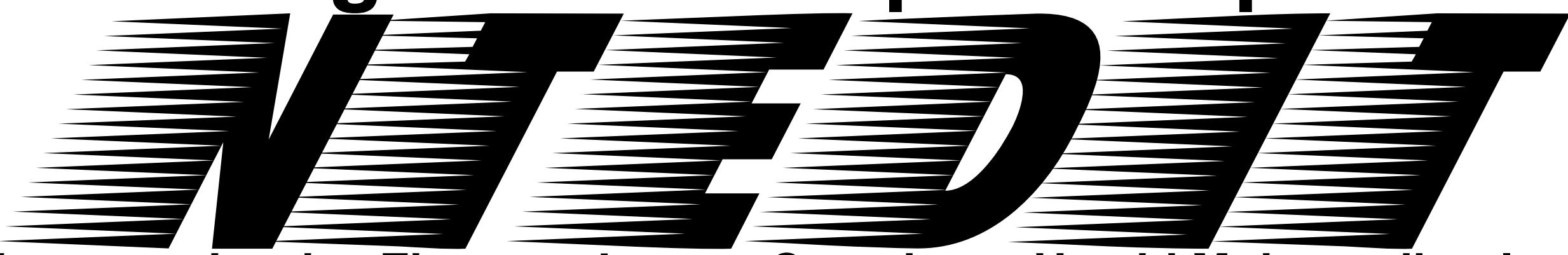
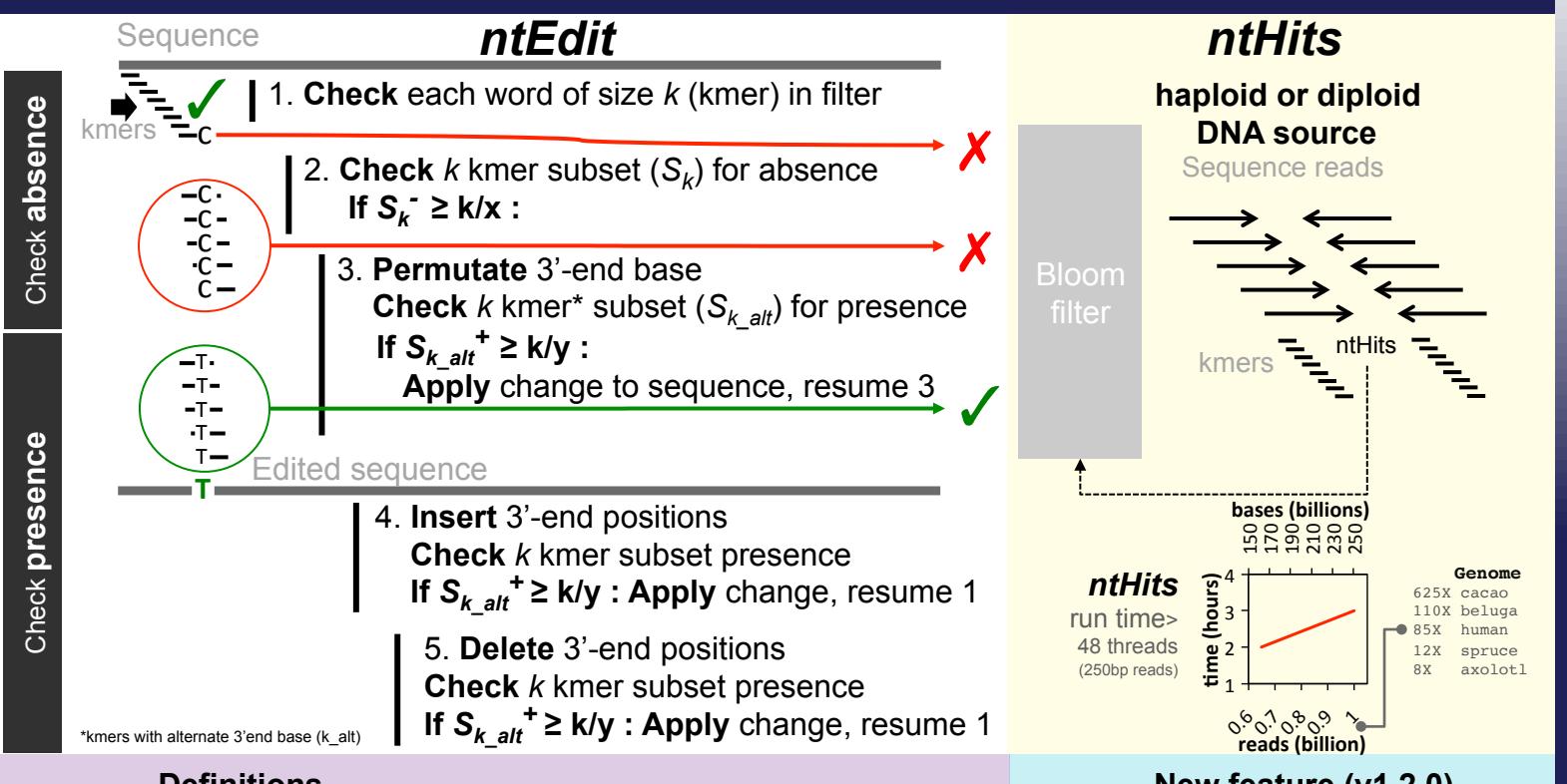


