**Plant and Environmental Biotechnology Laboratory, Department of Biochemistry and Biotechnology, University of Thessaly, Larissa, Greece (**[**http://plantenvlab.bio.uth.gr/news/newsfeed/**](http://plantenvlab.bio.uth.gr/news/newsfeed/)**)**

We are seeking a highly motivated **bioinformatician** to join the Plant and Environmental Biotechnology Laboratory at the Department of Biochemistry and Biotechnology, University of Thessaly, starting asap. This position will involve working with a multi-disciplinary team of plant scientists, microbiologists, molecular biologists, biochemists and bioinformaticians in providing data analysis support. The candidate will be involved in and carry out independently, analysis of plant and microbial omics (genome/transcriptome/proteome/metabolome) and meta-omics data. He/she will use and develop programming tools in UNIX environment for developing and executing algorithms and analysis pipelines. The position is open for 3 years.

**Principal Responsibilities**

* Design and implement reusable bioinformatics analysis pipelines for processing next-generation sequencing, genomics and proteomics data.
* Perform comparative analysis across genomes/transcriptomes/proteomes/metabolomes to identify putative genetic differences responsible for phenotypic variation, and for producing insights about evolutionary processes.
* Develop rapid prototypes and custom scripts for one-off type of analysis requests
* Use of algorithms and integrated data visualization applications
* Collaborate closely with Principal Investigators and lab members on research projects including defining the scope of the collaboration, researching the scientific topics and implementing the appropriate bioinformatics solutions that meet project requirements
* Properly document the procedures used in computational analysis and provide summary report of results suitable for group meetings, national and international conferences, inclusion in manuscripts and grant applications

**Required Qualifications and Skills**

* Master's degree in Computer Science or Bioinformatics or a related computational discipline, or equivalent experience
* Familiarity with biology and genomics of plants and microorganisms (prokaryotic and eukaryotic)
* Strong background with UNIX-like (e.g. Linux, Mac) operating systems, good familiarity with bioinformatics (and other necessary) tools repositories, and demonstrated programming skills with the BASH terminal.
* Knowledge of the R interpreter-based statistical software.

**Additional/Preferred Qualifications**

* Background in programming and algorithms. E.g. good knowledge of a programming language other than BASH and R (Python, C, C++ or Java, Perl)
* Experience using genome alignment software (bowtie2, bwa, tophat, etc.)
* Experience working with BIG DATA (NGS data)
* Experience using relational databases, SQL and / or structured data formats (e.g. HDF5)
* Web programming experience (PHP, Django, JavaScript, JQuery, JSON, REST API) is a plus
* Co-authorships on peer-reviewed publications are preferred

The posting will remain open until the position is filled.

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