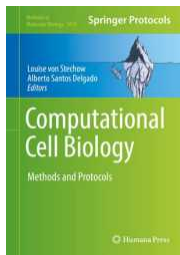


Alum

Department of Biosystems Science and Engineering

Machine Learning & Computational Biology Lab

all-GWAS: Virtual Machine



Anja C. Gumpinger, Damian Roqueiro,
Dominik G. Grimm and Karsten M.
Borgwardt

Methods and Tools in Genome-wide Association Studies

Book series on Methods in Molecular Biology, published by Springer.

Summary

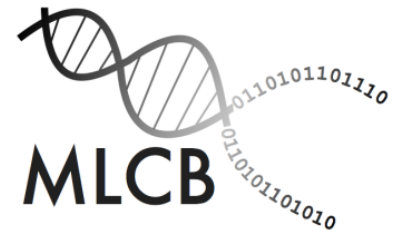
The book chapter: **Methods and Tools in Genome-wide Association Studies** (GWAS) presents the theoretical foundations of the most frequently used statistical models in GWAS. The theory is supplemented with step-by-step protocols on how to run GWAS with different tools and software.

As supplementary material for this book chapter, we have created an instance of a virtual machine (VM) with preinstalled software and with all the example scripts presented in the chapter. The VM allows the user to reproduce all the analyses that are presented as examples. As a word of caution, some of these analyses are better suited for a computing environment with multiple cores, and as a result of this, the execution on the VM will take a significantly longer amount of time. See Table 1 (p. 112) in the chapter for details on the execution times for different scripts.

all-GWAS Virtual Machine

The VM can be downloaded and instantiated on any platform by following these steps:

1. Download [VirtualBox](#) for your specific platform



Open Positions

Currently, we do not have any open positions at the MLCB lab.

Contact

ETH Zurich
Dep. Biosysteme

Prof. Dr. Karsten M. Borgwardt
BSB G 4
Mattenstrasse 26
4058 Basel
Switzerland

[+41 61 387 34 20](#)

[E-mail](#)

[V-Card \(vcf, 1kb\)](#)

2. Download the all-GWAS virtual machine [all-gwas.vdi](#), ~8.0 Gb,
MD5=dfab677d036b31a5e0048c51acea910b
3. Import the VM from within VirtualBox
Note: Depending on your version of VirtualBox, the instructions below may require clicking "Continue" to move to the next selection.
 - Click the "New" icon at the top to create a new VM
 - Type "all-GWAS" to set the name of the VM
 - Select "Linux" as the Type of operating system
 - Select "Ubuntu (64-bit)" as Version
 - Select 4,096 Mb as memory size
 - Select "Use an existing virtual hard disk file" and then search for the file all-gwas.vdi downloaded in step 2
4. Now a new VM will show up in the left panel of Virtual Box. The VM will be marked as "Powered Off"
5. Right-click on the VM and select "Settings". Go to "System" and then to "Acceleration". Make sure that:
 - [For Linux] the options "Enable VT-x/AMD-V" and "Enable Nested Paging" are selected
 - [For macOS and Windows] the option "Enable Nested Paging" is selected (this is normally the default behavior)
6. To start the VM, click the "Start" icon at the top
7. Log in with the user account: **gwasuser** with password **genome\$NP**

Code

All the scripts referenced in the chapter can be downloaded from [here \(GZ, 35.3 MB\)](#). This file also contains the data used by the scripts.

Technical Aspects of the VM

The list of software packages installed on the VM can be found below.

Programming Languages

Name	Version
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Python	2.7.12
R	3.3.1

The Wiki page in the VM contains a detailed list of what packages and libraries are installed for Python and R, respectively.

Software Tools

Name	Version
BOLT-LMM	2.2
dmGWAS	3.0
EIGENSOFT	5.0.1
FaST-LMM	0.2.26
PLINK	1.07
PLINK	1.90
VEGAS	1.0

Contact anja.gumpinger@bsse.ethz.ch or damian.roqueiro@bsse.ethz.ch for questions regarding usage of the VM or of the tools/scripts installed in it.