

Scalable solutions for *de novo* genome assembly

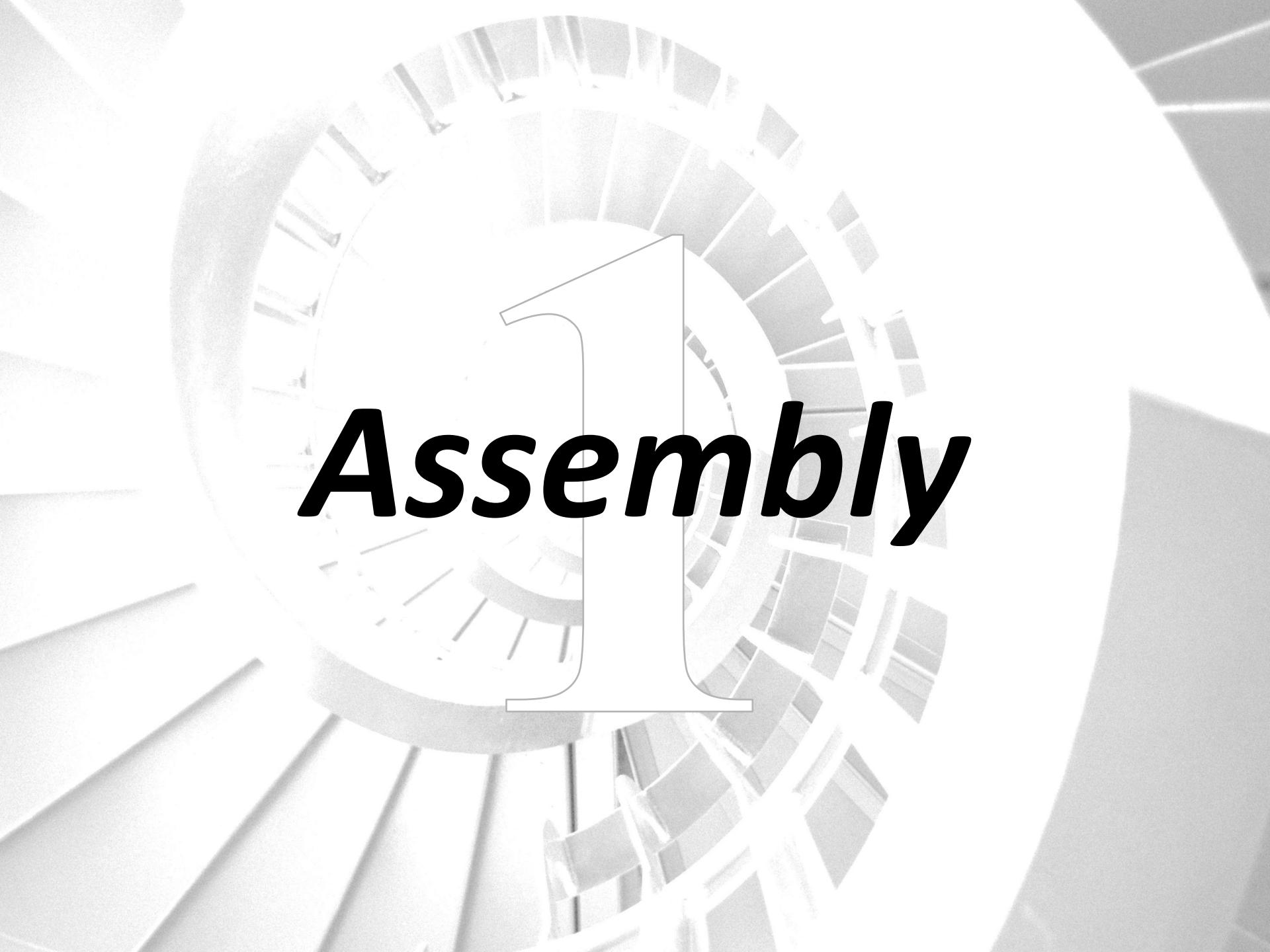
step

René L Warren 2019



CANADA'S MICHAEL SMITH
GENOME
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Assembly



