



### **CALL FOR EXPRESSIONS OF INTEREST**

Multiple available positions for computational scientists (from post-master to postdoc fellowships) at the Laboratory of Computational Metagenomics at CIBIO, Trento (Italy)

The <u>Laboratory of Computational Metagenomics</u> (<a href="http://segatalab.cibio.unitn.it/">http://segatalab.cibio.unitn.it/</a>) led by Prof. Nicola Segata (<a href="mailto:nicola.segata@unitn.it">nicola.segata@unitn.it</a>) at the <a href="mailto:Department CIBIO">Department CIBIO</a> at <a href="mailto:University of Trento">University of Trento</a> (Italy) is looking for highly-motivated students and postdoctoral researchers willing to work in close cooperation with a team of biologists and bioinformaticians to develop and to apply novel computational tools for the analysis of large-scale metagenomic data in the context of an European ERC grant and international and national projects.

## **Expression of interest #1**

Two Research positions on the link between the human microbiome and cancer (two positions available). 1) 2+ year postdoctoral fellowships for computational biologists in metagenomics and human microbiome research, 2) developer / systems analyst position for computer scientist / bioinformatician.

We are looking for one post-doctoral researcher and one developer / systems analyst to perform cutting-edge research in the field of computational metagenomics and the human microbiome.

The successful candidates will develop new innovative software tools and large-scale databases with public web front-ends for hosting, organizing, and analyzing metagenomic data. The successful candidates will also have the possibility to analyse microbiome data interfaced by the above-mentioned software, for testing biomedical scientific questions and specifically on the link between the human microbiome and cancer incidence, development, and treatment.

Specific topics will include strain-level metagenomic profiling, large-scale comparative metagenomics, phylogenetics, metagenome-based phylogeny clocking, functional potential profiling, metatranscriptomics, virome profiling, metagenomic assembly, and integration of multi meta'omics data. New research lines will also be considered and scientific curiosity toward related research areas will be welcome.

These positions will be part of the United States NIH Grant "Exploiting public metagenomic data to uncover cancer-microbiome relationships". One position will be based in Trento (Segata Lab) and supervised by prof. Nicola Segata (co-supervision by prof. Levi Waldron), the other in New York (Waldron Lab) and supervised by prof. Levi Waldron





(co-supervision by prof. Nicola Segata) with the possibility of exchanges between the two laboratories.

#### Tasks:

- Development of innovative software tools and their maintenance in R/Bioconductor and/or Python
- Development of large-scale databases with public web front-ends for hosting metagenomic data
- Analysis of microbiome data in connection with cancer data
- Analysis of microbiome data interfaced by the above-mentioned software, for testing biomedical scientific questions
- Network with our international partners and represent our works in large consortia
- Present results at international meetings
- Write scientific articles

## Requirements:

- Bachelor's or PhD (as appropriate) in computer science, computational biology, bioinformatics, or a related field
- Programming experience in R/Bioconductor or Python
- Experience with the analysis of large datasets, ideally genomic or metagenomic data
- Ability to work with different analysis packages in a Linux/Unix environment
- Excellent knowledge (written and spoken) of the English language (professional level)

#### We offer:

- A two-year full-time position with possibility of extension
- Competitive salary
- Access to cutting-edge data and high-performance computing resources
- Attractive living and working conditions
- Support and mentoring toward research independence

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### Earliest start date: June 2020

Potential candidates are invited to contact Prof. Nicola Segata (<u>nicola.segata@unitn.it</u>), Prof. Levi Waldron (<u>levi.waldron@sph.cuny.edu</u>), and Federica Pinto (<u>federica.pinto@unitn.it</u>) via email with "Expression of interest #1" in the subject and attaching a CV, the contact information of at least two references, and a brief description of the main areas of interest.





## **Expression of interest #2.**

Research position on microbiome analysis of fecal microbiome transplantation cohorts. 2+ year postdoctoral contract for a bioinformatician/microbiologist for analysing the microbiota transplantation (FMT) as a novel therapeutic treatment for recurrent *C. difficile* infection.

We are looking for a postdoctoral fellow with a background in microbiology and advanced expertise in computational biology who will be part of a novel investigation to understand whether a targeted microbiota modulation can improve clinical outcomes in Advanced Renal Cell Carcinoma (aRCC) patients.

The successful candidate will be part of a multidisciplinary research project in direct contact with clinicians. She/He will analyse metagenomic data from aRCC patients after a targeted FMT treatment. The successful candidate will associate the microbiome profiles of aRCC patients candidate to Immune checkpoint inhibitors (ICIs) with their clinical response and will evaluate the efficacy of targeted FMT (from donors whose microbiome features are similar to those of ICIs responders) in improving response rates to ICIs in subjects with aRCC. The analysis will also include strain-level evaluation of FMT engraftment levels.

## Requirements:

- PhD in Bioinformatics, Microbiology, Biology or a related field
- Experience in the analysis of metagenomic data
- Experience in machine learning for genomic data (optional)
- Ability to work with different analysis packages in a Linux/Unix environment
- Excellent knowledge (written and spoken) of the English language (professional level)
- Ability to work in a multidisciplinary group

# We offer:

- A two-year full-time position
- Competitive salary
- Access to cutting-edge data and high-performance computing resources
- An international and multidisciplinary work environment
- Attractive living and working conditions
- Support and mentoring toward research independence

Earliest start date: June 2020

Potential candidates are invited to email Prof. Nicola Segata (<u>nicola.segata@unitn.it</u>) and Federica Pinto (<u>federica.pinto@unitn.it</u>) with "Expression of interest #2" in the subject and attaching a CV, the contact information of at least two references, and a brief description of the main areas of interest.





## **Expression of interest #3**

Research position in computational biology / metagenomics. Two-year contract for a computational / data scientists in computational biology

The laboratory of Computational Metagenomics (<a href="http://segatalab.cibio.unitn.it/">http://segatalab.cibio.unitn.it/</a>) led by Prof. Nicola Segata at the Department CIBIO (University of Trento, Trento, Italy), is looking for a computational and data scientist to hire. The successful candidate will be responsible for tasks related to the implementation, deployment, maintenance, and development of software pipelines to analyze large datasets (in the order of hundreds of TBs) on a dedicated high-performance computing infrastructure.

The laboratory's main research focus is on the characterization of the human-associated microbial communities and their biomedical applications. The successful candidate will work in an international team of multidisciplinary scientists with the opportunity of developing a career in research.

The ideal candidate for this paid position has a **very strong computer science background** (i.e. a degree in computer science, information engineering, or equivalent). No previous expertise in biology and bioinformatics is required.

The main requirements for the position are:

- Good theoretical and practical knowledge of Unix and Bash
- Advanced programming skills in Python (or another relevant programming language).
- Familiarity with at least one of the following languages: Python, R, Java
- Motivation and mindset to work collaboratively with a multidisciplinary team

The following skills will be favourably considered (but are not mandatory):

- Experience and knowledge of HPC management software (e.g. PBS)
- Experience as a system administrator
- Experience in parallel computing
- Experience with tools such as Anaconda, Docker, and Git versioning

#### What we offer:

- An exciting scientific and research environment
- Development of bioinformatic/computational skills
- Development of multi-disciplinary skills
- Opportunity to be part of a team developing biomedical solutions
- Future possible transition toward a Ph.D. program if it is of interest for the candidate

Earliest start date: June 2020

Potential candidates are invited to contact Prof. Nicola Segata (<u>nicola.segata@unitn.it</u>) and Federica Pinto (<u>federica.pinto@unitn.it</u>) with "Expression of interest #3" in the subject and attaching a CV and a brief motivation statement.