

Unified detection, classification, and phasing of germline, somatic, and denovo variation from sequencing data

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Abstract

High throughput sequencing technology has seen the rise of powerful methods to detect genetic variation directly from raw data. Most notably, haplotype-based variant calling has become defacto for identifying germline variation.

First bit

If you want to ramp your text straight onto the title page, start the text at something that does not cause a page break, like a section. Here's a handy place to introduce some of your woofy conventions, like quotes in equations.

Chapter 1

New Page

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