



CIBIO - Centre for Integrative Biology
Trento, Italy

CALL FOR EXPRESSIONS OF INTEREST

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

The [Laboratory of Computational Metagenomics](http://segatalab.cibio.unitn.it/) (<http://segatalab.cibio.unitn.it/>) led by Prof. Nicola Segata (nicola.segata@unitn.it) at the [Centre for Integrative Biology](#) (CIBIO) at [University of Trento](#) (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 novel computational tools for the analysis of large-scale metagenomic data in the context of an European ERC grant and international collaborations.

Research Position Type 1 (two positions available). 2+ year postdoctoral (or doctoral) fellowships for computational biologists in metagenomics and human microbiome research.

We are looking for two outstanding post-doctoral researchers (or potentially also PhD fellowships) to perform cutting-edge research in the field of computational metagenomics and the human microbiome.

The successful candidates will perform analysis of metagenomics data both for our internal human microbiome studies (five distinct projects with hundreds of shotgun metagenomic samples each) as well as for our integrative ERC project which considers a panel of >10,000 publicly available samples (already available locally and partially processed). The successful candidates will also have the possibility to develop new computational tools along the lines of those recently published in the laboratory (see <http://segatalab.cibio.unitn.it/tools/>).

Specific topics can 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. Multiple projects are available in the mentioned research lines, and the successful applicants will be given the possibility to choose the preferred ones.

The two postdoctoral positions will be part of the ERC project MetaPG described at the following link: https://cordis.europa.eu/project/rcn/209129_en.html

Tasks:

- Analyze large shotgun metagenomic datasets (>10,000 samples) and interpret results
- Perform comparative microbial genomics analysis on many thousands of genomes and strains profiled from metagenomic samples
- Write new computational pipelines to be developed, shared, maintained, validated, and published as open-source software



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- Network with our international partners and represent our works in large consortia
- Present results at international meetings
- Write scientific articles

Requirements:

- PhD in computational biology, bioinformatics or a related field
- Mastering of at least one programming language, such as Python, R, or C/C++
- Familiarity with code development and, ideally, at least one computational tool released open-source to the scientific community
- Experience with the analysis of large datasets, ideally genomic or metagenomic data
- Ability to work with different analysis packages in a Linux/Unix environment

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

Earliest start date: May 2018

Potential candidates are invited to contact Prof. Nicola Segata (nicola.segata@unitn.it) via email with "Application for Research Position Type 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.

Research Position Type 2 (one position available). 2+ year postdoctoral contract for a computational scientist for organizing, handling, and developing large-scale computational analyses on high-performance computing infrastructure.

We are looking for a computer scientist and system administrator to be in charge of the several high-performance computing tasks that are routinely carried out in the Laboratory of Computational Metagenomics and to develop software tools in close collaboration with other bioinformaticians in the lab. The successful candidate is expected to be able to handle for the lab the optimized execution of CPU-intensive and memory-demanding metagenomic tools on a set of available high-performance servers and clusters. The results of such tools will be at the basis of multiple data-driven investigations that are central to the mission of the laboratory. Moreover, the successful candidate will contribute to the maintenance, optimization, and further development of computational tools (please see <http://segatalab.cibio.unitn.it/tools/> for an overview of the methods from the lab). Effective interactions with the other members of the lab (15 researchers) will be required.



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Requirements: Excellent knowledge of the Unix command line and of at least one scripting or programming language (e.g. Python, R, or C/C++). Familiarity with high-performance computing infrastructures. Familiarity in dealing with complex data structures and complex algorithms. Basic biological knowledge or previous experience in bioinformatics is a plus, but not strictly required.

Earliest start date: May 2018

Potential candidates are invited to email Dr. Francesco Asnicar (francesco.asnicar@unitn.it) and Prof. Nicola Segata (nicola.segata@unitn.it) with "Application for Research Position Type 2" in the subject and attaching a CV.

Research Position Type 3 (one position available). One year contract for a junior software developer

We are looking for a highly-motivated software developer with a recent Bachelor or Master degree in computer science or related areas to work in close cooperation with biologists and bioinformaticians to develop a software that will help synthetic biologists in their everyday bench-work. The project aims at developing a user-friendly bioinformatic tool for application in microbial genetic engineering.

The project is a collaboration between Dr. Christopher Johnston (Forsyth Institute, Boston, US) and Prof. Nicola Segata (CIBIO, Trento).

The candidate will conduct his/her research project mainly at CIBIO, and will closely collaborate with Dr. Johnston remotely. The project already includes full travelling support for at least one two-week visit to the laboratories in Boston.

Contract type and salary will depend on the experience and career stage of the applicant.

Requirements: Good knowledge of Python, R, or other scripting or programming languages. Basic biological knowledge or previous experience in bioinformatics would be a plus, but exceptional candidates without biological experience will also be considered.

Earliest start date: May 2018

Potential candidates are invited to contact Dr. Serena Manara (serena.manara@unitn.it) and Prof. Nicola Segata (nicola.segata@unitn.it) with "Application for Research Position Type 3" in the subject and attaching a CV.