

# User Manual ZLIMS

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MGI Tech Co., Ltd.



To Enable Effective and Affordable Healthcare Solutions for All



#### About the user manual

This user manual is applicable to MegaBOLT Bioinformatics Analysis Accelerator (MegaBOLT\_scheduler). The edition is 1.0 and the software version is V2.1.0.

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Figures in this manual are all illustrations. The contents might be slightly different from the software, please refer to the software purchased.

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### **Manufacturer information**

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## **Revision history**

Revision	Date
1.0	November 30, 2019

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1

# Introduction

MegaBOLT bioinformatics analysis accelerator (hereinafter called MegaBOLT) is an MGI self-developed and NGS-concentrated hardware (FPGA, Field-Programmable Gate Array) accelerating system and multi-task scheduling system for bioinformatics analysis. MegaBOLT supports the analysis of Whole Genome Sequencing (WGS), Whole Exome Sequencing (WES), and Panel Sequencing on Germline or Somatic data, fulfilling from FASTQ input of sequencing data to BAM output of alignment result and VCF/gVCF output of variant calling result. And it is 20 times faster than the traditional GATK approach.

The MegaBOLT Rack Server mode is a rack server equipped with the MegaBOLT analysis system for large-scale data analysis scenarios in a cluster environment. It is flexible because it supports a variety of analysis processes, and it is suitable for users with background of bioinformatics analysis.

The MegaBOLT Workstation mode is a workstation equipped with the MegaBOLT analysis system for small to medium data analysis scenarios. It provides one-stop services from sequencing to WGS/WES analysis. It provides an interactive web interface and analysis report, which is easy to operate and suitable for most users with non-biological information analysis backgrounds.

2

Configuration requirements

ltem	Minimum configuration	Recommended configuration
CPU	2 × Intel Xeon E5-26XX Series	2 × Intel Xeon Gold 62XX Series
Memory	96 GB	128 GB
Storage	1 TB HDD	>2 TB SSD
OS	CentOS 7.3-7.5	CentOS 7.3-7.5
Network card	1 Gbps	>10 Gbps

# 3

# Procedure

To use MegaBOLT in ZLIMS system, perform the following steps:

- 1. Access ZLIMS through the approaches below:
  - 1) Launch Google Chrome browser, enter *127.0.0.1* in the address bar, and press Enter.
  - 2) Double-click the ZLIMS shortcut on the desktop.
- 2. Input the user name "user" and password "123" to log into the ZLIMS system.



Figure 1 Logging into ZLIMS

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3. Select **Experiment > Task** to enter the task page, and click **Create**.

Figure 2 Creating a task

4. Set Task Type to megabolt, set Product to WGS or WES, and set Sequencing Type to PE.

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Figure 3 Adding sample information

5. Click Add outside sample to add sample information and click Submit.



- Items marked with "\*" are required.
- Multiple lines of sample information can be added.
- More optional parameters could be specified in Global parameters, Filter and alignment parameters, and BQSR and variant calling parameters. For details about commandline parameters, refer to MegaBOLT\_user\_manual.

Procedure

You will be prompted when the submission succeeds and the newly added task will be listed in the task page for analysis.

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Figure 4 Submitting a task

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Figure 5 Specifying optional parameters

6. Wait till the analysis completes.

You can check the status of the submitted task in the **Task Status** column on the task page.

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Figure 6 Checking task creation status

7. After the **Completion Status** of the task turns to **success**, click the task ID to enter the **Task Summary** page.

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Figure 7 Checking task completion status

8. On the **Task Summary** page, you can click the icons in the **Analysis Report** or **Result Files** column to view the results.

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#### Figure 8 Viewing analysis report and results





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