

# Detailed steps for GMATA installation

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Here are detailed installation steps:

The software GMATA comes with original codes which work well in different platforms once you installed prerequisite programming free software of perl, R and Java after following step 1, 2 and 3, which can be ignored if your computer has them installed.

Installation steps can be divided into two parts: Part 1 and Part 2. Part 1 can be ignored in most Mac and Linux systems.

After completion of Part 1, you do not to do anything. And then you can go to Part 2 for installation of GMATA. The GMATA installation is simple and very easy.

If the GMATA did not produce any result files, it means that your prerequisite software in Part I is not installed correctly.

Follow these steps below to get GMATA work.

## **Part 1: Preparation of prerequisite programming software:**

## Step1: perl installation

Mac and Linux system already have perl installed so you do NOT need to install perl. If your computer has no perl installed, you have to install the latest release of perl version 5. Click the link below to download and follow instruction to install perl.

<https://www.perl.org/get.html>

The screenshot shows the 'Perl Download' page from the official Perl website. The browser's address bar displays 'https://www.perl.org/get.html'. The page features a dark blue header with the 'Perl' logo and navigation links: ABOUT, DOWNLOAD (highlighted), LEARN, DOCS, CPAN, and COMMUNITY. A version indicator '5.26.2' is visible near the DOWNLOAD link. Below the header, the main heading 'Perl Download' is followed by the subtext 'Getting started quickly'. A section titled 'Perl runs on over 100 platforms!' includes a recommendation to use the latest stable version (5.26.2). The page is divided into three columns for different operating systems: Unix/Linux (with a penguin icon), Mac OSX (with an Apple icon), and Windows (with a Windows icon). Each column indicates that Perl is 'Included (may not be latest)' and provides a 'GET STARTED' button. Below the operating system sections, there is a specific section for 'Unix' with the text 'Running Linux, Solaris, AIX, HP/UX, or any other UNIX-like system?'.

**Perl**

ABOUT DOWNLOAD LEARN DOCS CPAN COMMUNITY







5.26.2

## Perl Download

Getting started quickly

**Perl runs on over 100 platforms!**

We recommend that you always run the latest stable version, currently 5.26.2. If you're running a version older than 5.8.3, you may find that the latest version of CPAN modules will not work.

Unix/Linux	Mac OSX	Windows
 Included (may not be latest)	 Included (may not be latest)	 Strawberry Perl & ActiveState Perl
 GET STARTED	 GET STARTED	 GET STARTED

