René Warren

warrenlr@gmail.com   778 . 386 . 4192   http://renewarren.ca

20+ years experience in 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 crystal.

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 **Concordia University**
Computer Science

2000

MSc **University of British Columbia**
Biochemistry & Molecular Biology

1997

BSc **Université de Montréal**
Biochemistry *(Honours)*

1994

PUBLICATIONS

Selected from 63 peer-reviewed | 23 lead author

Warren RL, *et al.* 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics. doi: 10.1093/bioinformatics/btz400*

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 upon request