

# Package ‘GxEscanR’

May 1, 2026

**Type** Package

**Title** Run GWAS/GWEIS Scans Using Binary Dosage Files

**Version** 3.0.0

**Description** Tools to run genome-wide association study (GWAS) and genome-wide by environment interaction study (GWEIS) scans using the genetic data stored in a binary dosage file. The user provides a data frame with the subject's covariate data and the information about the binary dosage file returned by the `BinaryDosage::getbinfo()` routine.

**Suggests** testthat (>= 2.1.0), knitr, rmarkdown

**VignetteBuilder** knitr

**License** GPL-3

**Encoding** UTF-8

**Language** en-US

**RoxygenNote** 7.3.3

**Depends** R (>= 3.5.0)

**Imports** lsReg, BinaryDosage

**NeedsCompilation** no

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**Date/Publication** 2026-05-01 16:40:12 UTC

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gweis.mem

*Routine to allocate memory needed to perform a GWEIS.***Description**

Routine to allocate memory needed to perform a GWEIS.

**Usage**

```
gweis.mem(gemdl, subids, tests, gomdl = NULL)
```

**Arguments**

gemdl	The results from glm for the gene-environment model. This model contains the outcome and all covariates of interest with the last covariate listed in the model being the covariate that the gene interaction is being tested for.
subids	A character vector of subject IDs that line up with the data that was used in the models that are passed to this routine
tests	The list of tests to perform. These can be any combination of the following values "bg_go", "bg_ge", "bg_gxe", "bgxe", "joint", "bg_eg", "bg_case", "bg_ctrl"
gomdl	The results from glm for the gene-only model. This model contains the outcome and all the covariates except the covariate that the gene interaction is being tested for. Required (non-NULL) when "bg_go" is included in tests; ignored otherwise.

**Value**

List containing allocated memory to perform the specified GWEIS. This value is passed to the `rungweis` routine. Returns 1 if any value in `tests` is not a recognised test name.

**Examples**

```
## Not run:
bdinfo <- BinaryDosage::getbdinfo(system.file("extdata", "gendata.bdose",
                                             package = "GxEScanR"))
subdata <- readRDS(system.file("extdata", "subdata.rds", package = "GxEScanR"))
subdata <- subdata[complete.cases(subdata), ]
subdata <- subdata[subdata$subid %in% bdinfo$samples$sid, ]

linearmodel <- glm(y_linear ~ x2 + x1, data = subdata)
linearmem <- gweis.mem(gemdl = linearmodel,
                      subids = subdata$subid,
                      tests = c("bg_ge", "bg_gxe", "bgxe", "joint"))

## End(Not run)
```

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rungweis	<i>Routine to run a GWEIS</i>
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**Description**

Routine to run a GWEIS

**Usage**

```
rungweis(gweismem, bdfinfo, snps, outfile, maf = 0.01)
```

**Arguments**

gweismem	Models and memory allocated by gweis-mem to run the GWEIS.
bdfinfo	Information about a Binary Dosage file that contains the genetic data to run the GWEIS
snps	List of SNPs in the Binary Dosage file to perform the GWEIS on.
outfile	Name of the file to contain the output
maf	Minimum minor allele frequency of SNPs needed to run test on.

**Value**

Called for its side effect of writing tab-delimited results to outfile. Returns NULL invisibly.

**Examples**

```
## Not run:
bdfinfo <- BinaryDosage::getbdfinfo(system.file("extdata", "gendata.bdose",
                                               package = "GxEScanR"))
subdata <- readRDS(system.file("extdata", "subdata.rds", package = "GxEScanR"))
subdata <- subdata[complete.cases(subdata), ]
subdata <- subdata[subdata$subid %in% bdfinfo$samples$sid, ]

linearmodel <- glm(y_linear ~ x2 + x1, data = subdata)
linearmem <- gweis.mem(gemdl = linearmodel,
                     subids = subdata$subid,
                     tests = c("bg_ge", "bgxe", "joint"))
outfile <- tempfile(fileext = ".txt")
rungweis(gweismem = linearmem, bdfinfo = bdfinfo,
        snps = 1:nrow(bdfinfo$snps), outfile = outfile)

## End(Not run)
```

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