# scalable genome sequence polishing

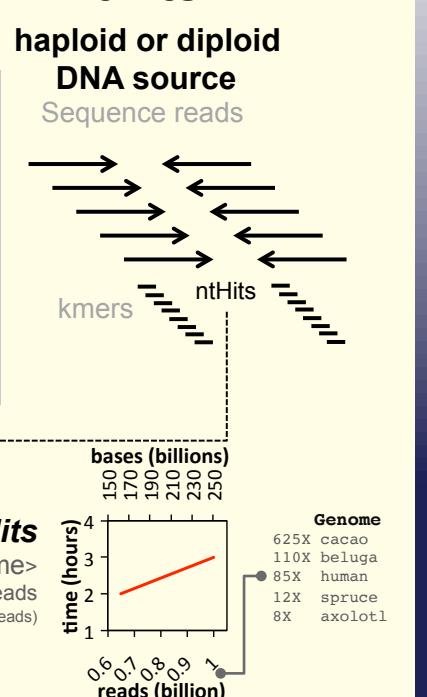


René Warren • Jessica Zhang • Lauren Coombe • Hamid Mohamadi • Inanç Birol

## Method



## ntHits



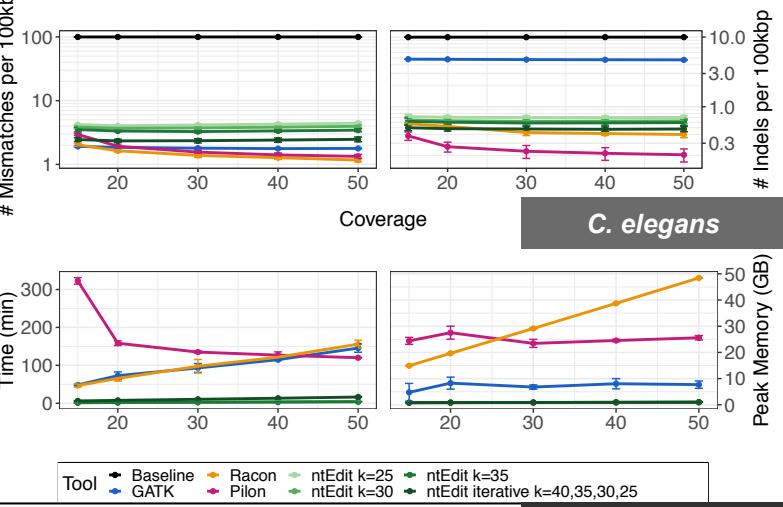
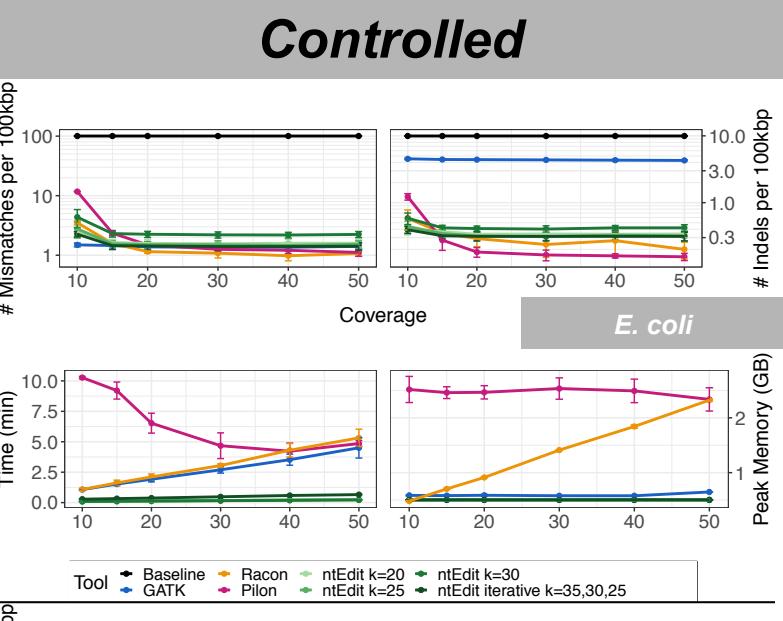
## New feature (v1.2.0)

