

# 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 *Rhodococcus*, *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

### Coordinator

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

### Officer

**NRC – Biotechnology Research Institute**, Montréal  
Engineered gene expression regulation technology  
Designed, fabricated, tested DNA “gene switch”  
Collaborated with stakeholders, scientists

## EDUCATION

**Certificate** Comp. Science | **Concordia U.**

**MSc** Biochemistry & Molecular Biology | **UBC**

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

## 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 USA **talk**  
2007 **Synthetic Biology**, Zürich **talk**

## PUBLICATIONS

*61 peer-reviewed [23 lead author], \*co-first*

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

**Warren RL, et al.** 2015. LINKS: scalable scaffolding of 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* in colorectal carcinoma. *Genome Res.* 22:299

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

**IT Skills:** Python, PERL, R, MySQL, HTML/js, unix/mac/win, MSOffice, Git **Projects:** SAM, SSAKE, TASR, HLaminer, LINKS, XMV, RAILS, ARCS, ntEdit

*References available upon request*