## How to run test cases

1. Checkout the tests directory from the project repo on github.
2. Change working directory to the test-case directory. setwd("tests/testthat/")
3. Initialize the testing environment. source("setup.R")
4. Run test cases test\_file("test-function\_preprocess.R",reporter = c("Check","Location"))

## Test Report

Start test: sanityCheckEBVdesc() works for basic valid data test-function\_preprocess.R:22:3 [success]End test: sanityCheckEBVdesc() works for basic valid dataStart test: sanityCheckEBVdesc() works for optional valid data test-function\_preprocess.R:31:3 [success]End test: sanityCheckEBVdesc() works for optional valid dataStart test: sanityCheckEBVdesc() detects illegal header test-function\_preprocess.R:41:3 [success]End test: sanityCheckEBVdesc() detects illegal headerStart test: sanityCheckEBVdesc() reports illegal header test-function\_preprocess.R:54:3 [success]End test: sanityCheckEBVdesc() reports illegal headerStart test: sanityCheckEBVdesc() detects missing header test-function\_preprocess.R:67:3 [success]End test: sanityCheckEBVdesc() detects missing headerStart test: sanityCheckEBVdesc() detects duplicate headers test-function\_preprocess.R:76:3 [failure]End test: sanityCheckEBVdesc() detects duplicate headersStart test: sanityCheckEBVdesc() checks 'ID' exists test-function\_preprocess.R:87:3 [success]End test: sanityCheckEBVdesc() checks 'ID' existsStart test: sanityCheckEBVdesc() checks classifiers exist test-function\_preprocess.R:100:3 [success]End test: sanityCheckEBVdesc() checks classifiers existStart test: sanityCheckEBVdesc() checks for unknown classifiers test-function\_preprocess.R:113:3 [success]End test: sanityCheckEBVdesc() checks for unknown classifiersStart test: sanityCheckEBVdesc() checks for Accuracy-Trait mismatch test-function\_preprocess.R:123:3 [failure]End test: sanityCheckEBVdesc() checks for Accuracy-Trait mismatchStart test: sanityCheckEBVdesc() checks for identical order numbers test-function\_preprocess.R:134:3 [success]End test: sanityCheckEBVdesc() checks for identical order numbersStart test: sanityCheckEBVdesc() checks for missing order numbers test-function\_preprocess.R:146:3 [failure]End test: sanityCheckEBVdesc() checks for missing order numbersStart test: sanityCheckEBVdesc() checks for missing group numbers test-function\_preprocess.R:159:3 [failure]End test: sanityCheckEBVdesc() checks for missing group numbersStart test: sanityCheckEVdesc() works for basic valid data test-function\_preprocess.R:172:3 [success]End test: sanityCheckEVdesc() works for basic valid dataStart test: sanityCheckEVdesc() detects illegal header test-function\_preprocess.R:182:3 [success]End test: sanityCheckEVdesc() detects illegal headerStart test: sanityCheckEVdesc() reports illegal header test-function\_preprocess.R:196:3 [success]End test: sanityCheckEVdesc() reports illegal headerStart test: sanityCheckEVdesc() reports duplicate headers test-function\_preprocess.R:208:3 [success]End test: sanityCheckEVdesc() reports duplicate headersStart test: sanityCheckEVdesc() checks 'Index' exists test-function\_preprocess.R:219:3 [success]End test: sanityCheckEVdesc() checks 'Index' existsStart test: sanityCheckEVdesc() checks if required classifiers exist test-function\_preprocess.R:232:3 [success]End test: sanityCheckEVdesc() checks if required classifiers existStart test: sanityCheckEVdesc() checks for unknown classifiers test-function\_preprocess.R:246:3 [failure]End test: sanityCheckEVdesc() checks for unknown classifiersStart test: sanityCheckEVdesc() checks if trait(s) in the EV description file matches with those in the EBV description file test-function\_preprocess.R:261:5 [success]End test: sanityCheckEVdesc() checks if trait(s) in the EV description file matches with those in the EBV description fileStart test: sanityCheckEBV() works for basic valid data test-function\_preprocess.R:274:3 [success]End test: sanityCheckEBV() works for basic valid dataStart test: sanityCheckEBV() reports duplicate headers test-function\_preprocess.R:286:3 [success]End test: sanityCheckEBV() reports duplicate headersStart test: sanityCheckEBV() checks if the list of trait(s) in the EBV data file matches with that in the EBV description file test-function\_preprocess.R:302:5 [success]End test: sanityCheckEBV() checks if the list of trait(s) in the EBV data file matches with that in the EBV description fileStart test: sanityCheckEBV() checks if traits in the EBV data file are present in the EBV description file test-function\_preprocess.R:319:5 [success]End test: sanityCheckEBV() checks if traits in the EBV data file are present in the EBV description fileStart test: sanityCheckEBV() checks if traits values in the EBV data file are character strings instead of numbers test-function\_preprocess.R:335:5 [success]End test: sanityCheckEBV() checks if traits values in the EBV data file are character strings instead of numbersStart test: sanityCheckEV() works for basic valid data test-function\_preprocess.R:349:3 [success]End test: sanityCheckEV() works for basic valid dataStart test: sanityCheckEV() checks if first column is Index test-function\_preprocess.R:363:13 [success]End test: sanityCheckEV() checks if first column is IndexStart test: sanityCheckEV() checks if 'Index' column is duplicated test-function\_preprocess.R:375:13 [success]End test: sanityCheckEV() checks if 'Index' column is duplicatedStart test: sanityCheckEV() checks if a column header is duplicated test-function\_preprocess.R:386:13 [success]End test: sanityCheckEV() checks if a column header is duplicatedStart test: sanityCheckEV() checks for mismatch between the column headers in the input and description files test-function\_preprocess.R:402:5 [success]End test: sanityCheckEV() checks for mismatch between the column headers in the input and description filesStart test: sanityCheckEV() checks if there is a column header in the input file that does not exist in the description file test-function\_preprocess.R:419:5 [success]End test: sanityCheckEV() checks if there is a column header in the input file that does not exist in the description fileStart test: sanityCheckWt() works for basic valid data test-function\_preprocess.R:433:3 [success]End test: sanityCheckWt() works for basic valid dataStart test: sanityCheckWt() checks if 'Index' column is duplicated test-function\_preprocess.R:445:13 [success]End test: sanityCheckWt() checks if 'Index' column is duplicatedStart test: sanityCheckWt() checks if indices are not recorded in the economic value file test-function\_preprocess.R:460:13 [success]End test: sanityCheckWt() checks if indices are not recorded in the economic value fileStart test: sanityCheckWt() checks if character strings are detected in the 'weight' column of the index weight file test-function\_preprocess.R:476:5 [success]End test: sanityCheckWt() checks if character strings are detected in the 'weight' column of the index weight fileStart test: sanityCheckWt() checks if NA's are detected in the 'weight' column of the index weight file test-function\_preprocess.R:493:5 [success]End test: sanityCheckWt() checks if NA's are detected in the 'weight' column of the index weight file

