Genome analysis

RAMPART: a workflow management system for de novo genome assembly

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Abstract

Motivation: The de novo assembly of genomes from whole-genome shotgun sequence data is a computationally intensive, multi-stage task and it is not known a priori which methods and parameter settings will produce optimal results. In current de novo assembly projects, a popular strategy involves trying many approaches, using different tools and settings, and then comparing and contrasting the results in order to select a final assembly for publication.

Results: Herein, we present RAMPART, a configurable workflow management system for de novo genome assembly, which helps the user identify combinations of third-party tools and settings that provide good results for their particular genome and sequenced reads. RAMPART is designed to exploit High performance computing environments, such as clusters and shared memory systems, where available.

Availability and implementation: RAMPART is available under the GPLv3 license at: https://github.com/TGAC/RAMPART.

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Supplementary information: Supplementary data are available at Bioinformatics online. In addition, the user manual is available online at: http://rampart.readthedocs.org/en/latest.

1 Introduction

The de novo genome assembly of whole genome sequence data is a complex task and typically involves testing multiple tools, parameters and approaches to produce the best possible assembly for downstream analysis. This is necessary because it is not always known a priori, which tools and settings will work best on the available sequence data given the organism’s specific genomic properties, such as size, ploidy and repetitive content. Despite advances in computing hardware and sequencing technologies, de novo assembly, particularly for more complex eukaryotic genomes, remains a non-trivial task and an ongoing challenge.

Recently, several tools, such as iMetAMOS (Koren et al., 2014) and A5 (Tritt et al., 2012), approach this problem by exhaustively testing many tools in parallel and then identifying and selecting the best assembly. However, these pipelines focus on prokaryote assemblies, where the computational demands are manageable and the genomes are easier to assemble. The complexities of eukaryotic genomes prohibit exhaustive testing of all tools and parameters with current computing hardware. For these projects the user must use the literature and their own experience to decide which avenues are worth considering.

2 RAMPART

This article presents a workflow management system for de novo genome assembly called RAMPART, which allows the user to design and execute their own assembly workflows using a set of third-party open-source tools. This reduces human error and relieves the burden of organizing data files and executing tools manually. Frequently, this helps to produce better assemblies in less time than is possible otherwise.

RAMPART gives the user the freedom to compare tools and parameters to identify the effect these have on the given data sets. The flexibility to roll-your-own workflow enables the user to tackle both
2.2 Assembly comparison and selection

To compare assemblies, RAMPART measures properties of each assembly relating to contiguity, conservation and assembly problems using third-party tools. The user can control which analysis tools, if any, are executed in their pipeline. To function as a fully automated pipeline, RAMPART, at particular stages, must be capable of selecting the best assembly to proceed with. We address this by assigning a single score to each assembly using a method similar to that described by Abbas et al. (2014), which groups and weights individual assembly metrics before assigning a single score. The user has the option to override the default weightings for automatic selection, or can select an assembly manually at their discretion. Please see Supplementary Material Section 2 for more information.

2.3 High performance computing support

Experimenting with de novo assembly for large, complex genomes is a computationally intensive process. Therefore, RAMPART is designed to exploit high performance computing environments, such as clusters or shared memory machines, by executing tools in parallel where possible via the system’s job scheduler. However, RAMPART still runs on desktop and server machines sequentially with sufficient resources. RAMPART currently supports both the Platform Load Sharing Facility and Portable Batch System schedulers, with plans to support Sun Grid Engine in the future.

3 Concluding remarks

RAMPART is a workflow management system for de novo genome assembly that provides an effective means of producing quality prokaryotic and eukaryotic assemblies by reducing the amount of manual work required in such projects. In addition, it offers a way for users to better understand differences in their genomic sequence data, assemblies and assembly tools. RAMPART is already used in production workflows at The Genome Analysis Centre, is under active development and is updated regularly to adapt to the latest challenges, tools and data.

As sequencing costs have come down it has been possible to sequence multiple isolates of the same species in parallel, these kinds of projects present additional challenges for the bioinformatician in terms of managing the numbers of files and comparing results of de novo assemblies across isolates. RAMPART contains some preliminary scripts for managing these kinds of projects. It also enables the rapid functional annotation of prokaryote genomes via PROKKA (Seemann, 2014). In the future we would like to improve these scripts and workflows and to provide the ability to annotate eukaryote genomes.

Over time, the community will develop a better understanding of what assembly workflows are appropriate for certain types of genomes with certain types of sequence data. For example, the ALLPATHS-LG ‘recipe’ (Grieff et al., 2011) has been shown to produce high-quality assemblies of mammalian genomes. We plan to encourage this process in the future by allowing users to share their own RAMPART workflows and metrics describing their results on a website for appraisal by the community.

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References
Abbas, M.M. et al. (2014) Assessment of de novo assemblers for draft genomes: a case study with fungal genomes. BMC Genomics, 15(Suppl 9), S10.

Gnerre, S. et al. (2011) High-quality draft assemblies of mammalian genomes from massively parallel sequence data. Proc. Natl Acad. Sci., 108, 1513–1518.

Koren, S. et al. (2014) Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 15, 126.

Seemann, T. (2014) Prokka: rapid prokaryotic genome annotation. Bioinformatics, 30, 2068–2069.

Tritt, A. et al. (2012) An integrated pipeline for de novo assembly of microbial genomes. PLoS One, 7, e42304.