

René



Warren

warrenlr [at] g m a i l [dot] com

<https://warrenlr.github.io>

20+ Years Experience - Biotechnology | Genomics | Informatics

Developed first *de novo* genome assembly software (SSAKE) with short DNA sequences

Discovered *Fusobacterium* in colon cancer, a Time Magazine's 2011 top ten breakthrough

Coordinated bioinformatics analyses of *Rhodococcus*, *Cryptococcus*, bullfrog & spruce genomes

Seeking New Challenges

Additional Leadership

EXPERIENCE

ACCOLADES

Group Leader

BC Cancer – Genome Sciences Centre Vancouver
Research project concept, management, guidance
Interview, supervise, mentor staff / students

Bioinformatics Coordinator

BC Cancer – Genome Sciences Centre Vancouver
Lead bioinformatics R&D
Interviewed, taught, trained, supervised staff

Technical Officer

NRC – Biotechnology Research Institute Montréal
Engineered gene expression regulation technology
Collaborated with stakeholders / scientists

2017-current

2002-17

2000-01

2015, 16 **Awarded** John Jambor Knowledge Fund
2011 **Interview** *Fusobacterium* cancer discovery
2009 *Genome Technology* **interview**, next-gen. seq.
2007 *GenomeWeb* **interview**, SSAKE development
1998 **Awarded** MSc UBC Graduate Fellowship
1997 **Awarded** BSc FRSQ bursary
1996 **Awarded** BSc FRSQ honour's research project
1995 **Worked** at NASA, CMIX-4 payload

PRESENTATIONS

Selected from 17 lead author

2017, 18 **RECOMB** Hong Kong / Paris **talks**
2015, 16, 19 **ISMB** Dublin / Orlando / Basel **talks**
2008, 12, 15 **Pac. Symp. Biocomputing** Hawaii **posters**
2010 **SFAF** Santa Fe **talk**
2007 **Synthetic Biology** Zürich **talk**

EDUCATION

PUBLICATIONS

Certificate Computer Science
Concordia University

MSc Biochemistry / Molecular Biology
University of British Columbia

BSc Biochemistry (*Honours*)
Université de Montréal

2001

1999

1997

*Selected from 70 peer-reviewed, 25 lead author, *co-first*

Warren RL, et al. 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics*. 35:4430

Warren RL, et al. 2015. LINKS: scalable, alignment-free scaffolding [...] genomes with long reads. *GigaScience*. 4:35

Warren RL, et al. 2012. Derivation of HLA types from shotgun sequence datasets. *Genome Med*. 4:95

Castellarin M*, Warren RL*, et al. 2012. *Fusobacterium* infection [...] in colorectal carcinoma. *Genome Res*. 22:299

Warren RL, et al. 2007. Assembling millions of short DNA sequences using SSAKE. *Bioinformatics*. 23:500

IT Skills Python PERL R MySQL HTML/js Git unix/mac/win Office

Projects SSAKE TASR HLAMiner LINKS XMV RAILS ARCS ntEdit ntJoin

References Available