[ FAIL 5 | WARN 5 | SKIP 0 | PASS 32 ]

== **Failed tests** =====================================================================================================**1]**

-- **Failure** (test-function\_preprocess.R:76:3): sanityCheckEBVdesc() detects duplicate headers ---------------------------**Function:** sanityCheckEBVdesc()

**Test:** Check if the function can return the correct error message

if duplicate headers are detected in the input file.

**Test File:** desc\_bv\_dup\_header.xlsx

**Expected:** “Breeding values: file description error:\n",

" Duplicated headers "

**Actual:** Breeding values: file description error:\n Illegal header. Please use 'column\_labelling' and 'classifier'.\n

**2]**-- **Failure** (test-function\_preprocess.R:123:3): sanityCheckEBVdesc() checks for Accuracy-Trait mismatch ---------------------------**Function:** sanityCheckEBVdesc()

**Test:** Check if the function can return the correct error message

when an ACC classifier does not have a corresponding 'TraitACC' entry

in the column\_labelling colum of the input file.

**Test File:** desc\_bv\_mismatch\_acc\_trait.xlsx

**Expected: “**Breeding values: file description error:\n",

" Accuracy names do not match trait names.

**Actual: “**Economic values: file description error:\n Unknown classifier:\nACC, ACC\n”

**3]**

-- Failure (test-function\_preprocess.R:146:3): sanityCheckEBVdesc() checks for missing order numbers ---------------------------**Function:** sanityCheckEBVdesc()

**Test:** Check if the function can return the correct error message

when there are missing ordering values for trait label/EBV rows

in the input file. While the order column is optional, every

trait label/EBV row should have an order value if the order

column is present.

**Test File:** desc\_bv\_missing\_order.csv

**Expected:** “Breeding values: file description error:\n",

" Missing order for trait(s)\n”

**Actual:** “Breeding values: file description error:\n Missing order for trait(s)\nTrait2\n”

**4]** -- Failure (test-function\_preprocess.R:159:3): sanityCheckEBVdesc() checks for missing group numbers ---------------------------**Function:** sanityCheckEBVdesc()

**Test:** Check if the function can return the correct error message

when there are missing group assignments for traits in the input file.

While the group column is optional, every trait label/EBV row should have a group value if the group column is present in the input file.

**Test File:** desc\_bv\_missing\_group.csv

**Expected:** "Breeding values: file description error:\n",

" Missing group for trait(s) "

**Actual:** NULL

**5]**

-- Failure (test-function\_preprocess.R:246:3): sanityCheckEVdesc() checks for unknown classifiers ---------------------------**Function:** sanityCheckEBVdesc()

**Test:** Check if the function can return the correct error message

when one the classifiers are not one of ID (for ID),

ClassVar (for categorical variables), EV (for trait EV) and

Group (group assignment for traits).

**Test File:** Take desc\_ev. Change classifier for ‘TARSPOT' trait from ‘EV’ to 'GEV'**.**

**Expected:** Economic values: file description error:\n",

" Unknown classifier:\n\

**Actual:** NULL