

Peer-Reviewed Publications

*Authors contributed equally

60. Helbing CC, Hammond SA, Jackman SH, Houston S, **Warren RL**, Cameron CE, Birol I. 2019. Antimicrobial peptides from *Rana [Lithobates] catesbeiana*: Gene structure and bioinformatic identification of novel forms from tadpoles. *Sci. Reports*. TBD
59. Jackman SD, Coombe L, Chu J, **Warren RL**, Vandervalk BP, Yeo S, Xue Z, Mohamadi H, Bohlmann J, Jones SJM, Birol I. 2018. Tigmint: correcting assembly errors using linked reads from large molecules. *BMC Bioinformatics*. 19:393 doi:10.1186/s12859-018-2425-6
58. Xue Z, **Warren RL**, Gibb EA, MacMillan D, Wong J, Chiu R, et al. 2018. Recurrent tumor-specific regulation of alternative polyadenylation of cancer-related genes. *BMC genomics*. 19:536 doi:10.1186/s12864-018-4903-7
57. Coombe L*, Zhang J*, Vandervalk B, Chu J, Jackman S, Birol I, **Warren RL**. 2018. ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. *BMC Bioinformatics*. 19:234 doi:10.1186/s12859-018-2243-x
56. **Warren RL**. 2018. Visualizing genome synteny with xmatchview. *Journal of Open Source Software* 3:497 doi:10.21105/joss.00497
55. Khan H, Mohamadi H, Vandervalk BP, **Warren RL**, Chu J, Birol I. 2018. ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. *Bioinformatics*. doi:10.1093
54. Jones SJ, Haulena M, Taylor GA, Chan S, Bilobram S, **Warren RL**, et al. 2017. The Genome of the Northern Sea Otter (*Enhydra lutris kenyoni*). *Genes*. 8:379.
53. Jones SJM, Taylor GA, Chan S, **Warren RL**, Hammond SA, Bilobram S, et al. 2017. The Genome of the Beluga Whale (*Delphinapterus leucas*). *Genes*. 8:378.
52. Hammond SA, **Warren RL**, Vandervalk BP, Kucuk E, Khan H, Gibb EA, Pandoh P, Kirk H, Zhao Y, Jones M, Mungal AJ, Coope R, Pleasance S, Moore RA, Holt RA, Round JM, Ohora S, Walle BV, Veldhoen N, Helbing CC, Birol I. 2017. The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. *Nature Comm*. 8:1433 doi:10.1038/s41467-017-01316-7
51. Yeo S*, Coombe L*, Chu J, **Warren RL***, Birol I. 2017. ARCS: Scaffolding genome drafts with linked reads. *Bioinformatics*. 34:725-731.