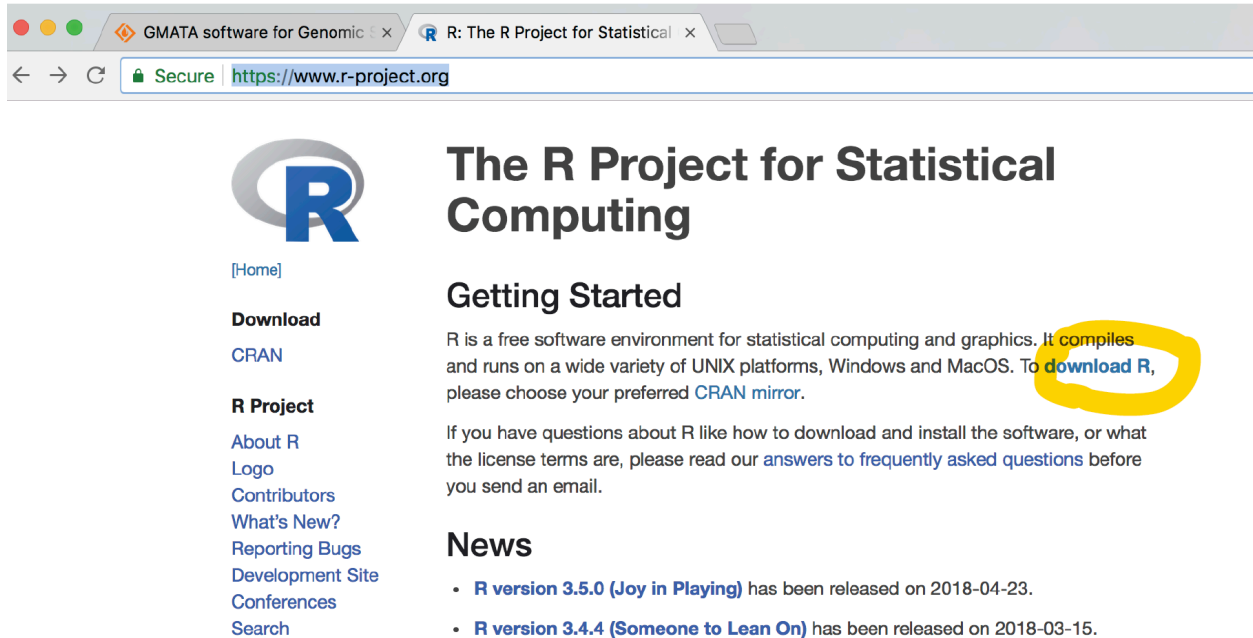
### Unix

Running Linux, Solaris, AIX, HP/UX, or any other UNIX-like system?

## Step2: R installation

Go to the website below to download the newest version of R, click “download R” and install R following the prompted instruction.

<https://www.r-project.org/>



The screenshot shows a web browser window with two tabs: "GMATA software for Genomic" and "R: The R Project for Statistical Computing". The address bar shows "Secure https://www.r-project.org". The website features the R logo, a navigation menu on the left, and main content sections for "Getting Started" and "News".

**The R Project for Statistical Computing**

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**Getting Started**

R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred [CRAN mirror](#).

If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

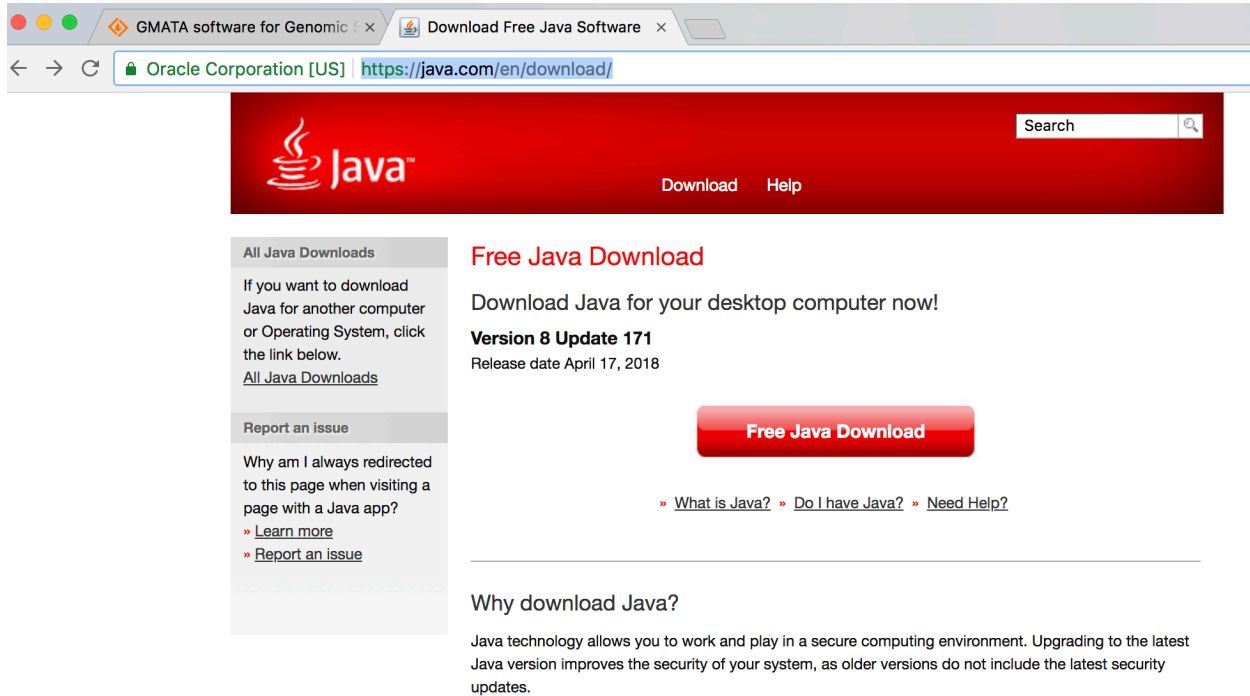
**News**

- **R version 3.5.0 (Joy in Playing)** has been released on 2018-04-23.
- **R version 3.4.4 (Someone to Lean On)** has been released on 2018-03-15.

