



RICARD ILLA

DATA ENGINEER BACKEND DEVELOPER

CONTACT

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PERSONAL

Date of birth 15/10/1990

Nationality Spanish

Languages Catalan
Spanish
English

EXPERIENCE

June 2019 - October 2020

company **LEAD RATINGS**

position *Data Engineer*

duties Develop and maintain a data-centered ML SaaS platform
Assist Data Scientists' internal workflow
Develop connectors to third party platforms

technologies Python
Django
Amazon web services
Docker and Docker Swarm
Redis
MySQL
Elasticsearch
Numpy and Pandas
Git

July 2018 - June 2019

company **SELLBYTELL GROUP**

position *GCP Support Engineer (Big Data and ML specialist)*

duties Provide Big Data and Machine Learning technical support to
Google Cloud Platform users
Troubleshoot and debug customer's issues

technologies Google Cloud Platform
BigQuery
Google Dataflow / Apache Beam
Google Composer / Apache Airflow
Google Cloud Pub/Sub
Python

November 2013 - April 2018

institution **INSTITUTE FOR RESEARCH IN BIOMEDICINE (BARCELONA)**

group *Molecular Modeling and Bioinformatics*

position *PhD Student*

duties Perform bioinformatics research on Nucleosome Positioning
Develop and implement statistical analysis methods
Develop and maintain R packages
Integrate my code into bigger genomics frameworks

technologies R
C
Python
Bioconductor
Sun Grid Engine
MongoDB

EDUCATION

2013-2018 **PhD in BIOMEDICINE (unfinished)**
Universidad de Barcelona

2012-2013 **MSc in BIOINFORMATICS**
Universidad Autònoma de Barcelona

2008-2012 **BSc in BIOCHEMISTRY**
Universidad Autònoma de Barcelona

RESEARCH PUBLISHED SOFTWARE

name	NucleosomeDynamics
language	<i>R and C</i>
function	Suite for nucleosome positioning analysis using MNase-seq
forms	Standalone R package Backend to the NucleosomeDynamics web service Tool integrated within the VRE of the Multiscale Genomics European project

CONGRESSES ATTENDED

	2016
name	15th European Conference on Computational Biology
location	<i>World Forum Convention Center (The Hague, Netherlands)</i>
poster presented	NucleosomeDynamics: a web portal to analyze and visualize MNase-seq data
name	XIII Symposium in Bioinformatics
location	<i>Universidad politécnica de Valencia (Valencia, Spain)</i>
talk given	NucleosomeDynamics: a web portal to analyze and visualize MNase-seq data

WORKSHOPS GIVEN

	2017
name	Multi-scale study of 3D Chromatin Structure
location	<i>European Bioinformatics Institute (Cambridge, UK)</i>
topic I covered	MNase-seq data analysis using the MuG research environment
name	Multi-scale genomics
location	<i>Barcelona Supercomputing Center (Barcelona)</i>
topic I covered	MNase-seq data analysis using the MuG research environment
	2016
name	3DAROC 2016
location	<i>Instituto Gulbenikan de la ciência (Lisboa, Portugal)</i>
topic I covered	MNase-seq data analysis using the NucleosomeDynamics portal

INTERSHIPS

	2011 - 2013
description	<i>Master's internship / Colaboration scholarship / Degree's internship</i>
group	Protein folding and conformational diseases
institution	Institute of Biotechnology and Biomedicine (Barcelona)
	2012
description	<i>Internship</i>
group	Peptide synthesis and protein structure
institution	Institute for Research in Biomedicine (Barcelona)
	2012
description	<i>Exchange Student</i>
group	Biophysics and radiation biology
institution	Semmelweis University (Budapest)

PUBLICATIONS

- Buitrago D, Codó L, Illa R, et al. Nucleosome Dynamics: a new tool for the dynamic analysis of nucleosome positioning. *Nucleic Acids Res.* 2019;47(18):9511-9523. doi:10.1093/nar/gkz759
- Dans PD, Daniłane L, Ivani I, et al. Long-timescale dynamics of the Drew-Dickerson dodecamer. *Nucleic Acids Res.* 2016;44(9):4052-4066. doi:10.1093/nar/gkw264
- Zambrano R, Conchillo-Sole O, Iglesias V, et al. PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores. *Nucleic Acids Res.* 2015;43(W1):W331-W337. doi:10.1093/nar/gkv490
- Navarro S, Diaz-Caballero M, Illa R, Ventura S. Aggregation propensity of neuronal receptors: potential implications in neurodegenerative disorders. *Future Sci OA.* 2015;1(2):FSO39. Published 2015 Sep 1. doi:10.4155/fso.15.39
- Fraga H, Graña-Montes R, Illa R, Covaleda G, Ventura S. Association between foldability and aggregation propensity in small disulfide-rich proteins. *Antioxid Redox Signal.* 2014;21(3):368-383. doi:10.1089/ars.2013.5543