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MegaBOLT

生信分析加速器 *Bioinformatics Analysis Accelerator*

快速上手指南

Quick Start Guide

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仅供科研使用

Research Use
Only

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关于本指南

本指南适用于 MegaBOLT 生信分析加速器，指南版本 1.0，软件版本 V2.1.0。

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About this guide

This guide is applicable to MegaBOLT Bioinformatics Analysis Accelerator. The edition is 1.0 and the software version is V2.1.0.

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Figures in this guide 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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目录

1	快速开始	1
	硬件安装.....	1
	进入操作系统	1
	进入命令行终端.....	2
	查看帮助文档	3
	投递任务.....	3
2	使用 ZLIMS	5
3	MegaBOLT 文档导航.....	6
	文档简介.....	6
	获取文档.....	7

Contents

1	Quick start	9
	Assembling the device	9
	Logging into the system	9
	Starting the terminal	10
	Viewing Help.....	11
	Submitting a task	11
2	Working with ZLIMS	13
3	MegaBOLT documents	14
	Brief introduction	14
	Accessing the documents	15

1

快速开始

硬件安装

连接主机、显示器、键盘与鼠标，将加密锁插入任意 USB 接口，接通电源，即可开机。



图 1 加密锁

进入操作系统

主机开机后，操作系统进入用户验证界面，如下图所示：

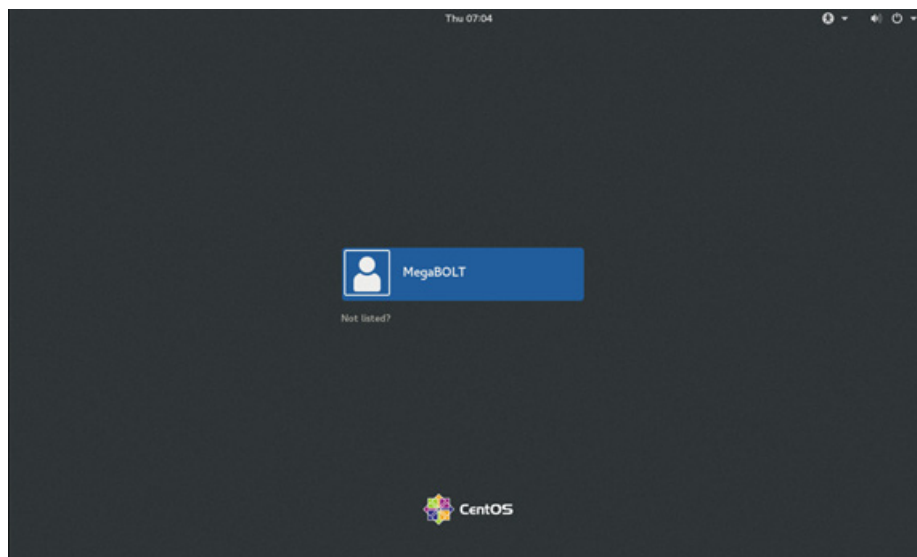


图 2 用户验证界面

点击选择系统用户“MegaBOLT”，输入密码“megabolt”，即可进入操作系统。

进入命令行终端

进入操作系统桌面后，点击桌面左上角的【Applications】>【Favorites】>【Terminal】，启动命令行终端。

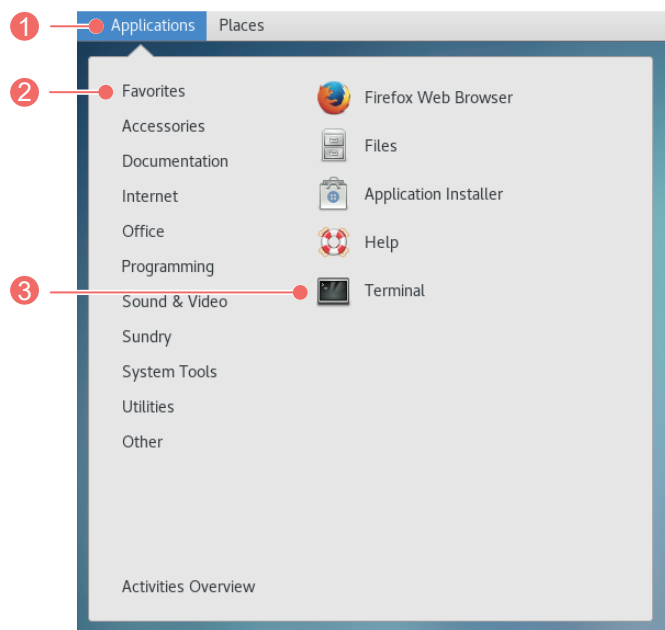


图 3 启动命令行终端

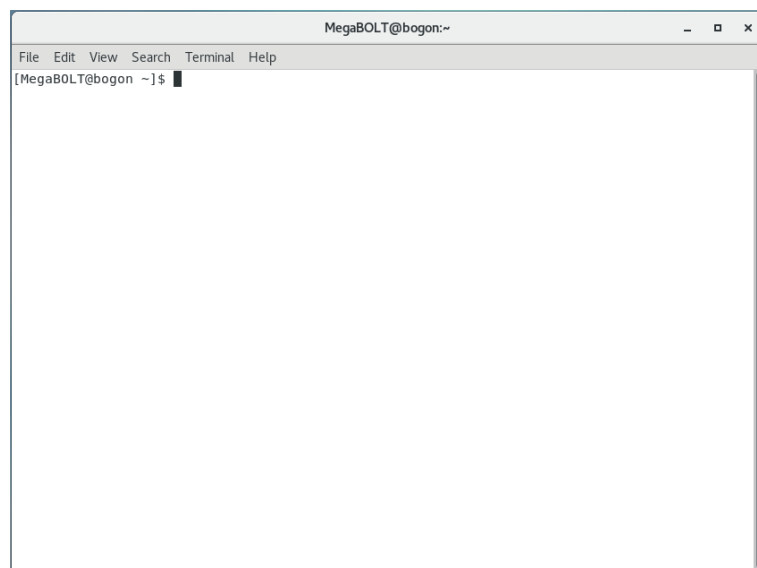


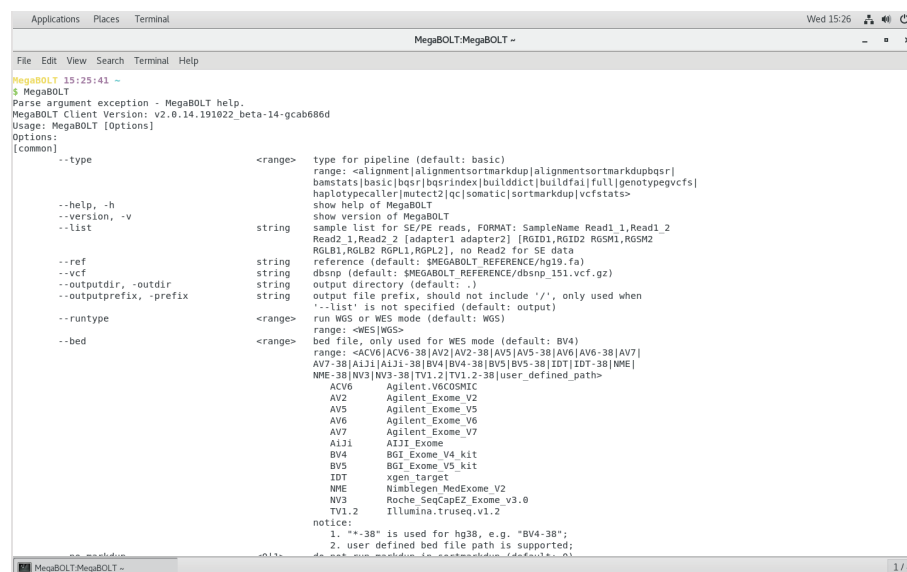
图 4 命令行终端

查看帮助文档

在命令行终端中输入如下命令：

MegaBOLT

按【Enter】执行，即可查看 MegaBOLT 帮助文档，如下图所示：



```
MegaBOLT 15:25:41 ~
$ MegaBOLT
Parse argument exception - MegaBOLT help.
MegaBOLT Client Version: v2.0.14.191022_beta-14-gcab686d
Usage: MegaBOLT [Options]
Options:
[common]