### Step3: Java installation

Go to the website below to download the newest Java, click “Free Java Download” and install Java following the prompted instruction.

<https://java.com/en/download/>



### Part 2: GMATA installation

There are two options to install GMATA. You can choose any one of them. GMATA.jar or GMATAv2.2.jar is an executable file at Windows 8, 10, Linux and Mac OS. For advanced usage, please follow the instruction in user manual. If you want to see example data, example output and dependent software, you can download them from <https://sourceforge.net/projects/gmata/files/>

### Option1:

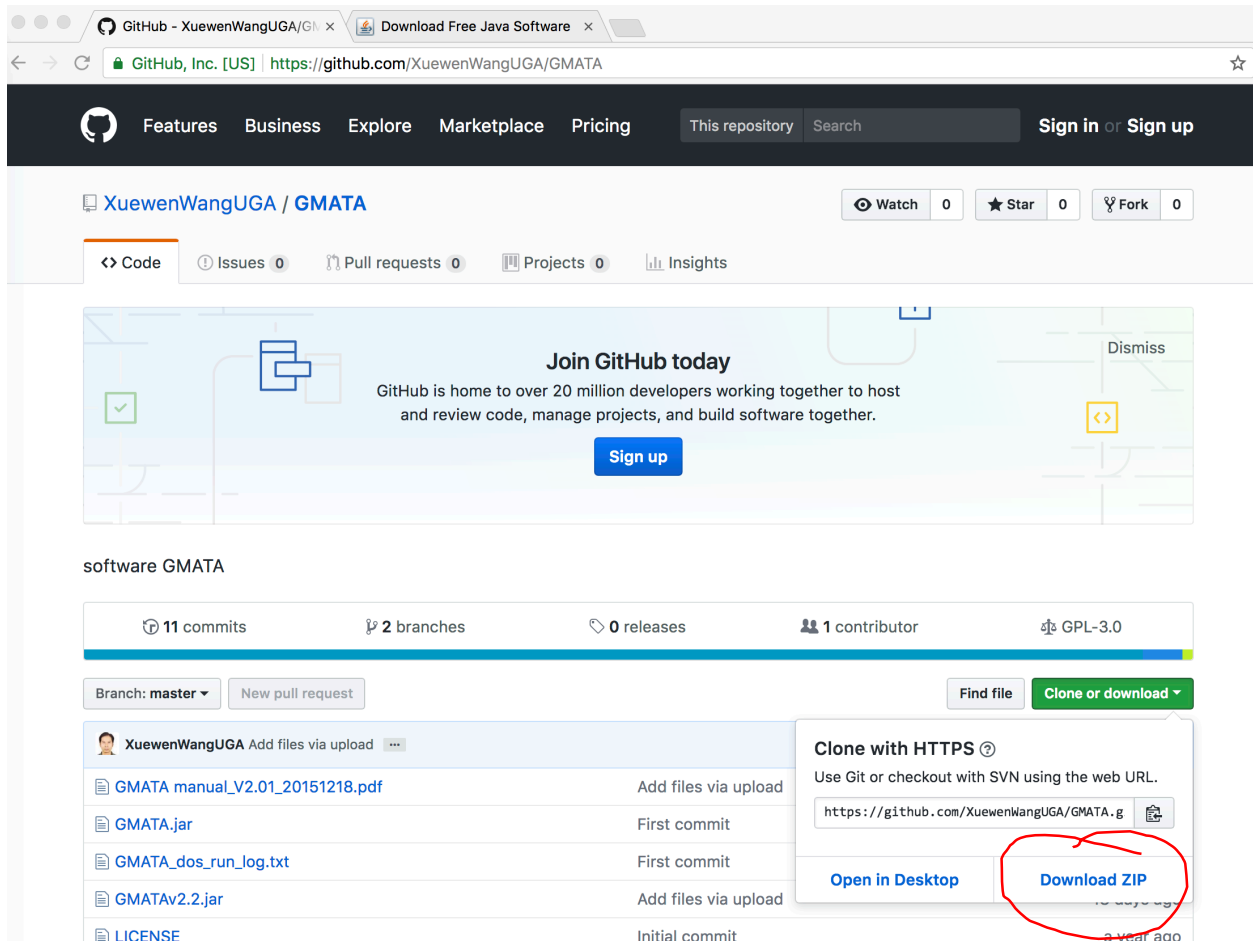
- 1) get GMATA for free:  
got to website: <https://sourceforge.net/projects/gmata/files/>
- 2) download software file package "binv2.1.zip", unzip this file to a directory called "GMATA"
- 3) download "GMATA.jar" or "GMATAv2.2.jar", and copy it to the same directory "GMATA";
- 4) Go to directory "GMATA"; Then you double click the file "GMATA.jar" or the latest "GMATAv2.2.jar", You will find GMATA is working.

