DRAGEN^{TM} ORA Decompression v2.7.0 Software Release Notes

June 18, 2024

Introduction

These release notes detail the key changes for the DRAGEN™ ORA Decompression software v2.7.0 which decompresses *.fastq.ora files that have been compressed using DRAGEN ORA Compression software with the default human reference and with the additional supported references.

Changes are relative to DRAGEN ORA Decompression software v2.6.1 for Linux and Mac and v2.6.2 for Windows. The DRAGEN ORA Decompression software v2.6.1 and v2.6.2 are replaced with new version v2.7.0.

The v2.7.0 software package includes a binary installer that is compatible with the following Linux distributions:
- Centos 7 or later
- Ubuntu 14 or later
- Oracle 8 or later
- Debian 8
- Fedora 26

The following table lists the minimum requirements for the DRAGEN ORA Decompression Software.

Component	Minimum Requirements
System Memory	8 GB RAM
Free Disk Space	From 2 GB to 15 GB depending on how many different specific references are needed for decompression. For human data, 2 GB are required.
Compatible Linux Distributions	• Ubuntu 14.06 and later • CentOS 7 and later • Oracle 8 and later
Compatible Mac Distributions	Mac 10.15 (Apple silicon and Intel CPU processors)
Compatible Windows Distributions	Windows 10 and later

DRAGEN ORA Decompression software can be downloaded from the ORA support page. Refer to the User Guide for installation of DRAGEN ORA Decompression software.

New Features and command

- DRAGEN ORA Decompression software decompresses FASTQ.ORA files that have been compressed with all supported references. The default human reference is included in the Software and does not need to be downloaded.

  For decompression based on other supported references, the correct reference needs to be downloaded from the [DRAGEN ORA support](#) site and placed in the `oradata` folder. Note: the reference used at decompression, must be the same one as the one used at compression.

  Once the correct reference is placed in the `oradata` folder, no specific command is expected. The software looks automatically for the correct reference.

  The command `orad <*.fastq.ora> --info` prints the species/model used to compress the *.fastq.ora file.

  The list below provides the list of supported species/model at the time of this release. The whole database, or reference file for a specific species/model can be downloaded. To see the most up-to-date list of species/model supported check the DRAGEN ORA support site.

Latin name	Common name	Size (GB)
Homo_sapiens	Human	1.3
Homo_sapiens_bisulfite	Human_bisulfite	2.4
Sus_scrofa	Pig	0.80
Gallus_gallus	Chicken	0.34
Oryza_sativa	Rice	0.15
Arabidopsis_thaliana	Arabidopsis thaliana	0.04
Triticum_aestivum	Wheat	4.7
Bos_taurus	Cattle	1.1
Glycine_max	Soybean	0.31
Rattus_norvegicus	Rat	1.1
Zea_mays	Maze	0.71
Danio_rerio	Zebrafish	0.54
Mus_musculus	Mouse	1.1
Caenorhabditis_elegans	Roundworm	0.03

- Added batch decompression of FASTQ.ORA files located at top-level directory.

Known issues

- Although the option `-rm` to delete input file is not supported when input is located in the cloud, the software will not print any error message if the command is used in the cloud. The command is ignored and the input file is not deleted.

Limitations

- Although several ORA references can be stored locally, the command `--check-ora-reference-path` only returns the path to one reference.

- The ora file format supports concatenation of files, e.g. with : `cat file1.fastq.ora file2.fastq.ora > concatenated_files.fastq.ora`
  The "`concatenated_files.fastq.ora`" is a valid ora file whose decompression will yield the concatenated contents of file1 and file2. However, printing the file's statistics with option -i on the concatenated file (`orad -i concatenated_files.fastq.ora`) will print erroneous information.