doi:10.1093/bioinformatics/btx675

50. Hasan NA, **Warren RL**, Epperson LE, Malecha A, Alexander DC, Turenne CY, MacMillan D, Birol I, Pleasance S, Coope R, Jones SJM, Romney MG, Ng M, Chan T, Rodrigues M, Tang P, Gardy JL, Strong M. 2017. Complete Genome Sequence of *Mycobacterium chimaera* SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. *Genome Announc.* 5:e00963-17. doi: 10.1128/genomeA.00963-17.
49. Yang C, Chu J, **Warren RL**, Birol I. 2017. NanoSim: nanopore sequence read simulator based on statistical characterization. *GigaScience*. 6:1
48. Kucuk E, Chu J, Vandervalk BP, Hammond SA, **Warren RL**, Birol I. 2017. Kollector: transcript-guided de novo targeted assembly of genes. *Bioinformatics*. 33:1782
47. Jackman SD, Vandervalk BP, Mohamadi H, Chu J, Yeo S, Hammond SA, Jahesh G, Khan H, Coombe L, **Warren RL**, Birol I. 2017. ABySS 2.0: resource-efficient assembly of large genomes using a Bloom filter. *Genome Res.* 27:768
46. Chu J, Mohamadi H, **Warren RL**, Yang C, Birol I. 2017. Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. *Bioinformatics*. 33:1261
45. **Warren RL**. 2016. RAILS and Cobbler: Scaffolding and automated finishing of draft genomes using long DNA sequences. *The Journal of Open Source Software*. doi: 10.21105/joss.00116
44. Coombe L*, **Warren RL***, Jackman SD, Yang C, Vandervalk BP, Moore RA, Pleasance S, Coope RJ, Bohlmann J, Holt RA, Jones SJM, Birol I. 2016. Assembly of the complete Sitka spruce chloroplast genome using 10X Genomics' GemCode sequencing data. *PLoS ONE*. 11(9): e0163059
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39. **Warren RL**, Yang C, Vandervalk BP, Behsaz B, Lagman A, Jones SJ, Birol I. 2015. LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. *GigaScience*. 4:35
38. Paulino D*, **Warren RL***, Vandervalk BP, Raymond A, Jackman SD, Birol I. 2015. Sealer: a scalable gap-closing application for finishing draft genomes. *BMC Bioinformatics*. 16:230
37. **Warren RL***, Keeling C*, Yuen M, Raymond A, Taylor G, Vandervalk BP, Mohamadi H, Paulino D, Chiu R, Jackman S, Robertson G, Yang C, Hoffmann M, Weigel D, Ritland C, Isabel N, Jaquish B, Yanchuk A, Bousquet J, Jones S, Nelson D, Mackay J, Birol I, Bohlmann, J. 2015. Improved white spruce (*Picea glauca*) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. *The Plant Journal*. 83:189
36. Gibb EA, **Warren RL**, Wilson GW, Brown SD, Robertson G, Morin GB, Holt RA. 2015. Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. *Genome Med*. 7:22
35. Birol I, Mohamadi H, Raymond A, Raghavan K, Chu J, Vandervalk BP, Jackman S, **Warren RL**. 2014. Spaced seed data structures, Bioinformatics and Biomedicine (BIBM), 2014 IEEE International Conference, vol., no., pp.15, 2-5 Nov. 2014 doi: 10.1109/BIBM.2014.6999305
34. Vandervalk BP, Jackman SD, Raymond A, Mohamadi H, Yang C, Attali DA, Chu J, **Warren RL**, Birol I. 2014. Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph, Bioinformatics and Biomedicine (BIBM), 2014 IEEE International Conference, vol., no., pp.51, 2-5 Nov. 2014 doi: 10.1109/BIBM.2014.6999126
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7. Bakkeren G, Jiang G, **Warren RL**, Butterfield Y, Shin H, Chiu R, Linning R, Schein J, Lee N, Hu G, Kupfer DM, Tang Y, Roe BA, Jones S, Marra M, Kronstad JW. 2006. Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. *Fungal Genetics and Biology*. 43:655-666
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Phototransduction. *Novartis Found Symp.* 224:249-261. Publisher: John Wiley & Sons, N.Y.

1. Durocher D, Charron F, **Warren R**, Schwartz RJ, Nemer M. 1997. The cardiac transcription factors Nkx2-5 and GATA-4 are mutual cofactors. *EMBO J.* 16:5687-5696

Patents

1. E Allen-Vercoe, R Holt, R Moore, R Warren - US Patent App. 13/877,421, 2011. Detection of fusobacterium in a gastrointestinal sample to diagnose gastrointestinal cancer.

First-Author Conference Presentations

16. 22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018 (Poster)
15. 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB), Hong Kong, May 2017 (Selected talk)
14. American Society of Human Genetics (ASHG), Vancouver, Canada, October 2016 (Poster)
13. 24th Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track)
12. 23rd Intelligent Systems for Molecular Biology (ISMB), Dublin, Ireland. July 2015 (Invited talk – late breaking research track. Selected talk - HiTSeq)
11. Student Biotechnology Network, Vancouver, Canada. February 2015 (Invited talk)
10. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2015 (Poster)
9. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2012 (Poster)
8. Sequencing, Finishing and Analysis in the Future, Santa Fe, New Mexico, USA. June 2010 (Oral presentation)
7. Advances in Genome Biology and Technology, Marco Island, Florida, USA. February 2009 (2 Posters)
6. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2008 (Poster)

5. Synthetic Biology 3.0 conference, Zurich, Switzerland. June 2007 (Invited talk)
4. 5th CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. October 2005 (Poster)
3. 7th Annual Conference on Computational Genomics. Reston, Virginia, USA. October 2004 (Poster)
2. Genomes 2004: International Conference on Microbial Genomes analysis. Hinxton, UK. April 2004 (Poster)
1. 3rd CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. May 2003 (Poster)