--type                <range>    type for pipeline (default: basic)
                                range: <alignment|alignmentsortmarkdup|alignmentsortmarkdupbqsr|
                                bamstats|basic|bqsr|bqsrindex|buildidict|buildfai|full|genotypegvcfs|
                                haplotypical|metect2|qc|somatic|sortmarkdup|vcfstats>
--help, -h            show help of MegaBOLT
--version, -v         show version of MegaBOLT
--list                string      sample list for SE/PE reads, FORMAT: SampleName Read1_1,Read1_2
                                Read2_1,Read2_2 [adapter1 adapter2] [RGID1,RGID2 RGSMT1,RGSMT2
                                RGLB1,RGLB2 RGPL1,RGPL2], no Read2 for SE data
--ref                 string      reference (default: $MegaBOLT_REFERENCE/hg19.fa)
--vcf                  string      dbnsp (default: $MegaBOLT_REFERENCE/dbnsp_151.vcf.gz)
--outputdir, -outdir  string      output directory (default: .)
--outputprefix, -prefix string      output file prefix, should not include '/', only used when
                                '--list' is not specified (default: output)
--runtype              <range>    run WGS or WES mode (default: WGS)
                                range: <WES|WGS>
--bed                  <range>    bed file, only used for WES mode (default: BV4)
                                range: <ACV6|ACV6-38|AV2|AV2-38|AV5|AV5-38|AV6|AV6-38|AV7|
                                AV7-38|AIJ1|AIJ1-38|BV4|BV4-38|BV5|BV5-38|IDT|IDT-38|NME|
                                NME-38|NV3|NV3-38|TV1.2|TV1.2-38|user_defined_path>
                                ACV6      Agilent V6COSMIC
                                AV2       Agilent Exome V2
                                AV5       Agilent Exome V5
                                AV6       Agilent Exome V6
