

R Script is a programming language widely used among statisticians, data miners, and data analysis. The software is available from [CRAN Download R](#) and [Microsoft R Open](#). Data from T3 can be accessed by

1. Saving from T3 then reading into R
2. Using BrAPI R package to read directly into R

Download data from T3 website then read into R

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment

The screenshot shows the T3 website interface. The top navigation bar includes 'Select', 'Analyze', 'Download', 'Browse', 'Reports', 'Manage', and 'Resources'. The 'Select' dropdown menu is open, showing options: 'Wizard (Lines, Traits, Trials)', 'Lines by Properties', 'Lines by Phenotype', 'Lines by Haplotype', 'Lines by Genotype Experiment', 'Traits and Trials', 'Markers', 'Subset by Marker Polymorphisms', 'Genetic Map', and 'Clear selection'. The 'Lines by Genotype Experiment' option is highlighted. Below the menu, the 'Select Lines by Genotype Experiment' page is visible. It features a search bar, a 'platform' dropdown, an 'Experiments' dropdown, and a 'Lines' dropdown. A list of experiments is shown, including 'UC Davis', 'WorldwideDiversityPanel_9K', 'USDA-ARS, North Dakota', 'NSGCwheat9K_winter_fac', 'NSGCwheat9K_4X', and 'NSGCwheat9K_spring'. A list of lines is also shown, including 'ATLAS66', 'NW03666', 'SD07220', 'LOUISE', 'CITR14695', 'PI94530', 'PI173442', 'PI119350', and 'PI48147'. A 'Save selection' button is at the bottom.

2. Go to Select => Genetic Map

Map Sets

This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to ch

| select | markers (total) | markers (in selected lines) | map set name | comment (select item for complete te |
|----------------------------------|-----------------|-----------------------------|----------------------------------|--|
| <input type="radio"/> | 877 | | Aegilops tauschii, 2009 | From Luo et al, (2009) PNAS 106(37 |
| <input type="radio"/> | 19720 | | SynOp GBS BinMap, 2012 | Bin map of Synthetic W9784 x Opata bet |
| <input type="radio"/> | 1485 | | SynOp GBS AntMap, 2012 | Genetic linkage map of Synthetic W9 |
| <input type="radio"/> | 1625 | | KleinProteo x KleinChaja, 2012 | Contacts: Jorge Dubcovsky, Luxmi Tr |
| <input type="radio"/> | 3503 | | wsnp 2013 Consensus | Consensus wsnp map from C.R. Cav |
| <input type="radio"/> | 38832 | | 90K Array Consensus | From: Wang et. al. (2014) Characteri |
| <input type="radio"/> | 125340 | | CSS POPSEQ 2014 | A genetic map created by locating thi |
| <input type="radio"/> | 3393777 | | CSS GBS 2014 | A physical map of GBS markers start a |
| <input checked="" type="radio"/> | 168455 | | RefSeq v1.0 | A physical map from IWGSC RefSeq |
| <input type="radio"/> | 145004 | | Chromosome Survey Sequence, 2014 | A physical map from the Chromosom Genome |

3. Go to Download => Genotype and Phenotype Data - Select rrBLUP format
4. Select "Create File"

Download ▾
Browse ▾
Reports ▾
Manage ▾
Resources ▾

Genotype and Phenotype Data
SNP Alleles and Sequences
Marker Annotation
Bulk Download
Android Field Book
Weather Data
Genetic Maps

Genotype and Phenotype Data

to retrieve the results.

consensus ☒ Genotype single experiment

| Lines | Markers | Traits | Trials |
|--|---------|---------------|---------------|
| ATLAS66 NW03666 SD07220 LOUISE CITR14695 PI94530 PI173442 PI119350 PI48147 | All | none selected | none selected |

Minimum MAF ≥ 5 % Remove markers missing > 50 % of data

| Removed by filtering | Remaining |
|--|--------------|
| 73 markers have a minor allele frequency (MAF) less than 5% 0 markers are missing more than 50% of data 73 markers removed | 6232 markers |

Create file

SNP data coded as {A,C,T,G,N,+,-}
tab delimited
used by **TASSEL**

file type "Hapmap"
for genetic maps the value in pos column is multiplied by 1000 and cor

Create file

genotype coded as {AA=1, BB=-1, AB=0, missing=NA}
comma delimited
used by **rrBLUP**

read.table("snppfile.txt", header=TRUE, check.names=FALSE)
read.table("genotyp.hmp.txt", header=TRUE, check.names=FALSE)

Create file

genotype coded as {AA, AB, BB}
used by **Flapjack**

Create file

VCF format
used by **TASSEL**

Create file

VCF format
Impute missing genotypes using Beagle

using beagle.10Jun18.811.jar (version 5.0)

5. In the R script read in file

```
R version 3.5.0 (2018-04-23) -- "Joy in Playing"  
Copyright (C) 2018 The R Foundation for Statistical Computing  
Platform: x86_64-apple-darwin15.6.0 (64-bit)
```

```
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.
```

```
Natural language support but running in an English locale
```

```
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.
```

```
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.
```

```
> snp <- readTable("genotype.hmp.txt", header=TRUE, check.names=FALSE)
```

Use BrAPI R package to directly read data from T3 in R

The documentation for this package is at <https://github.com/CIP-RIU/brapi>. The current package (Aug 1, 2018) will direct you to t3sandbox.org. This will be fixed soon to point to triticeaetoolbox.org/wheat.

In R execute

```
install.packages("devtools")  
devtools::install_github("CIP-RIU/brapi")
```

```
library(brapi)  
library(magrittr)
```

```
t3wheat <- ba_db()$t3s
```

```
list available calls  
bp_calls(t3wheat)
```