TITLE1
TITLE2
TITLE3

Tong Dong Qiu

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Delft University of Technology

Abstract

DALIGNER or Daligner

TU Delft Delft University of Technology

CE Lab Computer Engineering Laboratory

TITLE

THESIS

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Faculty of Electrical Engineering, Mathematics and Computer Science
Delft University of Technology

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by AUTHOR

Abstract

Laboratory	:	Computer Engineering
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Advisor:		, CE, TU Delft
Chairperson:		, CE, TU Delft
Member:		, CE, TU Delft
Member:		, CE, TU Delft

Dedicated to my family and friends

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GPU Graphics Processing Unit

Acknowledgements

AUTHOR
Delft, The Netherlands
September 14, 2017

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MAIN IS TRUE

3.1 Pacbio reads

Daligner finds alignments between long, noisy reads. Pacific Biosciences has commercially launched its first sequencer in 2011. It is able to output reads with an average of 1000 bases, which is significantly longer than **NGS!** (**NGS!**) reads [1]. In 2014, a new polymerase-chemistry combination was released, called P6-C4. This version can output average read lengths of 10000-15000 bases, and its longest reads can exceed 40000 bases [**?**]. While the drawback is that these reads have an error rate of 12-15%, this can be compensated by the distribution of these errors [**?**]. First, the set of reads is a nearly Poisson sampling of the sampled genome. This implies that there exists a coverage c for every target coverage k, such that every region of the genome is covered k times [**?**]. Secondly, the work of Churchill and Waterman [**?**] implies that the accuracy of the consensus sequence of k sequences is $O(\epsilon^k)$, which goes to 0 as k increases. This means that if the reads are long enough to handle repetitive regions, in principle a near perfect de novo assembly of the genome is possible, given enough coverage.

Important points for de novo DNA sequencing are: what level of coverage is needed for high quality assembly? And how to build an assembler that is able to deal with high error rates and long reads? Most previous assemblers work with **NGS!** reads, which are much shorter and have much lower error rates. Some algorithms used in these assemblers, such as **DBG!** (**DBG!**) [**?**] would grow too large for high error rates and long reads. Since Daligner was build, new methods of using **DBG!** with long reads have been developed, but they rely on a short read based **DBG!** to correct errors in long reads.

4 Specification

5 Experiments

6 Conclusion

Bibliography

[1] K. Davies, "Get smrt: Pacific biosciences unveils software suite with commercial launch," April 2011. [Online]. Available: http://www.bio-itworld.com/news/04/29/2011/Pacific-Biosciences-software-commercial-launch.html

List of definitions

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