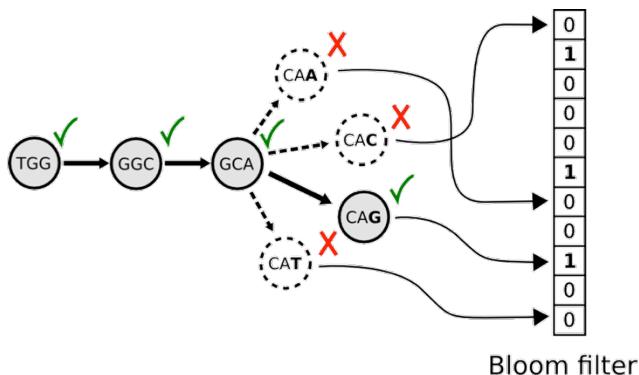
Short reads *de novo* genome assembly

2009 Parallel DBG assembler

- MPI to aggregate memory
- Assembled 20 Gb spruce genome

2017 Bloom filter representation

- 1/10th RAM
- Large genomes, single computer



GENOME
RESEARCH

ABYSS: A parallel assembler for short read sequence data

Jared T. Simpson,¹ Kim Wong, Shaun D. Jackman, Jacqueline E. Schein, Steven J.M. Jones, and İnanç Birol²

GENOME
RESEARCH

Method

ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter

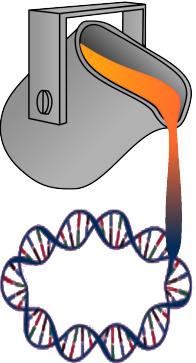
Shaun D. Jackman,¹ Benjamin P. Vandervalk,¹ Hamid Mohamadi, Justin Chu, Sarah Yeo, S. Austin Hammond, Golnaz Jahesh, Hamza Khan, Lauren Coombe, Rene L. Warren, and Inanc Birol

