Contact

www.linkedin.com/in/wayne-delport
(LinkedIn)

Top Skills

Bioinformatics
Computational Biology
Sequence Analysis

Languages

Afrikaans

Publications

A random effects branch-site model for detecting episodic diversifying selection.

The relatedness of HIV epidemics in the United States-Mexico border region.

Clinical, virologic, and immunologic correlates of HIV-1 intraclade B dual infection among men who have sex with men.

Using phylogeography to characterize the origins of the HIV-1 subtype F epidemic in Romania.

Characterization and evolution of the mitochondrial DNA control region in hornbills (Bucerotiformes).

Wayne Delport

CTO | Co-founder
San Diego, California, United States

Summary

Technology leader with >10 years' experience delivering computational biology solutions in the cloud. Dedicated to quality, well-versed in regulatory requirements for clinical genomics products, and skilled in leading cross-functional technology teams to meet product deliverables.

Experience

Simplify Genomics, Inc.

Chief Technology Officer
January 2022 - Present (2 years 11 months)
San Diego, California, United States

Human Longevity, Inc.

7 years 1 month

Vice President Of Technology and Bioinformatics
October 2019 - February 2022 (2 years 5 months)
Greater San Diego Area

Director of Bioinformatics
October 2017 - October 2019 (2 years 1 month)
Greater San Diego Area

Bioinformatics R&D Lead
October 2016 - October 2017 (1 year 1 month)
San Diego, California

Bioinformatics Scientist
February 2015 - October 2016 (1 year 9 months)
Greater San Diego Area

Prognosys Biosciences

4 years 3 months

Bioinformatics Scientist II
October 2012 - February 2015 (2 years 5 months)

Greater San Diego Area

- Responsible for processing of Next Generation Sequencing Data, including the development of custom analysis approaches for novel assays being developed in-house.

- Responsible for statistical analysis of large and complex sets of biological data, including microarray and next generation sequence data.

- Responsible for statistical power analyses, and defining robust statistical designs for biological experiments.

- Responsible for computational design of oligonucleotide probes for highly-multiplexed hybridization-based assays.

- Responsible for maintaining IT infrastructure and providing desktop support to users.

- Co-developed and launched web-based commercial software for analysis of RNA-Seq data. Major responsibilities included the development of web-based content management system, user-interface, data quality control procedures, automated management of Amazon Web Services compute resources and delivery of results (Technologies utilized: Python, MySQL, Unix shell scripting, Java, Java Applets, Java Web Start, Amazon Web Services, Django-Nginx-Gunicorn HTTP server, Oracle Grid Engine)

Bioinformatics Scientist I

December 2010 - October 2012 (1 year 11 months)

UC San Diego

Project Scientist

April 2009 - December 2010 (1 year 9 months)

- Developed and implemented novel phylogenetic models of evolution in the HyPhy (www.hyphy.org) phylogenetic analysis package (Technologies utilized: HyPhy Batch Language, Unix Cluster computing).

- Published papers in leading academic journals.

- Assisted students, postdoctoral students and clinicians with the analysis of DNA sequence data.

- Implemented several new evolutionary analyses methods on the datamonkey webserver (www.datamonkey.org), including Toggling Selection, Directional Evolution in Protein Sequences and Codon Model Selection (Technologies utilized: Perl, HyPhy Batch Language, Unix shell scripting).
Implemented a HIV-1 ultradeep sequence analyses pipeline (Technologies utilized: Perl, HyPhy Batch Language, Unix shell scripting).

- Co-supervised postdoctoral research students.

University of Cape Town
Postdoctoral Scientist
January 2006 - March 2009 (3 years 3 months)

- Development, testing and implementation of novel models of sequence evolution for HIV-1 sequence analysis (Technologies utilized: HyPhy Batch Language, Unix Cluster computing).

- Published papers in leading academic journals.

- Co-supervised MSc and undergraduate students in the Computational Biology Group

- Developed and maintained a Single Nucleotide Polymorphism MySQL database for two human genetics projects (Technologies utilized: Perl, MySQL).

- Performed population genetic genome-wide analyses and prepared manuscripts for publication (Technologies utilized: MySQL, Unix shell scripting, Perl).

- Presented research at local High Performance Computing and International Evolutionary Biology conference.

Education

University of Pretoria/Universiteit van Pretoria
MS, PhD, Zoology, Genetics · (1997 - 2005)

University of the Witwatersrand
BS, Biology · (1994 - 1996)