Genome-wide Association Mapping with
FarmCPU
By
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This tutoria...

Steps for Association Mapping
Step 1. Format the genotype and phenotype data needed for
FarmCPU.
Use this tutorial for dat...

ï· Genotype Map Data file
myGM <- read.table("mdp_SNP_information.txt", head = TRUE)
ï· Covariate Variable file (can be crea...

Step 3. Association Analysis
#Open R and Type this in R
install.packages("bigmemory")
install.packages("biganalytics")
lib...

# Results will be saved in myFarmCPU folder
Other ways of Analysis
1.
#Step 1: Set data directory and import files
myY <- ...

# Results will be saved in myFarmCPU folder
Other ways of Analysis
1.
#Step 1: Set data directory and import files
myY <- ...

Use this format for prior p-value SNPs
# Check results in myFarmCPU folder
Note:
ï· Use different software (GAPIT, PLINK, T...

<https://www.slideshare.net/AvjinderSingh/tutorial-for-association-mapping-with-farm-cpu>

<https://www.slideshare.net/AvjinderSingh/basic-tutorial-of-association-mapping-by-avjinder-kaler>

### Tutorial for association mapping with farm cpu

1. 1. Genome-wide Association Mapping with FarmCPU By Avjinder Singh Kaler University of Arkansas, Fayetteville, AR This tutorial can be used to perform association mapping with FarmCPU software alongwith other tutorial ( http://www.slideshare.net/AvjinderSingh/basic-tutorial-of- association-mapping-by-avjinder-kaler ) Software Needed: Download and Install these software. 1. R Software http://www.r-project.org/. 2. TEXTPAD: used to format the files. https://www.textpad.com/
2. [2.](https://image.slidesharecdn.com/tutorialforassociationmappingwithfarmcpu-160225091118/95/tutorial-for-association-mapping-with-farm-cpu-2-638.jpg?cb=1456391589)Steps for Association Mapping Step 1. Format the genotype and phenotype data needed for FarmCPU. Use this tutorial for data formatting http://www.slideshare.net/AvjinderSingh/basic-tutorial-of- association-mapping-by-avjinder-kaler Step 2. Four Files needed for this analysis and data reading in R. • Phenotype file myY <- read.table("mdp\_traits\_validation.txt", head = TRUE) • Genotype file (Numeric format, can be formatted using other software like GAPIT or TASSEL) myGD <- read.big.matrix("mdp\_numeric.txt", type="char", sep="t", head = TRUE)
3. [3.](https://image.slidesharecdn.com/tutorialforassociationmappingwithfarmcpu-160225091118/95/tutorial-for-association-mapping-with-farm-cpu-3-638.jpg?cb=1456391589)• Genotype Map Data file myGM <- read.table("mdp\_SNP\_information.txt", head = TRUE) • Covariate Variable file (can be created in other software like TASSEL, use 3-5 PC) myCV <- read.table("Copy of Q\_First\_Three\_Principal\_Components.txt", head = TRUE)
4. [4.](https://image.slidesharecdn.com/tutorialforassociationmappingwithfarmcpu-160225091118/95/tutorial-for-association-mapping-with-farm-cpu-4-638.jpg?cb=1456391589)Step 3. Association Analysis #Open R and Type this in R install.packages("bigmemory") install.packages("biganalytics") library("bigmemory") library("biganalytics") library("compiler") #this library is already installed in R source("http://zzlab.net/GAPIT/gapit\_functions.txt") source("http://zzlab.net/FarmCPU/FarmCPU\_functions.txt") library("bigmemory") library("biganalytics") library("compiler") #this library is already installed in R source("http://zzlab.net/GAPIT/gapit\_functions.txt") source("http://zzlab.net/FarmCPU/FarmCPU\_functions.txt") # Make a folder in C and name it myFarmCPU #Step 1: Set working directory and import data setwd("C:myFarmCPU") myY <- read.table("mdp\_traits\_validation.txt", head = TRUE) myGM <- read.table("mdp\_SNP\_information.txt", head = TRUE) myGD <- read.big.matrix("mdp\_numeric.txt", type="char", sep="t", head = TRUE) #Step 2: Run FarmCPU myFarmCPU <- FarmCPU( Y=myY[,c(1,8)], GD=myGD, GM=myGM )
5. [5.](https://image.slidesharecdn.com/tutorialforassociationmappingwithfarmcpu-160225091118/95/tutorial-for-association-mapping-with-farm-cpu-5-638.jpg?cb=1456391589)# Results will be saved in myFarmCPU folder Other ways of Analysis 1. #Step 1: Set data directory and import files myY <- read.table("mdp\_traits\_validation.txt", head = TRUE) myGM <- read.table("mdp\_SNP\_information.txt", head = TRUE) myGD <- read.big.matrix("mdp\_numeric.txt", type="char", sep="t", head = TRUE) myCV <- read.table("Copy of Q\_First\_Three\_Principal\_Components.txt", head = TRUE) #Step 2: Run FarmCPU myFarmCPU <- FarmCPU( Y=myY[,c(1,2)], GD=myGD, GM=myGM, CV=myCV ) 2. This method uses max loop to give best power and FDR #Step 1: Set data directory and import files myY <- read.table("mdp\_traits\_validation.txt", head = TRUE) myGM <- read.table("mdp\_SNP\_information.txt", head = TRUE) myGD <- read.big.matrix("mdp\_numeric.txt", type="char", sep="t", head = TRUE) #Step 2: Run FarmCPU myFarmCPU <- FarmCPU( Y=myY[,c(1,2)], GD=myGD, GM=myGM, maxLoop=10 ) 3. Use prior information of p-value for SNPs
6. [6.](https://image.slidesharecdn.com/tutorialforassociationmappingwithfarmcpu-160225091118/95/tutorial-for-association-mapping-with-farm-cpu-6-638.jpg?cb=1456391589)Use this format for prior p-value SNPs # Check results in myFarmCPU folder Note: • Use different software (GAPIT, PLINK, TASSEL) and models to compares results. • Try this tutorial too http://www.slideshare.net/AvjinderSingh/basic-tutorial-of- association-mapping-by-avjinder-kaler Acknowledge • Dr. Zhang’s Lab • Dr. Buckler’s Lab If you have any question, feel free to contact me. askaler@uark.edu