



André C. Guerra

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Expertise

Back-end Development

The back end of a software usually consists on multiple servers, an applications, and databases. A back-end developer builds and maintains the stack technology that powers those components and their intercommunication. I've extensive understanding on server-side languages and frameworks and have build several versioned, production-ready APIs with different bussiness logic associated.

Data Science and Analysis

From data to knowledge. In order to achieve such goal data must be processed, modelled and the produced results must be properly interpreted and displayed. I've considerable knowledge on big data processing frameworks along with modern modelling techniques based on multivariate data analysis, machine learning and artificial intelligence.

Software Engineering

Design, build, test and repeat. A software engineer main responsibility is the iterative management of software development in order to meet clients or business logic requirements. I've experience working in diversified teams of software engineers and developers under agile development environments and versioned production deployments.

Biotechnology

Biotechnology is the use living biological systems to yield products. Along with the technology and products, huge amounts of data are typically produced. Also, biotechnology is without a doubt the field with most diversity of data, from DNA to protein, from cell to process... I've dedicated most of my graduate studies developing models and processing data for biopharmaceutical and biotechnology.



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Experience

2019 - Present

COMPUTATIONAL BIOLOGIST

Alchemy Project - Amyris

UCP, Porto, Portugal

2015 - 2018

EARLY STAGE RESEARCHER

Marie Curie Scholarship, ITN Biorapid, Rapid Bioprocess Development

Newcastle University, Newcastle upon Tyne, United Kingdom

2012 - 2013

RESEARCH TRAINING COURSE D

Instituto de Tecnologia Química e Biológica

Oeiras, Portugal

Skills

LANGUAGES

Python, Java, R, Go, Javascript

Proefficient in Object Oriented Languages and Functional Programming.

DATABASES

MySQL, PostgreSQL, MongoDB, Neo4J, Redis

Good understanding of most SQL and No-SQL databases alongside with their ORMs.

WEBSERVERS

Django, Spring, ExpressJS, FastAPI

Intermediary knowledge on MVC platforms for rapid webserver prototyping.



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PROTOCOLS & APIS

RestAPI, AMQP, GraphQL, gRPC, Websockets

Diverse knowledge on protocols for back-end development.

DATA ACQUISITION

Streams, OPC UA, R Dataframes, Pandas, Numpy

Knowledge on online and off-line data collection.

DATA PROCESSING

Hadoop, Spark, Flume, KNIME, Dplyr

Efficient on data processing using conventional dataframe packages aswell as streaming frameworks.

MODELLING

Keras/Tensorflow, Caret, Scikit-learn, Statsmodels

Proefficiency on data modelling with major emphasis on statistical machine-learning model applications.

VISUALIZATION

GG Plot, Bokeh, Plotly, D3

Learning to present charts visualizations on dynamic WebGL platforms.

BUILD & TESTING

Gradle, Maven, JUnit, Mockito, Pytest, Tox, Hypothesis

Knowledge on automatic build tools for packaging and unit testing.

MICROSERVICES

Kubernetes, Docker

Good understanding of microservice architectures along with SOA best practices.

CI/CD & VCS

Jenkins, Jira, Gitlab, Github

Knowledge on integration of agile development with versioning deployments.



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PROVIDERS

AWS, GCC, Terraform, Pulumi

Intermediary usage of cloud providers and implementation of IaC.

Publications

Machine learning in biopharmaceutical manufacturing

The biotechnology industry is expected to increase the production of new biopharmaceuticals. Biopharmaceuticals require high-quality standards, high initial investments for approval and introduction into the market as well as continued investment in manufacturing.

Toward biotherapeutic product real-time quality monitoring

Biotherapeutics, such as those derived from monoclonal antibodies (mAbs), are industrially produced in controlled multiunit operation bioprocesses. Each unit operation contributes to the final characteristics of the bioproduct. The complexity of the bioprocesses, the cellular machinery, and the bioproduct molecules, typically leads to inherent heterogeneity and variability of the final critical quality attributes (CQAs). In order to improve process control and increase product quality assurance, online and real-time monitoring of product CQAs is most relevant. In this review, the recent advances in CQAs monitoring of biotherapeutic drugs, with emphasis on mAbs, and throughout, the different bioprocess unit operations are reviewed. Recent analytical techniques used for assessment of product-related CQAs of mAbs are considered in light of the analytical speed and ability to measure different CQAs. Furthermore, the state of art modeling approaches for CQA estimation in real-time are presented as a viable alternative for real-time bioproduct CQA monitoring under the process analytical technology and quality-by-design frameworks in the biopharmaceutical industry, which have recently been demonstrated.

Education



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2015 - 2018

EARLY STAGE RESEARCHER - PHD STUDENT IN CHEMICAL ENGINEERING

School of Engineering, Newcastle University
Newcastle upon Tyne, United Kingdom

Exploiting integrated rapid bioprocess monitoring methods for acceleration of process development

Integrate the analytical and modelling methods developed in all WPs into a framework for accelerated process development. Methods to build process model toolbox need to address knowledge diversity in addition to specifying process model structure and capability and the means by which the process model is parameterised. Among the important innovations is the ability of such models to incorporate a quantification of belief that can be utilised to determine the risk. Bayesian strategies offer both this capability and the opportunity to refine the representation as knowledge is accumulated. Another representational challenge is the ability to capture the behaviour of a whole process rather than individual unit operations. The difficulty involves the capture of unit to unit interactions and the representational requirements of other units to build a whole process description. Here agent based strategies offer great potential. Foremost among all the representational problems faced is the need to specify structure. Hybrid relationships offer a means of using mechanistic knowledge but other approaches can be used to capture structure, evolutionary computational approaches offer a practical alternative. This project will review the most appropriate methodology for general monitoring framework in bioprocessing and develop the overall rapid bioprocess development framework integrating all the model representations from the remaining BioRapid projects.

2014 - 2015

MASTER DEGREE IN BIOTECHNOLOGY

Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa
Caparica, Portugal

Genome-scale metabolic network reconstruction of Polaromonas JS666 strain for analyzing cDCE degradation rates and bioremediation improvement

Several bioinformatic tools were used in order to reconstruct the metabolic network from the partially annotated genome of Polaromonas sp. JS666, a microorganism capable of using cDCE as the sole carbon and energy source. After this initial curation, the model shall be correlated with published bibliographic data using Flux Balance Analysis. Hence the final model, iJS666, will be able to predict the optimum extracellular metabolites concentrations such that cDCE degradation rates would be maximized.



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2009 - 2013

BACHELOR DEGREE IN CELLULAR AND MOLECULAR BIOLOGY

Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa
Caparica, Portugal

Awards

2015

BEST STUDENT

Master in Biotecnology

Faculdade Ciencias e Tecnologia, Universidade Nova de Lisboa

Interests

BOOKS

I'm a huge fan of sci-fi and distopian books. All time favorite: Dune.

SPORTS

Sports are really not my expertise however I'm a passionate football and MotoGP fan.

OTHERS

Herpetology and Aquariofilia.

MISCELLANEOUS

European Driver's Licence (2013), Type A1, A & B1.