<https://github.com/bcgsc/abyss>



Correction

Tigmint



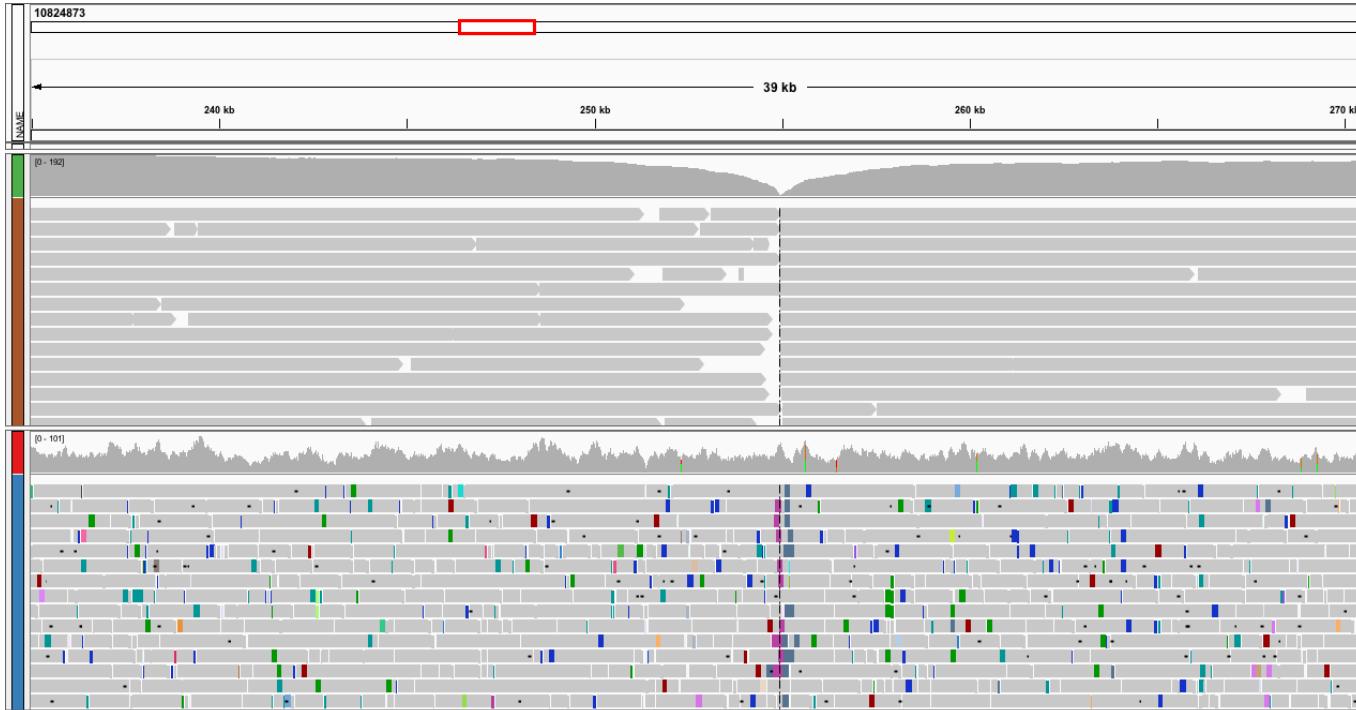
Linked reads misassembly correction



SOFTWARE

Tigmint: correcting assembly errors using linked reads from large molecules

Shaun D. Jackman^{1*} , Lauren Coombe¹, Justin Chu¹, Rene L. Warren¹, Benjamin P. Vandervalk¹, Sarah Yeo¹, Zhuyi Xue¹, Hamid Mohamadi¹, Joerg Bohlmann², Steven J.M. Jones¹ and Inanc Birol¹



Correct misassemblies



Scaffold

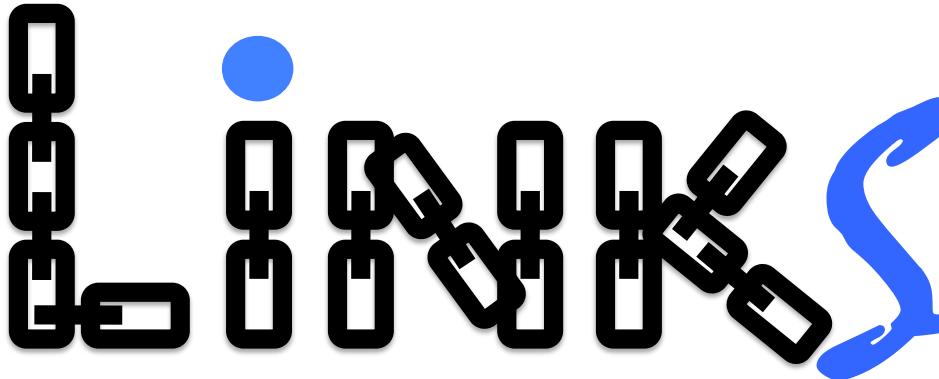


IGV screenshot: Tigmint breakpoint in human genome NA24143

<https://github.com/bcgsc/tigmint>



Scaffolding



Warren et al. *GigaScience* (2015) 4:35
DOI 10.1186/s13742-015-0076-3

(GIGA)ⁿ
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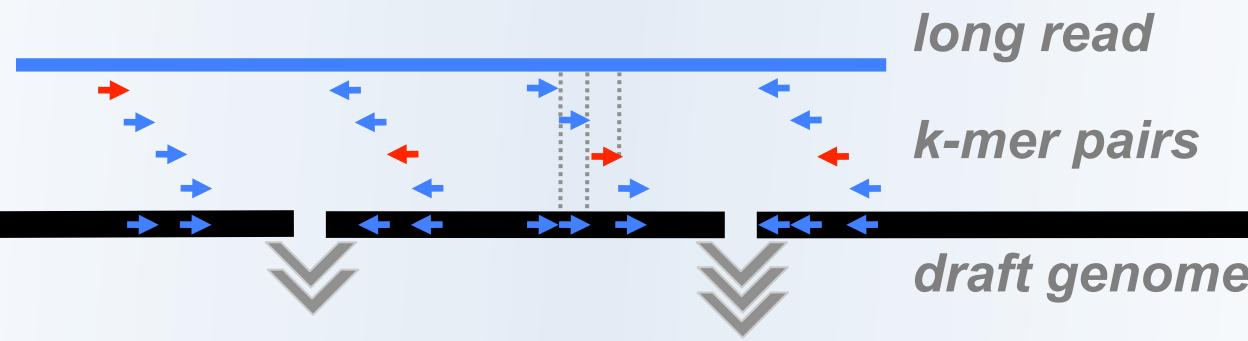