                                AV7       Agilent Exome V7
                                AIJ1      AIJ1 Exome
                                BV4       BGI Exome V4 kit
                                BV5       BGI Exome V5 kit
                                IDT       xgen target
                                NME       Nimblegen MedExome V2
                                NV3       Roche SeqCapEZ Exome v3.0
                                TV1.2     Illumina.truseq.v1.2
notice:
1. '--38' is used for hg38, e.g. "BV4-38":
2. user defined bed file path is supported;
do not use module as path (default: .)
1/4
```

图 5 MegaBOLT帮助文档

MegaBOLT 帮助文档和使用说明的详细信息参见《MegaBOLT 用户手册》。

投递任务

MegaBOLT 采用 Server-Client 结构设计，用户使用 MegaBOLT 程序投递分析任务到 MegaBOLT server 程序，由 MegaBOLT server 程序统一调度执行。

操作步骤如下：

1. 执行如下命令，运行 MegaBOLT 示例：

```
MegaBOLT --list /mnt/ssd/MegaBOLT/test/sample.list
```

其中，*sample.list* 示例文件包含待分析的样本信息，其内容为：

```
Test /mnt/ssd/MegaBOLT/test/read1.fq.gz /mnt/ssd/
MegaBOLT/test/read2.fq.gz
```

Sample.list 的详细格式参见《MegaBOLT 用户手册》的“List 文件”章节。

2. 查看输出。MegaBOLT 分析任务结束后，当前目录下会生成以分析样本名命名的文件夹。该文件夹用于存放分析结果，在本例中样本名为 **Test**，因此在命令行终端中执行如下命令，进入分析结果文件夹：

```
cd Test
```

再执行如下命令，可以查看分析流程的结果文件：

```
ll
```

```
Oct 11 20:15 Test.list
Oct 11 20:51 Test.log
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam.bai
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam.grp
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz.out
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz.tbi
Oct 11 20:51 Test.out
```

图 6 生成文件列表

至此，MegaBOLT 分析流程示例结束。

如有疑问，请查阅《MegaBOLT 用户手册》，或联系技术支持。

2 使用 ZLIMS

用户可登陆华大智造实验室信息管理系统 ZLIMS（Zebra Laboratory Information Management System）投递 MegaBOLT 分析任务，以及查看分析报告。ZLIMS 采用 Web 端设计，操作方式简单便捷。用户可直接在网页上提交任务并查看结果报告，无需生物信息技术背景，轻松安排计算任务。详细使用方式参见《MegaBOLT 用户手册 -ZLIMS》。



图 7 ZLIMS登录页面

3

MegaBOLT 文档导航

文档简介

MegaBOLT 产品配套用户文档简介如下：

表 1 MegaBOLT 文档

文档名	说明
MegaBOLT 快速上手指南	指导用户快速使用 MegaBOLT 完成示例分析和检查输出结果的正确性，并指示其余文档所在位置及其内容简介。
MegaBOLT 用户手册	指导用户使用 MegaBOLT 的所有基本特性和功能，并展示与功能对应的简单示例。
MegaBOLT 用户手册 -ZLIMS	指导用户使用 ZLIMS 实验室管理系统投递 MegaBOLT 任务，以及查看分析结果。
MegaBOLT 高级用户手册	介绍存储目录结构、存储挂载、部分软件工具的源代码路径、FAQ 以及指导用户使用 MegaBOLT 或 MegaBOLT 子模块进行流程开发等。

获取文档

本文档位于桌面，其它用户文档均可在桌面点击【Home】>【Documents】文件夹查看，如下图所示：

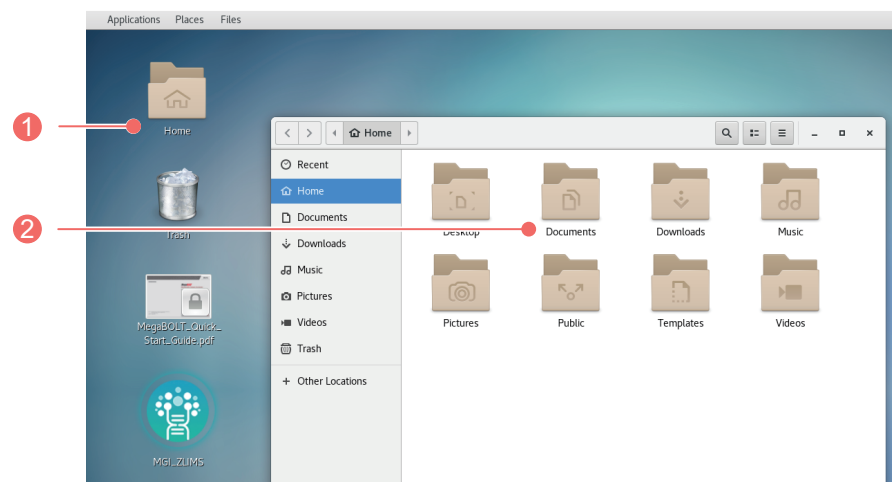


图 8 文档路径

这些文档在命令行终端中的访问路径为：

`/home/MegaBOLT/Documents`

--- 此页有意留白 ---

1 Quick start

Assembling the device

Perform the following steps:

1. Connect the server, monitor, keyboard, and mouse.
2. Insert the dongle to a USB port.
3. Connect to the power source and power on the device.



Figure 1 Dongle

Logging into the system

After you power on the device, the user verification interface is displayed, as shown in the figure below:

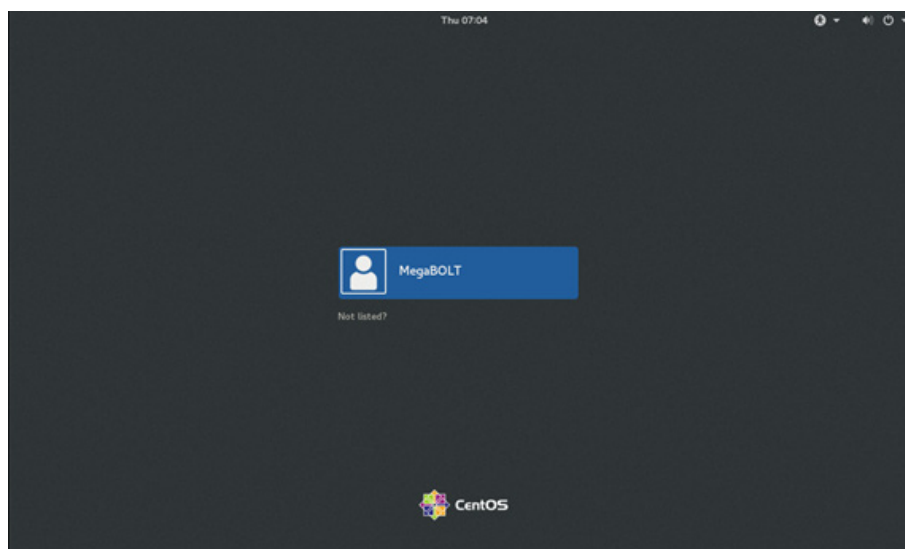


Figure 2 User verification interface

Select the account “MegaBOLT” and input the password “megabolt” to log into the system.

Starting the terminal

To start the terminal, click **Applications>Favorites>Terminal**.

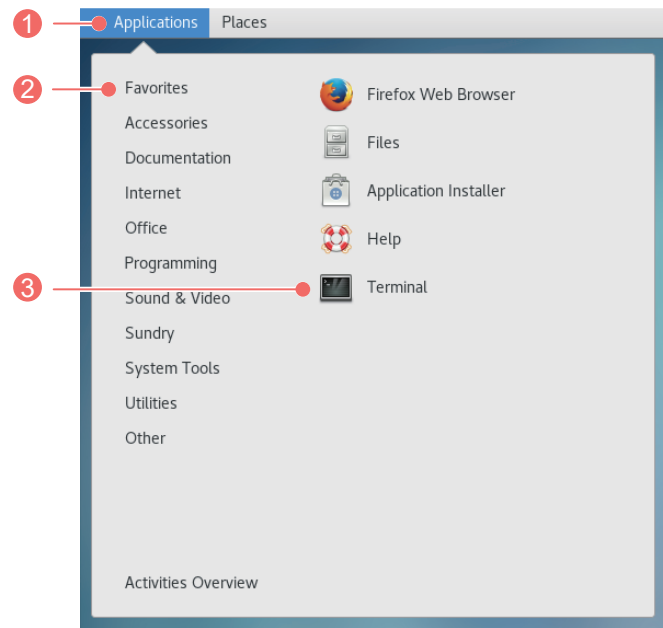


Figure 3 Starting the terminal

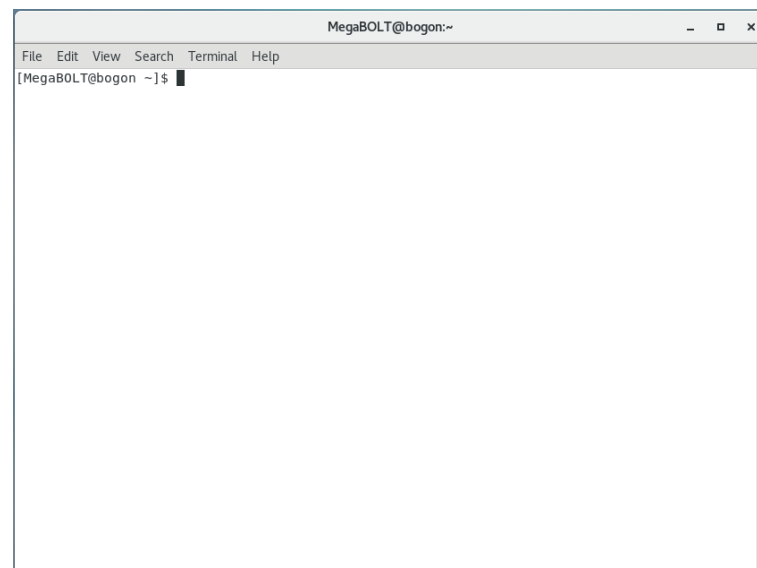


Figure 4 Terminal

Viewing Help

Input the following command on the terminal:

```
MegaBOLT
```

Press **Enter** to execute the command and MegaBOLT Help is displayed:

```
MegaBOLT 15:25:41 ~
$ MegaBOLT
Parse argument exception - MegaBOLT help.
MegaBOLT Client Version: v2.0.14.191022_beta-14-gcab686d
Usage: MegaBOLT [Options]
Options:
[common]
--type                <range>    type for pipeline (default: basic)
                                range: <alignment|alignmentsortmarkdup|alignmentsortmarkdupbqsr|
                                bamstats|basic|bqsr|bqsrindex|buildidict|buildfail|full|genotypegvcfs|
                                haplotypical|metect2|qc|somatic|sortmarkdup|vcfstats>
--help, -h            show help of MegaBOLT
--version, -v         show version of MegaBOLT
--list                string      sample list for SE/PE reads, FORMAT: SampleName Read1_1,Read1_2
                                Read2_1,Read2_2 [adapter1 adapter2] [RGID1,RGID2 RGSMT1,RGSMT2
                                RGLB1,RGLB2 RGPL1,RGPL2], no Read2 for SE data
--ref                 string      reference (default: $MegaBOLT_REFERENCE/hg19.fa)
--vcf                 string      dbnsp (default: $MegaBOLT_REFERENCE/dbnsp_151.vcf.gz)
--outputdir, -outdir string      output directory (default: .)
--outputprefix, -prefix string     output file prefix, should not include '/', only used when
                                '--list' is not specified (default: output)
--runtype              <range>    run WGS or WES mode (default: WGS)
                                range: <WES|WGS>
--bed                  <range>    bed file, only used for WES mode (default: BV4)
                                range: <ACV6|ACV6-38|AV2-38|AV5|AV5-38|AV6|AV6-38|AV7|
                                AV7-38|AIJ1|AIJ1-38|BV4|BV4-38|BV5|BV5-38|IDT|IDT-38|NME|
                                NME-38|NV3|NV3-38|TV1.2|TV1.2-38|user_defined_path>
                                ACV6      Agilent V6COSMIC
                                AV2       Agilent Exome V2
                                AV5       Agilent Exome V5
                                AV6       Agilent Exome V6
                                AV7       Agilent Exome V7
                                AIJ1      AIJ1 Exome
                                BV4       BGI Exome V4 kit
                                BV5       BGI Exome V5 kit
                                IDT       xgen target
                                NME       Nimblegen MedExome V2
                                NV3       Roche SeqCapEZ Exome v3.0
                                TV1.2     Illumina.truseq.v1.2
notice:
1. '**38' is used for hg38, e.g. "BV4-38":
2. user defined bed file path is supported;
   do not use module in path (e.g. "module.bed")
1/4
```

Figure 5 MegaBOLT Help

For details about the usage of MegaBOLT, refer to *MegaBOLT_User_Manual*.

Submitting a task

MegaBOLT adopts a Server-Client architecture. Analysis tasks are submitted to the MegaBOLT server for unified execution.

1. Execute the following command to run a DEMO analysis task to MegaBOLT:

```
MegaBOLT --list /mnt/ssd/MegaBOLT/test/sample.list
```

The list file contains the sample information to be analyzed, a sample file is shown as below:

```
Test /mnt/ssd/MegaBOLT/test/read1.fq.gz /mnt/ssd/
MegaBOLT/test/read2.fq.gz
```

For detailed format of the *Sample.list* file, refer to *MegaBOLT_User_Manual*.

2. After the analysis task finishes, a folder named after the sample is generated under the current directory to store analysis results.

3. Execute the following command to open the analysis result folder, taking the sample named “Test” for example:

```
cd Test
```

4. Execute the following command to view the result files of the analysis workflow:

```
ll
```

```
Oct 11 20:15 Test.list
Oct 11 20:51 Test.log
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam.bai
Oct 11 20:42 Test.mm2.sortdup.bqsr.bam.grp
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz.out
Oct 11 20:51 Test.mm2.sortdup.bqsr.HaplotypeCaller.vcf.gz.tbi
Oct 11 20:51 Test.out
```

Figure 6 Result files

If you have any doubts about the analysis workflow, refer to *MegaBOLT_User_Manual* or contact the technical support.

