Safe and complete genome assembly via omnitigs

Alexandru Tomescu
Department of Computer Science
University of Helsinki, Finland

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Central dogma of biology

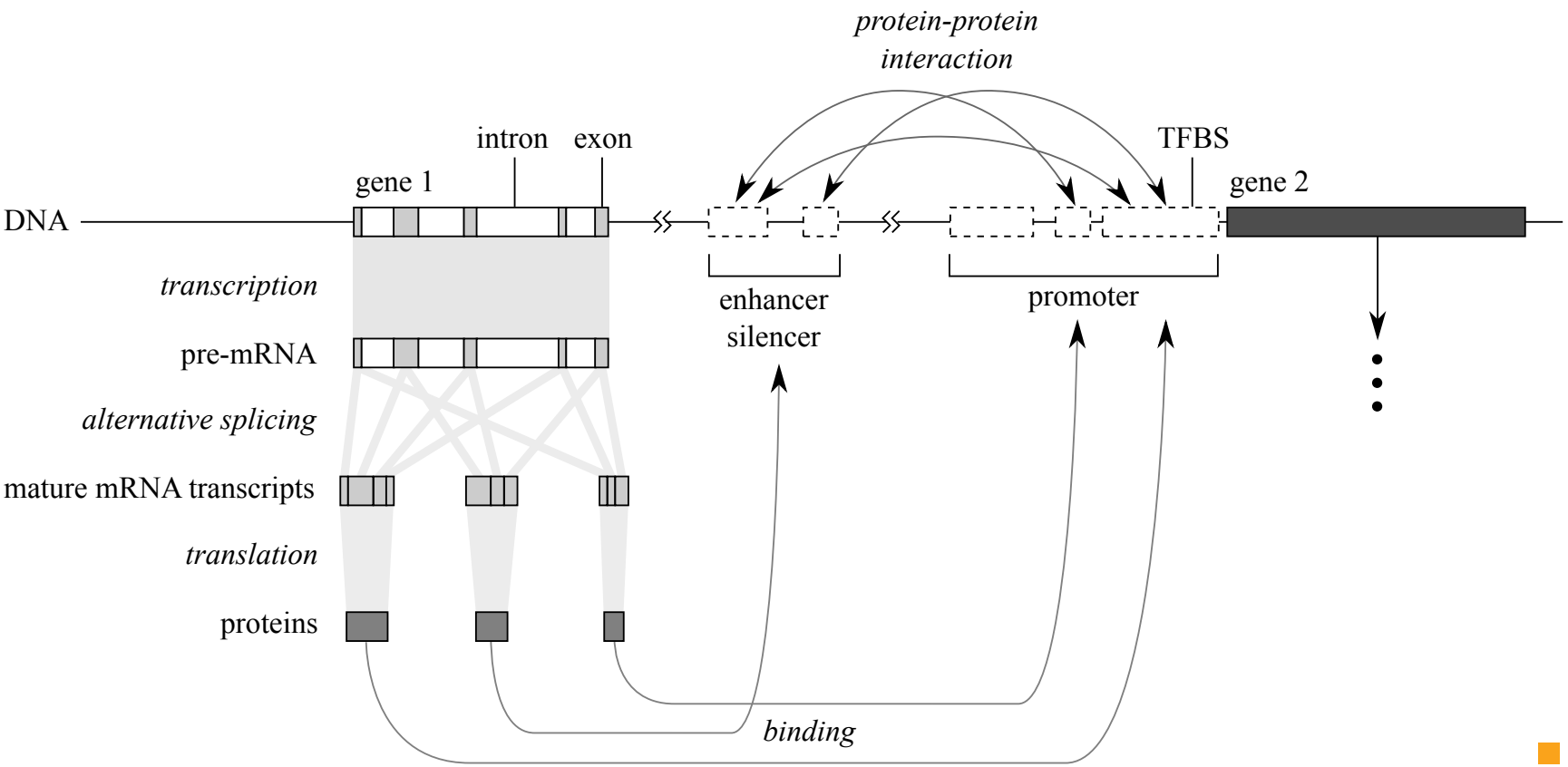


Image taken from