The screenshot shows a web browser window with two tabs: "GMATA software for Genomic" and "Download Free Java Software". The address bar shows the URL <https://sourceforge.net/projects/gmata/files/>. The page features the SourceForge logo and navigation links for Articles, Cloud Storage, and Business VoIP. The main heading is "GMATA software for Genomic..." with a subtitle "Genome-wide Microsatellite Analyzing Toward Application: GMATA" and "Brought to you by: xwvan". Below this is a navigation bar with links for Summary, Files, Reviews, Support, Wiki, Code, Tickets, Discussion, and Blog. A green button labeled "Download Latest Version" with a download icon and "GMATAv2.2.jar (77.6 kB)" is prominent, along with a blue "Get Updates" button and a blue RSS feed icon. The "Home" section contains a table of files.

Name	Modified	Size	Downloads / Week
<a href="#">GMATAv2.2.jar</a>	2018-04-14	77.6 kB	30
<a href="#">e-PCR.zip</a>	2017-04-24	16.5 MB	2
<a href="#">Gmatav2.1_figureOutput.BdistachyonGenome.zip</a>	2016-10-20	401.1 kB	2
<a href="#">Gmatav2.1_figureOutput.FoxtailmilletGenome.zip</a>	2016-10-20	459.5 kB	3
<a href="#">Gmatav2.1_figureOutput.CornGenome.zip</a>	2016-10-20	432.9 kB	4
<a href="#">Gmatav2.1_figureOutput.RiceGenome.zip</a>	2016-10-20	457.0 kB	2
<a href="#">datav21.zip</a>	2016-02-04	942.5 kB	3
<a href="#">binv21rel.zip</a>	2016-02-04	201.1 kB	7
<a href="#">GMATA manual_V2.01_20151218.pdf</a>	2015-12-18	1.2 MB	5

## Option2:

1. get GMATA for free:  
Go to website: <https://github.com/XuewenWangUGA/GMATA> , click “Clone or download”, choose “Download ZIP”. This will download a file “GMATA-master.zip” to your computer.
2. After downloading, unzip the downloaded file to a directory called “GMATA”
3. Go to directory “GMATA”; Then you double click the file "GMATA.jar" or the latest “GMATAv2.2.jar”. You will find GMATA is working.



## Working with GMATA:

Go to directory “GMATA”, click “GMATA.jar” or “GMATAv2.2.jar”, you will see interface like this. Enjoy.

GMATA v2.0

# GMATA

SSR identification | SSR statistical plotting | Gbrowse viewing | Marker designing | e-Mapping | About

Parameters

Sequence file (fasta format):

Motif unit

Min-length (nt):	<input type="text" value="2"/>	Min. repeat-times:	<input type="text" value="5"/>
Max-length (nt):	<input type="text" value="10"/>	Highlighted motif:	<input type="text" value="0"/> ▼

Running Information:

●●●GMATA v2.2 Build 20180415

GMATA

SSR viewing

Marker designing

e-Mapping

SSR Masking

About

SSR identification

Statistical plotting

Parameters

Sequence file (fasta format):

Browse

.fasta, fa, fastaq, fq

Motif unit

Min-length (nt):

2

Max-length (nt):

6

Min. repeat-times:

5

Highlighted motif:

0

Run

Clear

Exit

Running Information: