Educational Background

2014 - 2017	**PhD in Genetics and Microbiology**, *University of Florence, Dep. of Biology*.
2010 - 2014	**MSc Biological Sciences - Molecular Biology and Technology**, *University of Florence - Italy*.
Degree Mark	110/110

Theses

PhD Thesis

TITLE	Modeling biological systems: from genome sequences to functional insights
SUPERVISOR	Professor Alessio Mengoni, University of Florence

MSc Thesis

TITLE	Study of the distribution and phylogeny of nitrogen fixation process
ADVISOR	Researcher Marco Fondi, University of Florence, Italy
SUPERVISOR	Professor Renato Fani, University of Florence, Italy
SUPERVISOR	Professor Davide Pisani, University of Bristol, UK / University of Maynooth, IE

Research Projects and Work Experience

Post doctoral Fellowship - Research Project

2017	**FAS-SALUTE MICpROBIMM**.
SUPERVISOR	Professor Renato Fani

Project outline	Functional and metabolic characterization of the microbiome and the role of probiotics in the modulation of immuno-specific response in colorectal cancer patients. My role in this project is to analyse large RNA-Seq data (100 GB) of relevant microbial species and to integrate such data into host-community genome-scale metabolic models. The basic pipeline involves quality check of raw RNA-Seq sequences, mapping (Samtools, Cufflinks) and differential expression evaluation (Bioconductor packages in R). The obtained data are then integrated in GEMs trough Matlab environment (GIMME or iMAT). Modelling through COBRA Toolbox (Matlab and Python) and manual refinement follows.
Research Group	COMBO, Computational Biology Group, Biology Department
University	**University of Florence**
Funding	Regione Toscana, Italy

PhD Research Project

2016	**Modeling of patient-specific (RNA-seq based), genome-scale metabolic models of colorecatal cancer cells.**.
Project outline	The main goal was to identify new antimetabolites to be used as cancer treatments. COOBRA Toolbox and Raven have been used for the modeling phase. RNA-Seq data and metadata have been taken from TGCA database.
SUPERVISOR	Professor Jens Nielsen
Research Group	SYS^{2}BIO, Systems and Synthetic Biology Division
University	**Chalmers University of Technology** - Goteborg - Sweden
2014 - 2017	**From NGS data to systems metabolic modeling through genome-scale metabolic network**.
Project outline	During the three years of PhD program I have been involved in several projects which span from **genome assembly** and **annoatation** to **genome-scale metabolic models reconstruction and modeling for new drug target identification.** My main focus has been on the possibility to derive functional (phenotypic) clues based on genomic data.
SUPERVISOR	Professor Alessio Mengoni
Research Group	COMBO, Computational Biology Group, Biology Department
University	**University of Florence** - Florence - Italy

Undergraduate Research Project

2013	**Study of the distribution and phylogeny of nitrogen fixation process**, The study involved the analysis of large biological dataset, from data-mining phase, to multiple alignments editing, phylogenetic tree construction and evolutuionary model inference.
SUPERVISOR	Professor Davide Pisani
Research Group	Bioinformatics and Molecular Evolution Unit - School of Biological Sciences
University	**University of Bristol** - Bristol - UK

Research Interests

BIOLOGY	○ Computational Biology ○ Genetics ○ Microbiology

Teaching Experience

2014 - 2017 **Undergraduate students tutoring at COMBO**.

Languages

Italian	Native	
English	Professional	*IELTS - Cambridge English Assessment Language (2013)* *University of Bristol*
French	Fluent	*Diplôme d'Études en Langue Française (DELF)*

Skills

Programming	Python, R
Tools	PyCharm, Matlab, RStudio, Adobe Illustrator
Other Skills	Communication, Organization, Writing

MOOCs

Programming	*The Data Scientist's Toolbox* Johns Hopkins Bloomberg School of Public Health & Coursera
Bioinformatics	*Bioinformatics* UC San Diego & Coursera
Systems Biology	*Systems Biology and Biotechnology* Ichan School of medicine at Mount Sinai & Coursera

Conferences

2017 **Bionformatiha6**, *Oral communication*, Genome-scale metabolic modeling identifies new colorectal cancer chemotherapy candidates, Pisa.
Italy

