René Warren

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

20+ years experience in biotechnology, genomics & informatics

Developed the first *de novo* genome assembly software (SSAKE) with short DNA sequences
Discovered *Fusobacterium* in colon cancer, one of Time Magazine's 2011 top ten breakthrough
Coordinated bioinformatics analyses of *Rhodococus, Cryptococcus*, Bullfrog & Spruce genomes

Seeking new challenges & additional leadership

EXPERIENCE

Group Leader
BC Cancer – Genome Sciences Centre, Vancouver
Lead group, project management & guidance
Conceptualize, lead, develop genome technologies
Interview, supervise, mentor staff / students

2017-current

Bioinformatics Coordinator
BC Cancer – Genome Sciences Centre, Vancouver
Lead bioinformatics R&D
Published research (science journals, conferences)
Interviewed, taught, trained, supervised staff

2002-17

Technical Officer
NRC – Biotechnology Research Institute, Montréal
Engineered gene expression regulation technology
Designed, fabricated, tested DNA "gene switch"
Collaborated with stakeholders / scientists

2000-01

ACCOLADES

2015, 16	**Awarded** *John Jambor Knowledge Fund*
2011	NTN24 **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 for honour's research project
1995	**Worked** at **NASA**, CMIX-4 payload protein 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

2000

Certificate Computer Science | **Concordia U.**

1997

MSc Biochemistry & Molecular Biology | **UBC**

1994

BSc Biochemistry *(Honours)* | **U. de Montréal**

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