PERSONAL INFORMATION

Luigi Chiricosta

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Whatsapp, Telegram

Sex M | Date of birth 13/01/1993 | Nationality Italian

JOB APPLIED FOR / POSITION PREFERRED / JOB STUDIES APPLIED FOR / PERSONAL STATEMENT

Programmer in medical field, as bioinformatician.
Available for PhD opportunities.
Interested in machine and deep learning, images analysis, software development.

WORK EXPERIENCE

07/03/2018 –

Fellowship in “Development of next generation sequencing tools for the diagnosis of neurodevelopmental disorders”

Azienda Ospedaliera di Padova (AOP), Padua, Italy

- Creation of software pipeline (bash, phyton) to analyse data from gene panel and whole exome even by bioinformatics tools (E.g. samtools)
- Attendance to CAGI (Critical Assessment of Genome Interpretation)

Business or sector Bioinformatics, Computer Science.

01/10/2014 – 30/04/2015

Programmer

Antlia S.R.L., Milan, Italy

- Operating systems: Windows e Linux
- Programming languages and metalanguages: Android, Java, AJAX, jQuery, JSON, XML, HTML, SQL, MySQL, JavaScript, CSS.
- Other expperience: Vaadin, Jboss, Hibernate

Business or sector Programming.

EDUCATION AND TRAINING

01/10/2015 – 26/09/2017

Doctor in Bioinformatics (110/110)

Master's degree in Bioinformatics, Alma Mater Studiorum ,Bologna, Italy

- Next-Generation Sequencing (FastQ for raw data (Ion Proton, Illumina), SAM and VCF files)
- Machine learning (Hidden Markov Model, Support Vectors Machines, Artificial Neural Network, Decision trees, Ensemble methods, evaluation of classifiers)
- Personalized medicine (pipeline creation, pattern recognition, in silico prediction, homology modeling, molecular docking)
- Big data
- Cancer genomics (WES data from Baylor College of Medicine and Broad Institute)
- Databases (GnomAD, 1000 Genomes Project, ExAc, ESP, ClinVar, COSMIC, PDB, UNIPROT)
- Tools (ANNOVAR, VCFTools, ContrastRank, PhD-SNP^{g}, BLAST, Chimera, Rasmol)
- Operating System (Ubuntu)
- Programming languages (Python, R)
- Neuroscience and Complex Systems courses

01/09/2011 – 26/03/2015

Doctor in Computer Science (110/110 cum laude)

Bachelor's degree in Computer Science, University of Messina, Messina, Italy

- Client programming
- Web programming
- Database organization

PERSONAL SKILLS

Mother tongue(s) Italian

Other language(s)

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	B2	C1	B2	B2	B2
Spanish	A1	A1	A1	A1	A1

Levels: A1/A2: Basic user - B1/B2: Independent user - C1/C2 Proficient user
Common European Framework of Reference for Languages

Communication skills

Good communication skills gained through my experience in programming team during:

- bioinformatics master course
- internship

Job-related skills

- Good statistical analysis and programming about cancer genomics acquired during the 8 months of thesis works entitled “Detecting cancer causing genes and variants in Colonadenocarcinoma” using genome/exome data and machine learning procedures on Linux with Python
- Good hardware knowledge acquired by myself during the realization of the computer science thesis project (Arduino, Java and Android-based) titled “L'uomo, i robot e l'intelligenza artificiale” (“Human being, robots and artificial intelligence”)
- Firebase server usage
- OpenCV library on Java, Python and Android

Digital competence

SELF-ASSESSMENT				
Information processing	Communication	Content creation	Safety	Problem solving
Proficient	Proficient	Proficient	Proficient	Proficient

Levels: Basic user - Independent user - Proficient user
Digital competences - Self-assessment grid

Other skills

- Guitar player graduated by Yamaha level 6 course

Driving licence B

ADDITIONAL INFORMATION

Conference
29/05/2018

Workshop “Computational and Translational Methods for Cancer Genomics”

- Epigenomics and cancer – methylation as a marker in oncology
- Are tumor predictable? Inherited immune variation constraints tumor evolution
- Genomics of soft tissue sarcomas
- Computational methods to discover significant mutations in cancer genomes.
- Methodologies for data integration in cancer

Conference
23/05/2018 – 25/05/2018

FEBS advanced course “The molcular basis of diseases: can we infer phenotypes from protein variant analysis?”:

- How can we make better predictors for variant interpretation?
- The European Variation Archive: a database of genetic variation from all species
- Pre-mRNA splicing predictions and phenotype analysis: from simple to complex disease contexts.
- The regulatory genome of epithelial regeneration
- Effective diagnosis of neurodevelopmental disorders by computational analysis and Next Generation Sequencing
- The effect of variations on protein stability
- Towards the prediction and interpretation of deleterious coding variants in terms of stability and functional features
- Labeling tune-able protein positions for evaluating variation effects
- Position matters: roles for SNPs in protein biogenesis and function
- Genetic variation causes differential viral susceptibilities in the model organism *Caenorhabditis elegans*
- Determination of pathogenicity of mitochondrial DNA mutations and combinations of polymorphisms through the assessment of their functional effect
- Revealing and targeting the pathways that are perturbed in genetic diseases
- DisGeNET: a discovery platform to support translational research on human diseases
- Patient-past based precision medicine
- The disease comorbidity network
- k121Q polymorphism of ectonucleotide pyrophosphatase phosphodiesterase 1 increases the risk of insulin resistance in Javanese obese adults

Conference
22/02/2016 – 26/02/2016

Winter school “In Silico Markers for Precision Medicine”:

- In silico biomarkers: do we know them all?
- Precision medicine in vivo and in vitro
- Computational methods and systems biology
- Search for markers of cancer and genetic diseases
- Markers of cancer and genetic diseases in silico, in vitro and in vivo

Personal web site

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