2017 **Acinetobacter 2017 - 11th international symposium**, *Poster presentation*, Constraint-based modelling identifies new putative targets through colistin-resistant *Acinetobacter baumannii* infections, Seville.
Spain

2016

Bionformatiha 2016, *Oral communication*, Modelling Acinetobacter baumannii metabolic response to antibiotic stress, Florence.
Italy

2016

ICSB - International Conference on Systems Biology 2016, *Poster presentation*, Modelling *Acinetobacter baumannii* metabolic response to antibiotic stress, Barcellona.
Spain

2016

Cortona Procarioti, *Oral communication*, Modelling *Acinetobacter baumannii* metabolic response to antibiotic stress, Cortona.
Italy

2015

ProkaGENOMICS, *Poster presentation*, Genome-scale metabolic reconstruction of multiple *Acinetobacter buamannii* strains, Göttingen.
Germany

Publications

[Adessi et al., 2016] Adessi, A., Spini, G., Presta, L., Mengoni, A., Viti, C., Giovannetti, L., Fani, R., and De Philippis, R. (2016). Draft genome sequence and overview of the purple non sulfur bacterium rhodopseudomonas palustris 42ol. *Standards in genomic sciences*, 11(1):24.

[Fondi et al., 2016] Fondi, M., Bosi, E., Presta, L., Natoli, D., and Fani, R. (2016). Modelling microbial metabolic rewiring during growth in a complex medium. *BMC genomics*, 17(1):970.

[Maggini et al., 2017] Maggini, V., Presta, L., Miceli, E., Fondi, M., Bosi, E., Chiellini, C., Fagorzi, C., Bogani, P., Di Pilato, V., Rossolini, G. M., et al. (2017). Draft genome sequence of pseudomonas sp. strain ep r1 isolated from echinacea purpurea roots and effective in the growth inhibition of human opportunistic pathogens belonging to the burkholderia cepacia complex. *Genome Announcements*, 5(20):e00351–17.

[Miceli et al., 2017] Miceli, E., Presta, L., Maggini, V., Fondi, M., Bosi, E., Chiellini, C., Fagorzi, C., Bogani, P., Di Pilato, V., Rossolini, G. M., et al. (2017). New genome sequence of an echinacea purpurea endophyte, arthrobacter sp. strain epsl27, able to inhibit human-opportunistic pathogens. *Genome announcements*, 5(25):e00565–17.

[Presta et al., 2017a] Presta, L., Bosi, E., Fondi, M., Maida, I., Perrin, E., Miceli, E., Maggini, V., Bogani, P., Firenzuoli, F., Di Pilato, V., et al. (2017a). Phenotypic and genomic characterization of the antimicrobial producer rheinheimera sp. eprs3 isolated from the medicinal plant echinacea purpurea: insights into its biotechnological relevance. *Research in microbiology*, 168(3):293–305.

[Presta et al., 2017b] Presta, L., Bosi, E., Mansouri, L., Dijkshoorn, L., Fani, R., and Fondi, M. (2017b). Constraint-based modeling identifies new putative targets to fight colistin-resistant a. baumannii infections. *Scientific Reports*, 7(1):3706.

[Presta et al., 2015] Presta, L., Fondi, M., Emiliani, G., and Fani, R. (2015). *Molybdenum Cofactors and Their Role in the Evolution of Metabolic Pathways*. Springer.

[Presta et al., 2016a] Presta, L., Fondi, M., Perrin, E., Maida, I., Miceli, E., Chiellini, C., Maggini, V., Bogani, P., Di Pilato, V., Rossolini, G. M., et al. (2016a). Arthrobacter sp. eprs66 and arthrobacter sp. eprs71: draft genome sequences from two bacteria isolated from echinacea purpurea rhizospheric soil. *Frontiers in microbiology*, 7.

[Presta et al., 2016b] Presta, L., Inzucchi, I., Bosi, E., Fondi, M., Perrin, E., Miceli, E., Tutino, M. L., Giudice, A. L., de Pascale, D., and Fani, R. (2016b). Draft genome sequence of flavobacterium sp. strain tab 87, able to inhibit the growth of cystic fibrosis bacterial pathogens belonging to the burkholderia cepacia complex. *Genome announcements*, 4(3):e00410–16.

References

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