

A Standalone Tool for Compressing the Old Hybrid Scaffold Output

Xiang Zhou, Computational Biologist

Research Department, BioNano Genomics Inc.

xzhou@bionanogenomics.com

1. Introduction

compressHybridScaffold_forIrysView.sh is a tool for compressing a BioNano hybrid scaffold output generated by hybrid scaffold function in IrysView. The purpose of this tool is to facilitate the import of the IrysView hybrid scaffold output into the BioNano Access for visual display. It supports both automatic and manual run of hybrid scaffold output.

2. Structure of the Files and the folders

Automatic Cutting Mode	Manual Cutting Mode
./fa2cmap/*	./fa2cmap/*
./hybrid_scaffolds/*	./hybrid_scaffolds_M{\$i}/*
./alignmol_bionano/merge/*	./alignmol_bionano_M{\$i}/merge/*
./alignmol_hybrid/merge/*	./alignmol_hybrid_M{\$i}/merge/*
./cur_results.txt	./cur_results.txt
./*_status.txt	./*_status.txt

* The \$i should be replaced by the largest # found after “M” in all the output folders.

3. Usage

```
/home/users3/xzhou/HS_old_output/compressHybridScaffold_forIrysView.sh --targetFolder  
<path/to/hybrid/scaffold/output> --outputFolder <path/to/compressFileOutput> --prefix  
<name_for_output_file> --manual <0/1>
```

Options:

-t/--targetFolder Hybrid scaffold folder for compression (Required)

-o/--outputFolder	Output folder (Required)
-p/--prefix	Prefix of the output *.tar.gz file
-M/--manual	Whether the hybrid scaffold result to be compressed is from manual cut (1) or not (0)
-h/--help	Display the help message

4. Detailed Instructions

4.1 Instructions for Compression – Automatic Cut

Run hybrid scaffold using the automatic cut option. Then compress the output folder using this tool with option “--manual 0”. The compressed file generated with name “<prefix>.tar.gz” can be shared for import into BioNano Access.

4.2 Instructions for Compression – Manual Cut

Run hybrid scaffold using the manual cut option. Then compress the output folder using this tool with option “--manual 1”. The compressed file generated with name “<prefix>.tar.gz” can be shared for import into BioNano Access.

4.3 Instructions for Importing:

Download the compressed file “<prefix>.tar.gz”. From BioNano Access, use the “Import” feature to import the file.

Note: If there is no “hybrid_scaffold_informatics_report.txt” file in the original input folder, no report file will be shown on BioNano Access.