RESEARCH

LINKS: Scalable, alignment-free scaffolding
of draft genomes with long reads

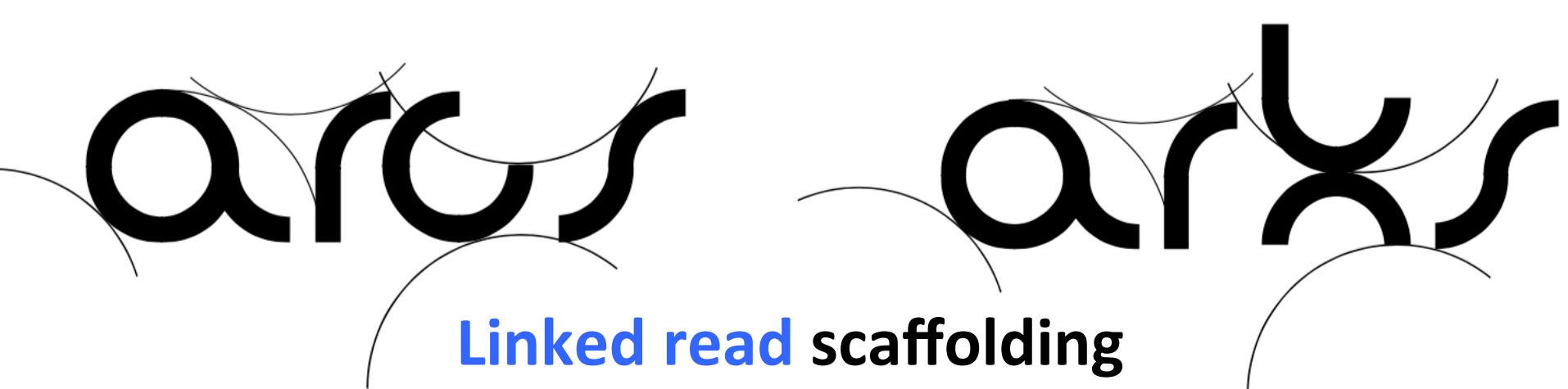
René L. Warren*, Chen Yang, Benjamin P. Vandervalk, Bahar Behsaz, Albert Lagman, Steven J. M. Jones
and Inanç Birol

Long read kmer scaffolding

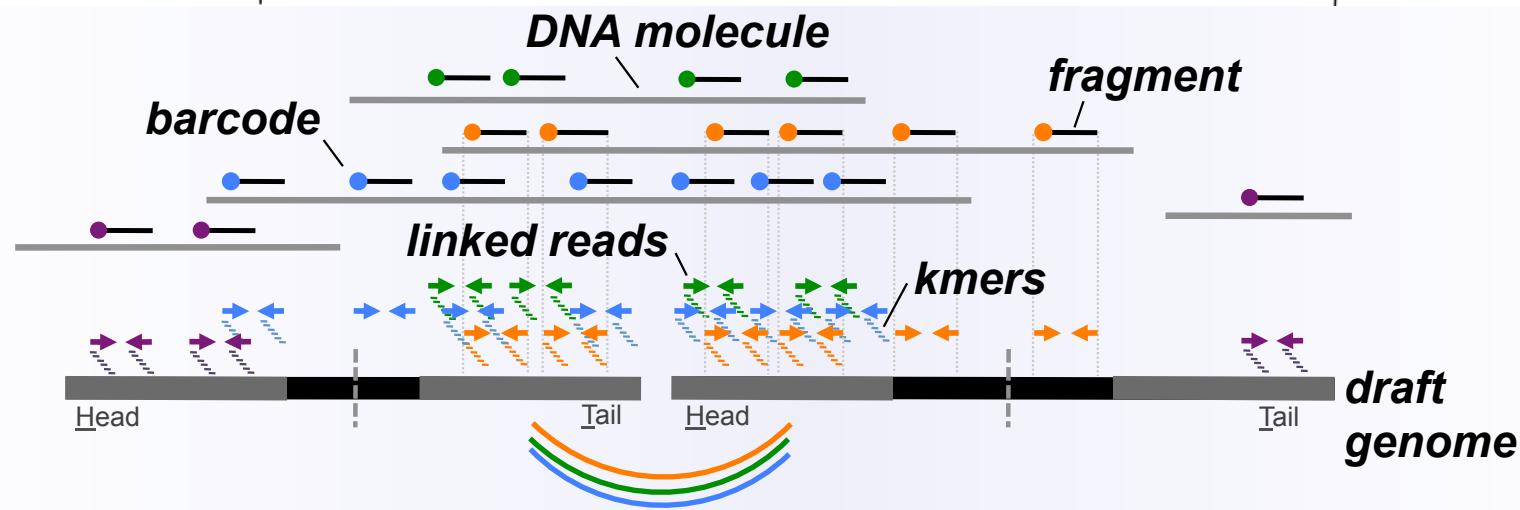


- **Scaffolder** order & orient sequences
- **k-mer based** no alignments, error tolerant = no error corrections
- **Vast k-mer space** no fragment length limitations
- **Versatile** long-reads, draft sequences, MPET

