Carlos Vigil Vásquez

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Academic Background

- **B.S. Biochemistry** — Santiago, Chile
  Pontificia Universidad Católica de Chile — *2015 - 2022*
  - Graduation exam grade: 6.3/7.0
  - Undergraduate thesis grade: 7.0/7.0
  - Bachelors grade: 6.0/7.0
  - Undergraduate thesis titled "Weak-link paradox for *de novo* prediction of pharmacological targets"

Work experience

- **Protein Designer**
  Protera Bioscience; Santiago, Chile — *September 2023 - today*
  - Implementation, validation and maintainance of computational biology modules for madi™, protera's propietary SaaS platform for protein design applications.
  - Conduct extensive analysis and modelling related to Protera's clients projects, utilizing bioinformatics, structural biology and protein design strategies.

- **Research Assistant - Neurobiology of Aging Laboratory** — Dra. Cheril Tapia-Rojas, Ph. D.
  Universidad San Sebastián; Santiago, Chile — *May - August 2023*
  - Conducted extensive bioinformatic analysis as part of a study investigating the correlation between mitochondrial protease Lonp1 and age-associated neurodegenerative diseases.
  - Contributed writing and creating figures for a manuscript and poster presentation related to the previously mentioned work.

- **Research Assistant & Thesis student - Molecular Design Laboratory** — Dr. Andreas Schüller, Ph. D.
  Pontificia Universidad Católica de Chile; Santiago, Chile — *July 2017 - June 2023*
  - *Summa cum laude* undergraduate thesis titled "Weak-link paradox for *de novo* prediction of pharmacological targets" between August, 2020 and June, 2022.
  - Proposal and implementation of "SimSpread", a novel predictive model that combines graph theory and the concept of chemical similarity for drug discovery and repositioning, its optimization using different cross-validation schemes, and evaluation of the predictive performance of the proposed models.
  - Related study on the discovery of drugs with antifungal activity using the SimSpread predictive model, discovering 4 new compounds with antifungal activity for 8 clinically relevant fungal organisms.
  - Authored `SimSpread.jl`, a software package for the `Julia` programming language that implements the SimSpread formalism for link prediction in graphs.
  - Advised in the initiation and development of 3 projects related to the SimSpread model, related to increasing its predictive power, and extending the application domain and accessibility of the method.
  - Authored a scientific publication, prepared multiple poster presentations and contributed to writing original research manuscript in the context of the SimSpread project and other projects developed at the laboratory.

- **Research secondee - REFRACT MSCA RISE PROJECT 2019** — Dr. Damien Devos, Ph. D.
  Universidad Pablo de Olavide; Sevilla, España — *September 2022 - December 2022*
  - Proposal and implementation of "ResidueFisher", an open-source bioinformatics protocol to aid remote homology search between proteins using sequence and structural information.
  - Lead the writing of the application note for the previously mentioned protocol.

- **Research Assistant - Psychophysiology Laboratory** — Dr. Diego Cosmelli Sánchez, Ph. D.
  Pontificia Universidad Católica de Chile; Santiago, Chile — *January 2022 - December 2022*
  - Implementation of analysis protocol based on machine learning, statistical modeling, and feature extraction of the trained models for a human study that resulted in the identification of the effect of different contemplative practices (e.g., meditation) on the well-being of the subjects studied.
  - Contributed writing the methods and results sections of a paper related to the work previously mentioned.

- **Teaching Assistant - Biostatistics** — Dr. Andreas Schüller, Ph. D.
  Pontificia Universidad Católica de Chile; Santiago, Chile — *July 2017 - December 2017*

Academic Productivity

1. Publications:

- "*De novo* prediction of drug targets and candidates by chemical similarity-guided network-based inference"; **C. Vigil-Vásquez** and A. Schüller. IJMS (2022). DOI:10.3390/ijms23179666

2. Poster presentations:

- "Changes in epigenetic control and loss of Lonp1 proteolytic protease activity induce abnormal protein accumulation and mitochondrial dysfunction in aging"; J. Llanquinao, C. Jara, M. Lira, **C. Vigil-Vásquez**, M. Sjöberg, A. Schüller, B. Kerr and C Tapia-Rojas. SBCCH (November, 2023)
- "De Novo Prediction of Pharmaceutical Targets Using Network-Based Inference Guided by Chemical and Structural Similarities."; M. Saez-Ortega, V. Valdes, **C. Vigil-Vásquez** and A. Schüller. PUC-IIBM Symposium (November, 2023)
- "SimSpread Ensemble Model and SimSpread web server for prediction of drug-target interactions"; F. Melo, V. Valdes, **C. Vigil-Vásquez**, A. Schüller. PUC-IIBM Symposium (November, 2023)
- "Antifungal drug discovery by chemical similarity-guided network-based inference"; **C. Vigil-Vásquez**, M. Jimenez-Socha, P. Ortiz-Bermudez and A. Schüller. Chilean Bioinformatics Society (January, 2022)
- "DDTNBI: *de novo* target prediction using a social network-derived method"; **C. Vigil-Vásquez** and A. Schüller. International Society for Computational Biology/European Conference on Computational Biology (August, 2021)
- "A computational chemogenomics method for the prediction of off-target interactions with coagulation factor Xa"; A. Schüller and **C. Vigil-Vásquez**. European Hematology Association (August, 2020)
- "Limits and potential of in silico target prediction by chemical similarity"; M. Ruiz, **C. Vigil-Vásquez** and A. Schüller. International Society for Computational Biology-LA (October, 2018)

3. Awards:

- **Undergraduate Research Contest - Summer 2020**: Project titled "Use of biochemical networks for the prediction of novel drugs for coagulation factor Xa."
- **Undergraduate Research Contest - Winter 2017**: Project titled "*In silico* prediction and prioritization of novel drug targets."

Languages

- **Spanish**: native
- **English**: TOEFL, 101/120 points; over 24 points over all categories

Skill set

- **Machine languages**: Julia, Python, LaTeX, Bash/Shell scripting, Lua
- **Predictive modelling**: Transfer learning, Machine learning (supervised and unsupervised models), conformal prediction, data processing, database management, REST API, data clustering and evaluation, predictive model evaluation, recommender systems, data visualization, biostatistics, statistics and probability, graph theory, network analysis, Scikit-Learn, Pandas, NumPy, Matplotlib, Seaborn, NetworkX, Pingouin
- **Bioinformatics**: Protein Language Model, Sequence alignment, MSA, structural alignment, molecular docking, structural biology, PyMOL scripting, AlphaFold modeling and evaluation, omics analysis, biostatistics, phylogenetic tree construction.
- **Cheminformatics**: Molecular descriptor preparation, chemical similarity analysis, confomer preparation, pharmacophoric modeling, RDKit, OpenBabel, computational representation of chemical compounds
- **Tools**: Git, GitHub, MySQL, SQLite, slurm
- **Platforms**: Linux, MacOS, docker

Extracurricular Activities

- **Co-delegate of the National Asociation of Biochemistry Students (ANEB)**: 2018
- **Member of the National Asociation of Biochemistry Students (ANEB)**: 2016 to 2021
- **Member of the International Society for Computational Biology (ISCB)**: 2018 & 2021
- **Author and maintainer of** `esqueleto.nvim`: 2023 - today
- **Author and maintainer of** `SimSpread.jl`: 2022 - today