**Daniella L. Matute, MSc.**

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**SUMMARY**

* **Synthetic & Computational Biologist** with 5+ years’ in BSL-2 labs and +6 years programming & data analysis experience.
* Specialty domain: Combining engineering principles (DBTL) & molecular biology techniques.
* Career Purpose: Make “The Century of Biology” a reality & transform biology into a formalized engineering field.
* Extroverted, analytical, data driven M.Sc. looking for a **multidisciplinary position with access to lab-automation platforms.**

**SKILLS**

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| **Laboratory Skills** | | |
| Molecular Biology  &  Biochemical / Biophysical Assays | * RNA isolation, DNA isolation, DNA restriction, electrophoresis, northern & southern blotting, RT/qPCR, Situ Hybridization & DNA microarrays, RNA-seq, sanger sequencing, Nanopore Sequencing, NGS (Illumina & ONT) prep. * Plasmid vector design, Golden Gate assembly, primer design, bacterial transformation, plasmid cloning, DNA library creation, Genome Editing Techniques (TALENs, CRISPR-Cas9), enzymatic digestion * Cell lysis (sonification, chemical), Protein Purification (Affinity tags, Ultra-centrifugation isolation, precipitation, immunoblotting), Protein Assay (Bradford, immunological), protein expression (Lac, T7), SDS-PAGE, ELISA. * UV-visible, circular dichroism, NMR, fluorescence (probe & structural) spectroscopy; light scattering, SAXS & SANS; mass spectrometry; surface plasmon resonance, ITC; liquid & gas chromatography. | |
| Cell Culture | Media preparation, daily maintenance, cryopreservation, resuscitation of epithelial carcinoma (A549) | |
| **Computation Skills** | | |
| Programming | **Interfaces:** Unix/Linux, command line.  **Code Editors:** Jupyter Notebooks, VSC, R Studio. | **Languages:** Python, SQL, R, MATLAB, HTML. **Other:** OOP, GIT Version control, Unit Testing. |
| Python Packages | Pandas, NumPy, Matplotlib, Scikit, Scipy, RShiny |  |
| Synthetic Biology / Bioinformatic Tools | * SnapGene (plasmid editor, assembly simulation, annotation), PyMOL biomacromolecules visualization, DNA & Protein database (NCBI, RefSeq, GeneBank, SwissProt, NEBCutter2, UniProt, Addgene, EMBL, Ensembl) * Sequencing Cleaning (FastQC), de novo assembly (SPAdes, Wtdbg2), Scaffolding (GapFiller), Quality assessment (BUSCO, N50), Read mapping (BWA, Bowtie), variant calling (SAM tools, Freebayes), 16S rRNA amplicon analysis (Qiime2, DADA2) | |
| Other | Research Tools: Zotero  Languages: Fluent Spanish & English | |

**RESEARCH EXPERIENCE**

**Edinburgh Genome Foundry** - Edinburgh, Scotland 05/2022 – 08/2022

*MSc Dissertation Project (self-lead) - Automation Engineer Intern*

* Scripted (Python) and automated the MetClo DNA assembly protocol on the Opentrons OT2 robot.
* Slashed assembly planning time of 96 well plate to <1min by scripting a computer aided design program.
* Generated a modular assembly pipeline that can be integrated into Biofoundries systems or small laboratories.

**Metagenomic/taxonomic analysis of Anaerobic Digestors in Wastewater Plants** -Edinburgh, Scotland 01-05/2022 & 01-05/2023

* Identified various taxonomic markers to evaluate the health of the reactors, and their ability to produce biogas.
* Assess the flux of antimicrobial resistance taxa throughout the plant from input sewage to its environmental release.
* Reported on the impact of organic overload on the microbiome and microbiota.

**Whole Genome Assembly quality assessment of Solanum stenotomun (Sst)** - Edinburgh, Scotland 04/2023 - 05/2023

* Evaluated the sequencing and whole genome assembly technologies used for Sst to previous sequencing results of related taxa.

**Stem Cell Lineage Determination Computational Model** - Edinburgh, Scotland 11/2021 - 12/2021

* Modeled differentiation transcription factors expression behaviors from published micro-array & ChiP-on-chip result equations.
* Computational mathematical modeling determined that the trophectoderm and differentiate to endoderm lineage without the need to return to the embryonic stem cell state, suggesting the system is pluripotent.

**Genetic and Cellular Disposition for Gefitinib Treatment in Non-Small Cell Lung Cancer** - Virginia, USA 05/2021 - 07/2021

* Explored susceptibility of L858R mutated small-cell-lung-cancer to enter epithelial-mesenchymal transition (EMT) by exposure to Gefitinib, a toxic and resistance-prone tyrosine kinase competitive-inhibitor.
* Assess the impact of drug toxicity and EMT commencement/progression by conducting: Gene & protein expression analysis, Immunochemical microscopy of EMT regulating transcription factors.

**WORK EXPERIENCE**

**Korean Institute of Ocean Science and Technology Busan, South Korea**

*Molecular Biology Research Intern* 06/2018 – 08/2018

* Designed plasmids and expressed/purified protein at various scales in anaerobic and aerobic prokaryotes.
* Functional relationship analysis between hydrogenase and target proteins in hyperthermophilic archaeon.

**ChongKunDang Pharmaceuticals Seoul, South Korea**

*Pharmaceutical Market Research R&D Intern*  04/2020 – 06/2020

**Boryung Pharmaceuticals Seoul, South Korea**

*Global Marketing and Regulatory Affairs Intern*  08/2019 - 10/2019

**EDUCATION**

**The University of Edinburgh (Scotland) -** Distinction Award & 4.0 GPA 12/2022

*Master of Science in Synthetic Biology & Biotechnology*

**George Mason University (VA, USA) -** Cum Laude Award & 3.63 GPA05/2019

*Bachelor of Science in Biology -*Concentration in Molecular biology and Biotechnology & Minor in Business

**Professional Development:** Machine Learning & Data Science Bootcamp (in progress), Unit-testing, Git Versioning.