<https://github.com/bcgsc/links>



Linked read scaffolding



ARCS: scaffolding genome drafts with linked reads  Sarah Yeo, Lauren Coombe, René L Warren  , Justin Chu, Inanç Birol Author Notes <i>Bioinformatics</i> , Volume 34, Issue 5, 1 March 2018, Pages 725–731, https://doi.org/10.1093/bioinformatics/btx675	<small>Coombe et al. <i>BMC Bioinformatics</i> (2018) 19:234 https://doi.org/10.1186/s12859-018-2243-x</small>
https://github.com/bcgsc/arcs	SOFTWARE  ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers  Lauren Coombe [†] , Jessica Zhang [†] , Benjamin P. Vandervalk, Justin Chu, Shaun D. Jackman, Inanc Birol and René L. Warren [*]

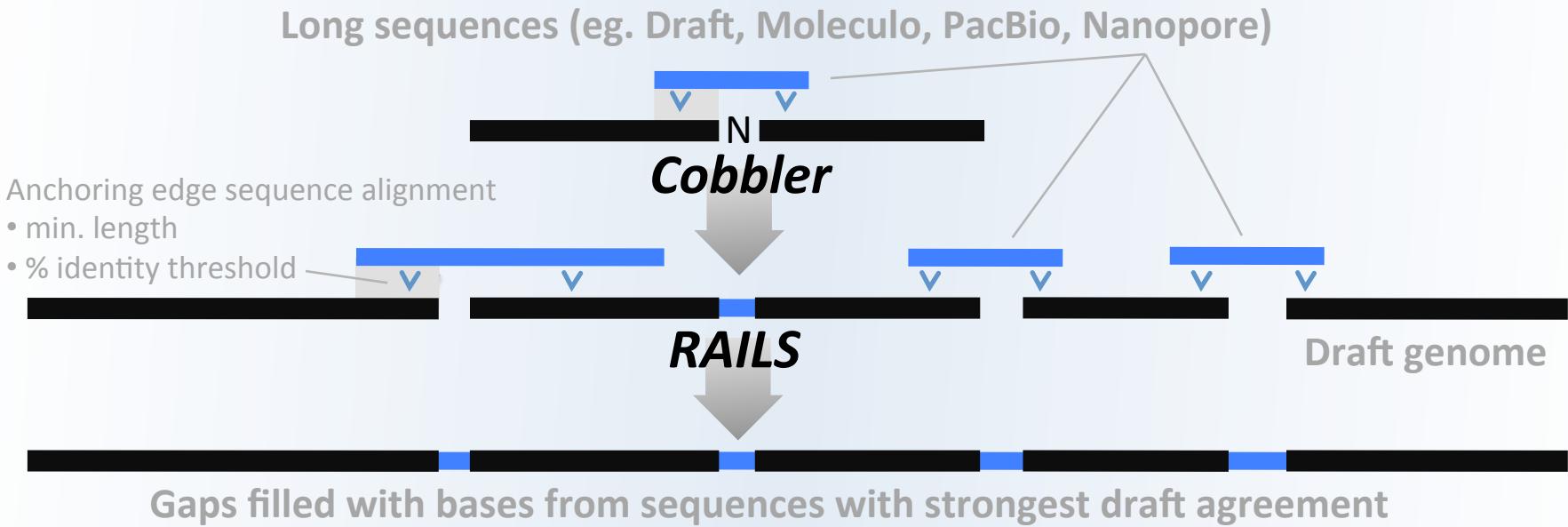
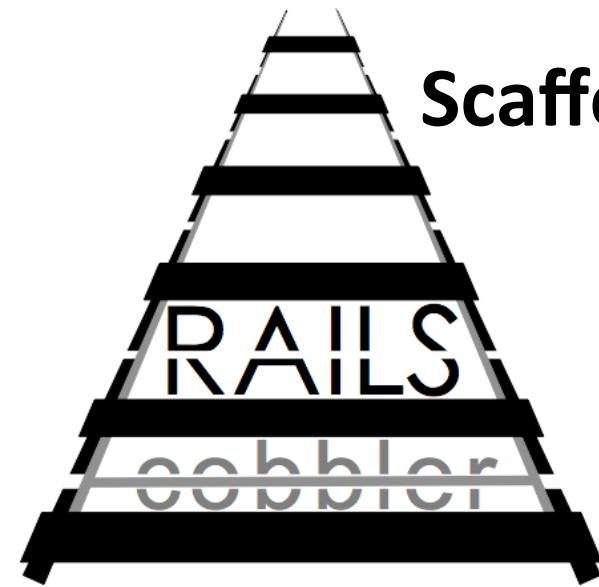
https://github.com/bcgsc/arcs	https://github.com/bcgsc/arks
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Gap-filling

