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, Time Magazine's 2011 top 10 breakthrough
Coordinated bioinformatics analyses of *Rhodococus, Cryptococcus*, bullfrog & spruce genomes

Seeking New Challenges

Additional Leadership

EXPERIENCE

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

2017-current

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

2002-17

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

2000-01

ACCOLADES

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

Certificate Computer Science
Concordia University

2001

MSc Biochemistry / Molecular Biology
University of British Columbia

1999

BSc Biochemistry *(Honours)*
Université de Montréal

1997

PUBLICATIONS

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 SAM SSAKE TASR HLAminer LINKS XMV RAILS ARCS ntEdit

References Available