



INTI MANUEL YABAR-PAGAZA

COMPUTATIONAL BIOLOGIST

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Lyngby, Denmark

PROFILE

I am a computational biologist with a background in biochemistry and a strong interest for math, physics and data science. I have experience with automation of data analysis, and enjoy teaching and communicating scientific and technical topics.

I find programming great for creating insightful and useful tools and I enjoy building programs that create value for many users.

EXPERIENCE

2019-2020

RESEARCH ASSISTANT

at **Technical University of Denmark**

Lyngby, Denmark

Computational and experimental investigation of biophysical properties of amyloid fibrils in the Protein Biophysics Group at Bioengineering led by Prof. Alexander K. Büll.

- calculated structural and energetic changes in amyloid fibrils upon mutations using Monte Carlo-based methods in Rosetta and PyRosetta.
- analyzed temperature and chemical dependence of fibril dissociation.
- set up protocols to automate liquid handling for high throughput biophysical experiments.

2014-2018

STUDENT HELPER

at **Novozymes**

Bagsværd, Denmark

- developed web application to facilitate overview of progress of gene library samples using Python and SQL.
- automated data analysis and visualization for numerous projects involving assays using JMP Scripting Language.
- created parsers to unify data in standard complying format extracting metadata.

2014-2017

ASSISTANT TEACHER

at **University of Copenhagen**

Copenhagen, Denmark

Assisted teaching in Biochemical Student Cafe and the summer Brush-up course for new attending biochemical students.

- taught and organized a week-long intensive math and chemistry course aimed to brush-up new students that are going to study biochemistry.
- helped first-year biochemistry students with weekly problem sets in mathematics, biology, organic chemistry and biochemistry.
- created explanatory solutions for problem sets for fellow assistant teachers.

IT SKILLS

Python



Experience with web apps (Flask, Dash), data analysis and visualization (pandas, matplotlib), and creating machine learning models (Pytorch).

SQL



Experience using MySQL databases connected to web apps.

Bash



I have been using linux systems and the bash shell language daily for 5+ years.

JSL



I have created several scripts to automate the analysis of high throughput screening data.

VBA



I have used VBA to automate data formatting for input to liquid handling robots working in Novozymes.

R



During the course *Statistics for Biochemistry* I analyzed data using various statistical models in R.

HTML and CSS



I have experience creating simple pages and stylesheets for project pages.

CERTIFICATES

IBM AI Engineering Specialization

at **Coursera**

I completed a 6 course Professional Certificate and gained a practical understanding of **Machine Learning (ML)** & **Deep Learning (DL)**. This provided me with the technical skills to build AI systems, and :

- Implement ML algorithms including Classification, Regression, Clustering, and Dimensional Reduction using scipy & scikitlearn.
- Perform ML on Big Data and deploy ML Algorithms and Pipelines on Apache Spark.
- Demonstrate understanding of Deep Learning models such as autoencoders, restricted Boltzmann machines, convolutional networks, recursive neural networks, and recurrent networks.
- Build deep learning models and neural networks using Keras, PyTorch and Tensorflow libraries.
- Demonstrate ability to present and communicate outcomes of deep learning projects.

Verify at: coursera.org/verify/professional-cert/HSNG3RS3VPJL



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EDUCATION

2016-2019

- MSC IN BIOCHEMISTRY (PROTEIN CHEMISTRY)**
 at **University of Copenhagen** Copenhagen, Denmark
 Courses in bioinformatics and biophysics with focus on structural biology.
 My thesis, *Characterization of San1p*, was supervised by Prof. K. Lindorff-Larsen, and focused on biophysical and bioinformatic characterization of a yeast ubiquitin ligase.
 During the biophysical characterization I carried out nuclear magnetic resonance spectroscopy and nano differential scanning fluorimetry.
 In the bioinformatic part of the I carried out coevolution analysis on the protein and analyzed the protein family of San1p using profile hidden Markov models.

2013-2016

- BSC IN BIOCHEMISTRY**
 at **University of Copenhagen** Copenhagen, Denmark
 Courses in mathematics, physical chemistry, statistics and bioinformatics.
 My thesis, *Understanding and Mapping Mutations in HIV-1 Protease*, was supervised by prof. K. Lindorff-Larsen, and focused on predicting the resistance of HIV-1 protease mutants to protease inhibitors used in HIV mutations.
 During the project I worked with the Rosetta software suite to predict $\Delta\Delta G$ of mutated protease structures and compared with experimental data from a resistance assay and clinical databases.

VOLUNTEER EXPERIENCE

2019-2020

- MATH INSTRUCTOR**
 at **Matematik Center** Copenhagen
 I weekly help middle and high school students with understanding mathematical concepts and solving mathematical problems.

2014-2015

- INTRODUCTORY TUTOR**
 at **University of Copenhagen** Copenhagen, Denmark
 organized social and academic events for 100+ biochemistry students throughout the academic year.

PROJECTS

HMMLOGO

Visualize profile hidden Markov models (pHMMs) in Python using the HMMLogo package.
hmmlogo.readthedocs.io

HMMLOGO VISUALIZER

Flask app that showcases functionality of HMMLogo. Where you can visualize pHMMs.
imyptest.herokuapp.com

LANGUAGES

Danish

Native speaker. Born and raised in Denmark.

English

Fluent proficiency written and spoken.

Spanish

Native speaker with peruvian descent.

PERSONAL SKILLS

Analytical

I enjoy problem solving, finding edge cases and studying complex systems.

Curious

I enjoy learning about new topics and understand how processes work.

Cooperative

I enjoy collaborations, reciving and giving feedback to colleagues.

ACADEMIC SKILLS

Project management

I can formulate, structure and carry out a project that aims out to question answer a scientific question.

Research

I can develop and apply biological and computational methods to generate new knowledge.

Data analysis

I can generate, assess, and analyze data and find potential sources of error, relevance of applied methods and validity of data.

REFERENCES

Kresten Lindorff-Larsen

Professor of Biomolecular Sciences
Department of Biology
University of Copenhagen

Alexander K. Büll

Professor of Protein Biophysics
Department of Biotechnology and Biomedicine
Technical University of Denmark