Scaffolding and gap-filling with long reads

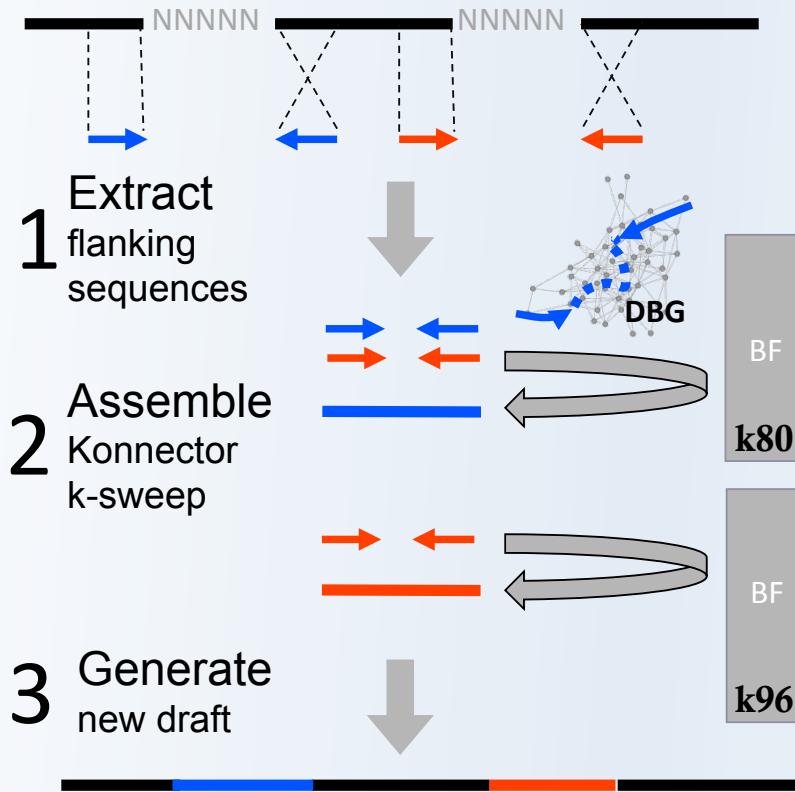
Uses LINKS scaffolding algorithm



<https://github.com/bcgsc/rails>

Sealer

Gap filling with short reads



Vandervalk et al. BMC Medical Genomics 2015, 8(Suppl 3):S1
http://www.biomedcentral.com/1755-8794/8/S3/S1



RESEARCH

Open Access

Konnecter v2.0: pseudo-long reads from paired-end sequencing data

Paulino et al. BMC Bioinformatics (2015) 16:230
DOI 10.1186/s12859-015-0663-4



SOFTWARE

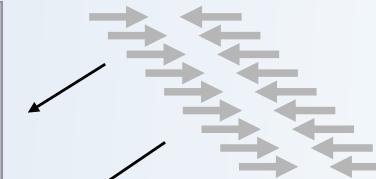
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Sealer: a scalable gap-closing application for finishing draft genomes



Build Bloom filters (BF) with Konnector

NGS reads k-mers



Gap-closing results, white spruce

Genotype/#Gaps	k	#Closed
WS77111/ 1.8M	64 80	461,196
	96	(25.5%)
PG29/ 2.9M	84 96	399,476
		(13.79%)