2

Working with ZLIMS

You can log into ZLIMS (Zebra Laboratory Information Management System) to assign a MegaBOLT analysis task and check the analysis report. ZLIMS adopts an easy-to-use web design. You can submit tasks and check the results on the website easily even if you have no bioinformatics background. For details, refer to *MegaBOLT_User_Manual_ZLIMS*.

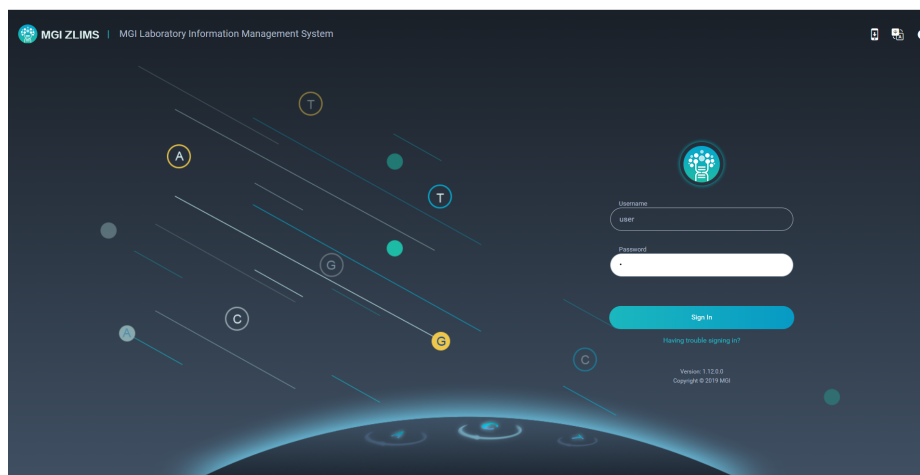


Figure 7 ZLIMS login page

3

Documentation

Brief introduction

The following documentation is provided with MegaBOLT:

Table 2 MegaBOLT documentation

Name	Description
MegaBOLT_Quick_Start_Guide	It is intended to guide the user through task analysis workflow and result confirmation, and provide basic information for the other three files.
MegaBOLT_User_Manual	It provides information about MegaBOLT's basic features and its functions with samples.
MegaBOLT_User_Manual_ZLIMS	ZLIMS is a laboratory management system of MGI. You can log into ZLIMS to assign a MegaBOLT analysis task and check the analysis results.
MegaBOLT_User_Manual_Advanced	It provides information about the storage structure, storage mounting, source code path for some software tools, and FAQ. It further guides the user to develop workflow with MegaBOLT and its submodules.

Accessing the documents

A digital version of this guide is available on the desktop. You can find the other documents by clicking **Home>Documents** on the desktop, as shown in the figure below:

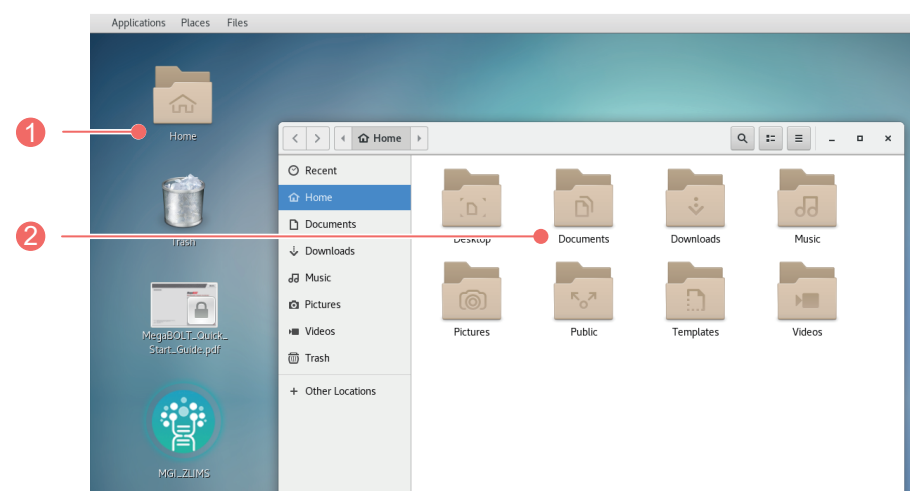


Figure 8 Document directory

You can also obtain the documents from the following directory:

/home/MegaBOLT/Documents

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