A Standalone Tool for Compressing IrysView *De Novo* Assembly Output

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1. Introduction

compressDeNovoAssembly_forImport.sh is a tool for compressing a Bionano *de novo* assembly output, and importing to IrysView and Bionano Access.

This document provides instructions for how to compress the results of the Bionano Genomics IrysSolve pipeline for *de novo* assembly. This script has not been fully validated and is currently not supported by Bionano.

2. Expected structure and required files of *de novo* assembly "output" folder
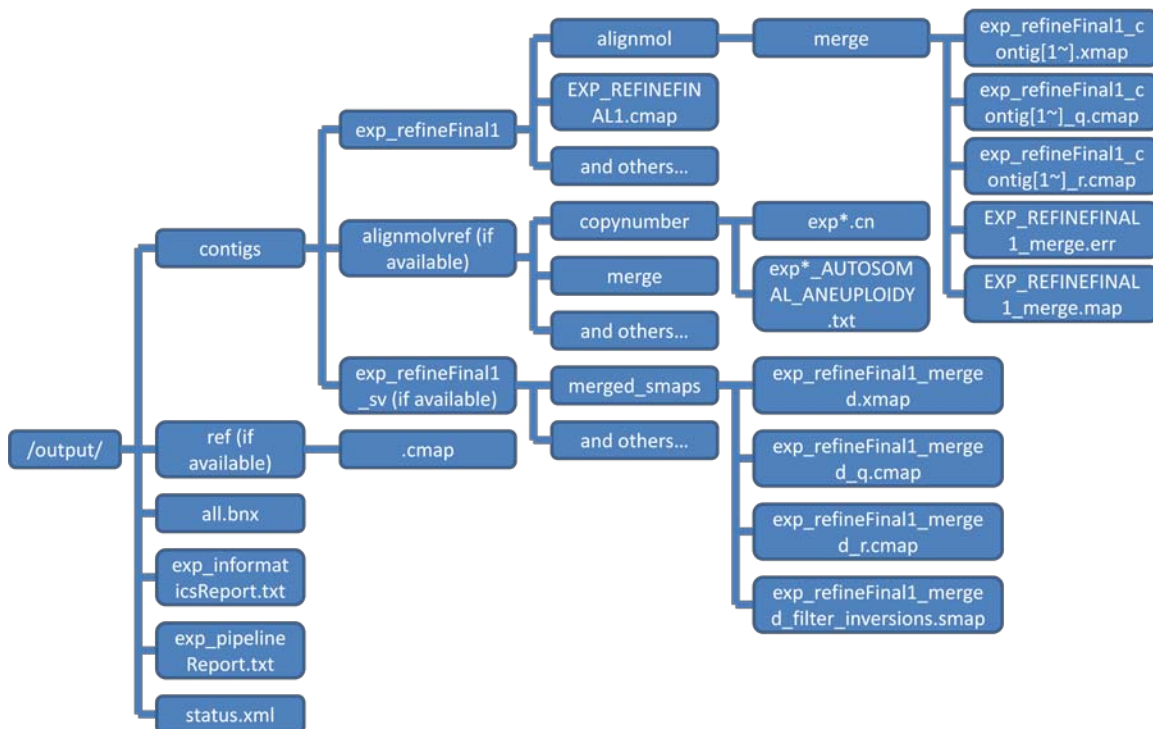
3. Usage

3.1 Copy the compression script to a location on a Linux system that has access to the "output" folder.

3.2 Change the permissions of the folder to enable executable privileges: eg. "chmod 755 compressDeNovoAssembly_forImport.sh".

3.3 The script requires minimum input parameters:

- --targetFolder: path/to/denovo/assembly/output
- --outputFolder: path/to/compressFileOutput/folder
- --prefix: name_for_output_file

Optional parameters:

- --gzip: force tar.gz gzip output
- --verbose: verbose output

3.4 Execute the script on the target folder: eg. "./compressDeNovoAssembly_forImport.sh --targetFolder ./output/ --outputFolder ./ --prefix denovoCompressTest --gzip --verbose"

3.5 The compressed file generated with name "prefix" can be imported into IrysView and Bionano Access.

4. Instructions for Importing

From IrysView, use the "Import" feature to import the compressed *de novo* assembly output. Please refer to **IrysView v2.5.1 Software Training Guide (30035 Rev. G, pg. 20)** for step-by-step instructions.

From Bionano Access, use the "Import" feature to import the compressed *de novo* assembly output. Please refer to **Bionano Access™ 1.0 Software User Guide (Document Number: 30142 Revision: A)** for step-by-step instructions.