4.5B Illumina reads Peak RAM: 44GB Time: 27h

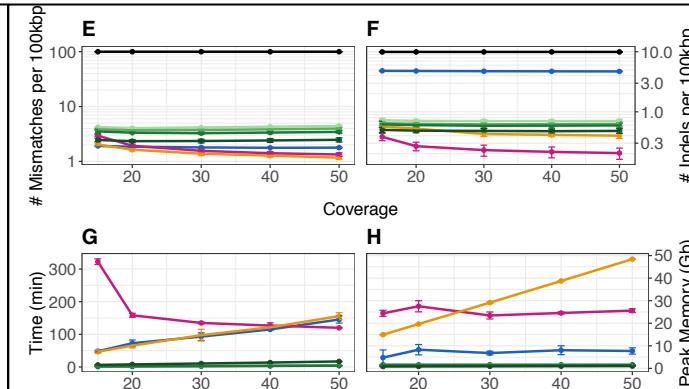
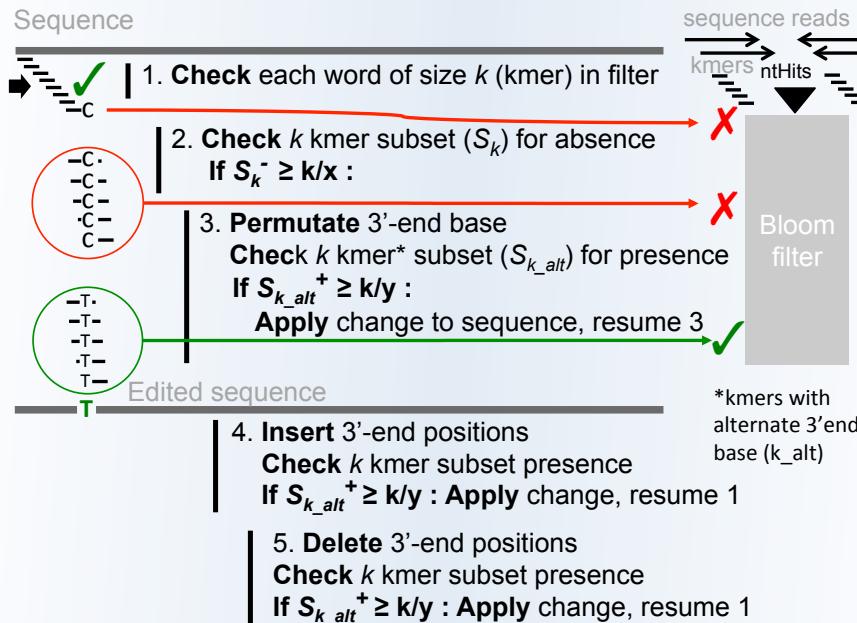
<https://github.com/bcgsc/abyss/tree/master/Sealer>

The background features a complex geometric pattern of concentric circles and radiating lines in shades of gray. The circles are composed of numerous small, rectangular segments that create a textured, gear-like appearance. Radiating from the center are several thick, light-gray lines that intersect the circles at various angles.

Polishing

WTD

Fast genome polishing with short reads



C. elegans

H. Sapiens chr21

- Human and spruce genomes in 4 and 25 minutes
- Fix frameshift errors in nanopore/pacbio assemblies