Genome-Scale Algorithm Design, Cambridge University Press, 2015

Sequencing atlas

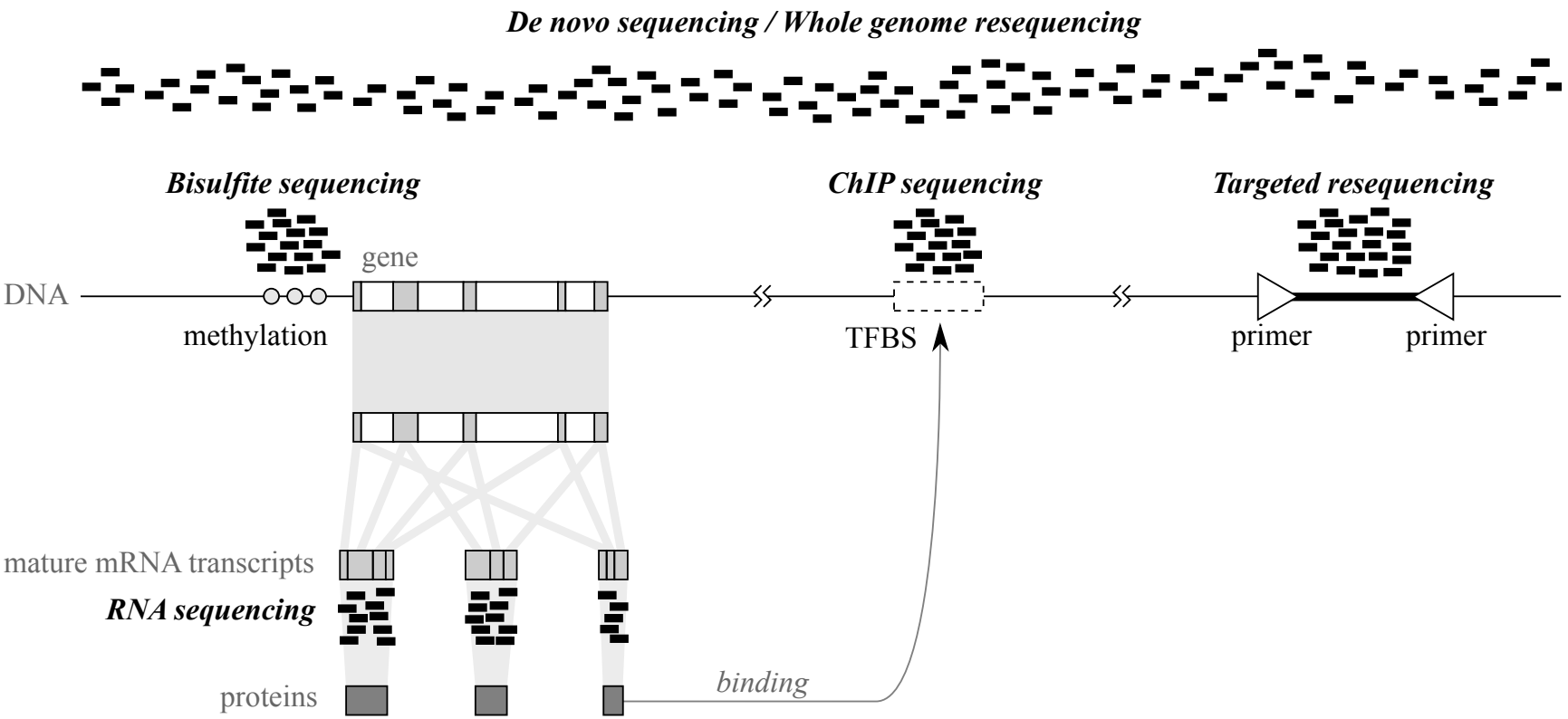


Image taken from
Genome-Scale Algorithm Design, Cambridge University Press, 2015

BLACKBOARD

The "safe and complete" framework is described in:

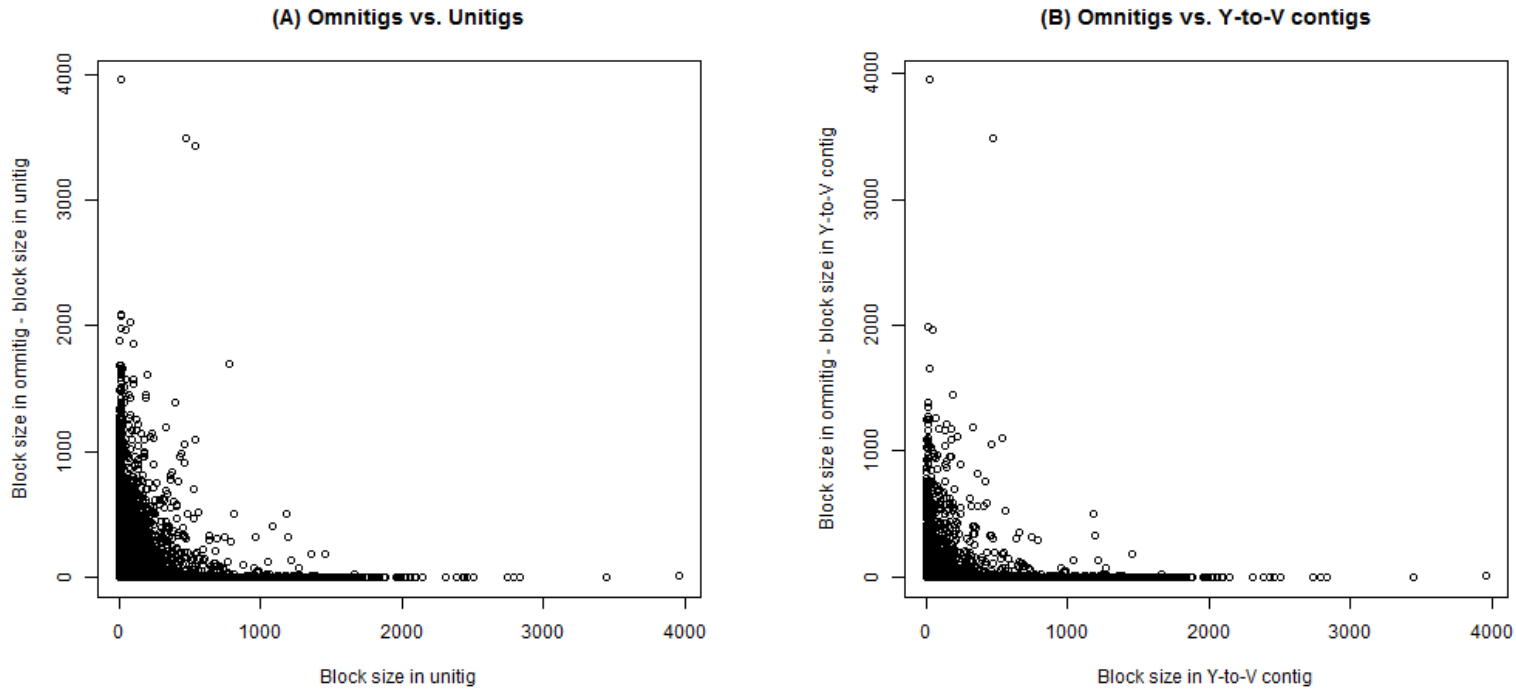
- A. I. Tomescu, P. Medvedev, *Safe and complete contig assembly via omnitigs* RECOMB 2016 - 20th Annual International Conference on Research in Computational Molecular Biology, LNCS 9649, 152-163, 2016.
  Extended version available at `http://arxiv.org/abs/1601.02932`

Experimental results

Table: Results for $DB^k_{ec}(R)$, where R is the set of all $(k+1)$-mers of the genome.

	E.coli ($k = 31$)				chr10 ($k = 55$)			
	# strings	avg len	E-size	time (s)	# strings	avg len	E-size	time (s)
unitigs	1,743	2,654	33,309	< 1	259,845	546	8,344	1
Y-to-V	1,004	4,682	33,632	< 1	159,101	878	8,376	2
omnitigs	983	4,832	34,557	< 1	158,236	887	8,401	1,046

Experimental results



Compared to unitigs, #SNPs whose block size

- increased: ~ 1.7 million (out of ~ 5.9 million)
- increased by more than 10: $\sim 137,000$

Compared to Y-to-V contigs, #SNPs whose block size

- increased: $\sim 266,000$ (out of ~ 5.9 million)