-m option editing mode 0-2 [default=0]

0: best substitution, or first supported indel  
1: best substitution, or best indel  
2: best edit overall (exhaustive)

## Results

### Controlled



### Experimental

#### I. Polishing

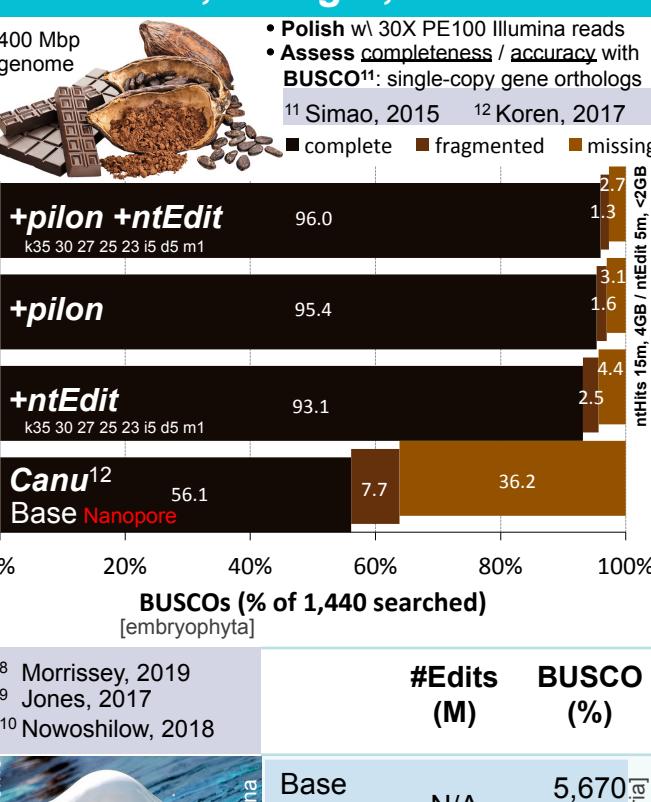
##### Human\*

Polish w/ 54X Illumina	Time**	Edits (M)	BUSCO (%)	Baseline
GATK <sup>4</sup>	41h45	0.97	5,654 (91.3)	7
ntEdit***	2h10	0.95	5,670 (91.6)	23
Racon <sup>5</sup>	45h54	N/A	5,681 (91.7)	34
GATK	42h21	2.66	5,285 (85.4)	0
ntEdit***	2h10	3.63	5,651 (91.3)	366
Racon	40h55	N/A	5,670 (91.6)	385

<sup>4</sup>McKenna, 2010 <sup>5</sup>Vaser, 2017 <sup>6</sup>Jain, 2018 <sup>7</sup>Pendleton, 2015

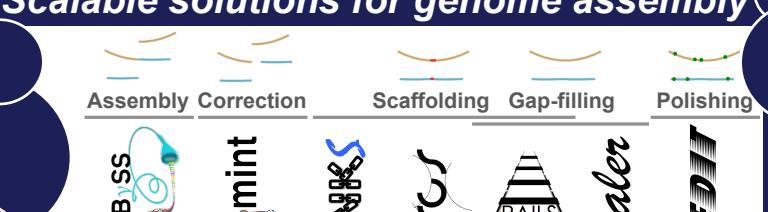
\*Single Molecule Sequencing draft genomes \*\*Time for pipeline \*\*\*15GB RAM ntHits 40GB

##### Cacao<sup>8</sup>, Beluga<sup>9</sup>, Axolotl<sup>10</sup>



## Summary

### Scalable solutions for genome assembly



### Read Technology

Short

Linked

Long

Illumina, SMS drafts (Nanopore/PacBio)

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

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

<https://birol-lab.ca>

<http://renewarren.ca>

<https://bcgsc.ca>

[NIH](http://nih.gov)

[Genome British Columbia](http://genomebc.ca)

[Genome Canada](http://genomesc.ca)

[BC CANCER FOUNDATION](http://bc-cancer.ca)

## Acknowledgements

### Reference

Warren et al. 2019. *Bioinformatics*.

DOI: 10.1093/bioinformatics/btz400

### Software

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

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

### Funding

<http://birol-lab.ca>

<http://renewarren.ca>

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