ntEdit: scalable genome sequence polishing

2019

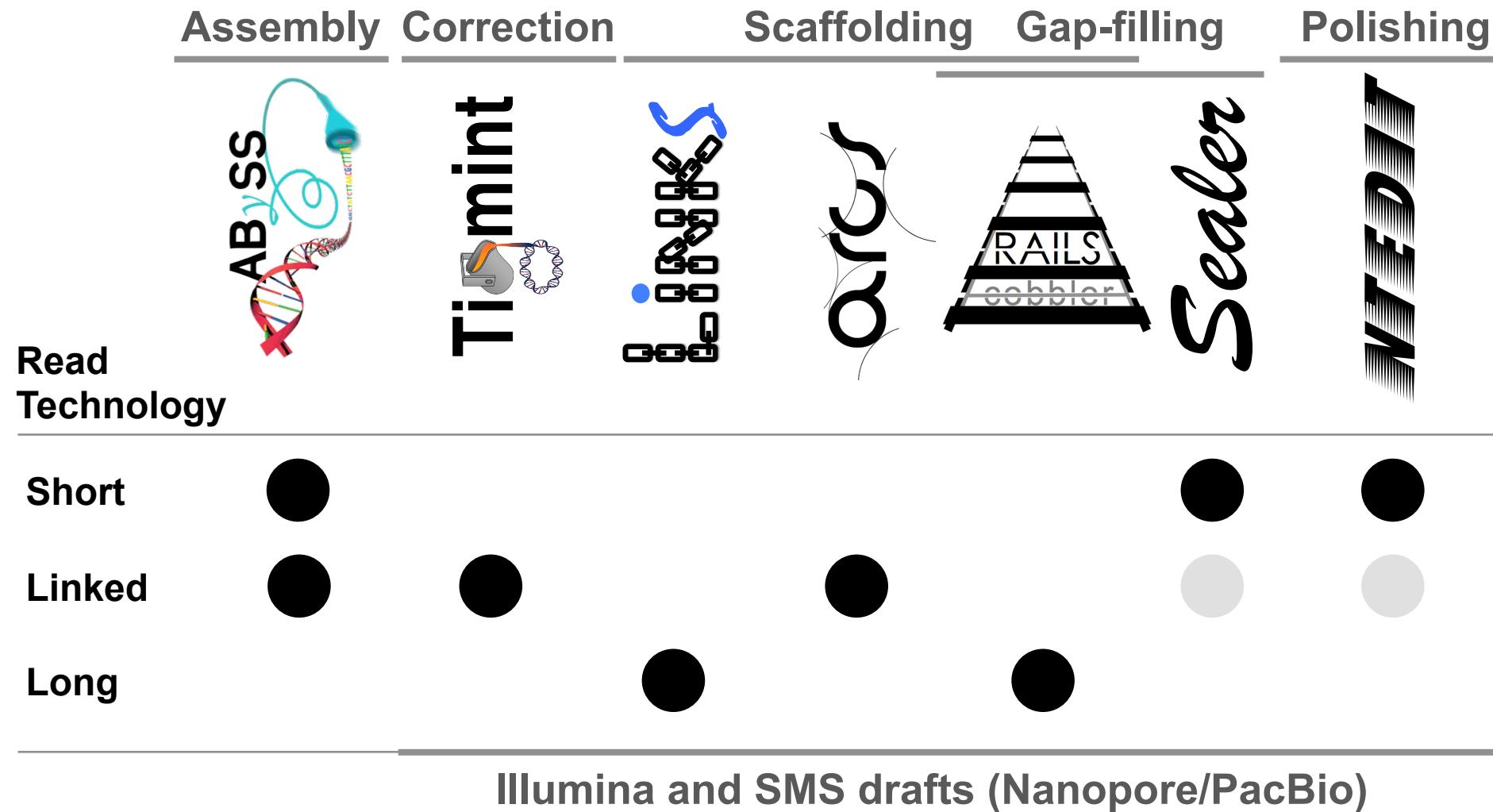
René L Warren, Lauren Coombe, Hamid Mohamadi, Jessica Zhang, Barry Jaquish, Nathalie Isabel, Steven JM Jones, Jean Bousquet, Joerg Bohlmann, Inanç Birol
doi: <https://doi.org/10.1101/565374>

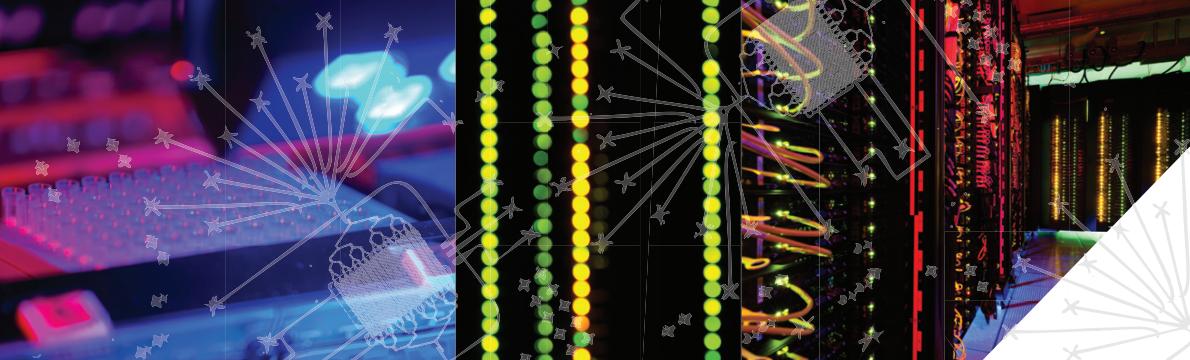


bioRxiv
THE PREPRINT SERVER FOR BIOLOGY

<https://github.com/bcgsc/ntedit>

Scalable solutions for genome assembly

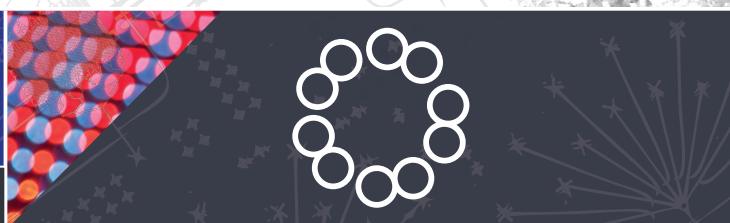




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>2 PETABASES SEQUENCED • A HUMAN GENOME EVERY 15 MINUTES • HIGH-PERFORMANCE COMPUTING



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