Documentation to the if else rules within the MM automated code

March 2012

Function 4: final genotype model

#the model depends on the output of keepgender, keepinteraction and keepweight questions where the output is yes or no

#Genotype is automatically included as the goal is to build a genotype model

#When weight is a dependent variable, you cannot have weight in the formula as an fixed effect so the keepweight question is irrelevant.

|  |  |  |  |
| --- | --- | --- | --- |
| Possible scenarios | Gender  Significant? | Interaction  Significant? | Formula |
| 1 | X | X | ~ genotype |
| 2 | X | ✓ | ~ genotype + gender + gender\*genotype\*1 |
| 3 | ✓ | X | ~ genotype + gender |
| 4 | ✓ | ✓ | ~ genotype + gender + gender\*genotype |

\*1 Here gender becomes included at you can’t have an interaction term without the main effects so they are carried in even though they were not significant on their own.

# For any other dependent variable beyond Weight

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Possible scenarios | Gender  Significant? | Interaction  Significant? | Weight  Significant? | Formula |
| 1 | X | X | X | ~ genotype |
| 2 | X | ✓ | X | ~ genotype + gender + gender\*genotype\*1 |
| 3 | ✓ | X | X | ~ genotype + gender |
| 4 | ✓ | ✓ | X | ~ genotype + gender + gender\*genotype |
| 5 | X | X | ✓ | ~ genotype + weight |
| 6 | X | ✓ | ✓ | ~ genotype + gender +weight + gender\*genotype\*1 |
| 7 | ✓ | X | ✓ | ~ genotype + gender +weight |
| 8 | ✓ | ✓ | ✓ | ~ genotype + gender + weight+ gender\*genotype |

Function 4: final null model

#the model depends on the output of keepgender ,keepinteraction and keepweight questions where the output is yes or no

#Genotype and interaction are never included in the null model

# You never include the interaction term as inclusion would also lead to the inclusion of genotype, however if it is significant then gender is automatically in the genotype model and to make the models as comparable as possible ie the only difference is genotype we need to include in the null model.

# When weight is a dependent variable, you cannot have weight in the formula as an fixed effect so the keepweight question is irrelevant.

|  |  |  |  |
| --- | --- | --- | --- |
| Possible scenarios | Gender  Significant? | Interaction  Significant?  As null never include | Formula |
| 1 | X | X | ~ 1 |
| 2 | ✓ | X | ~ gender |
| 3 | X | ✓ | ~ gender |
| 4 | ✓ | ✓ | ~ gender |

# For any other dependent variable beyond Weight

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Possible scenarios | Gender  Significant? | Interaction  Significant? | Weight  Significant? | Formula |
| 1 | X | X | X | ~ 1 |
| 2 | X | X | ✓ | ~ weight |
| 3 | ✓ | X | X | ~ gender |
| 4 | ✓ | X | ✓ | ~ gender +weight |
| 5 | X | Y | X | ~ gender |
| 6 | X | Y | ✓ | ~ gender +weight |
| 7 | ✓ | Y | X | ~ gender |
| 8 | ✓ | Y | ✓ | ~ gender +weight |

Building the model structure – part of Function 3, 6 & 7

F3 (model for Fixed test), F6 (testing genotype effect) and F7 (final model) uses the results of F1 (testing batch) and F2 (testing variance) to build the general model structure. The output of F1 and F2 are either yes or no.

#note 1 formula is an input object which is generated within the function

#note 2: method = REML for F3 and F7 but ML for F6

|  |  |  |
| --- | --- | --- |
| Keep batch (yes/no) | Keep equal variance (yes/no) | General formula |
| X | X | model=do.call("lme", args = list(formula, random=~1|Assay.Date, dataset, na.action="na.omit", method="REML")) |
| X | ✓ | model= do.call("lme", args = list(formula, random=~1|Assay.Date, dataset, weights=varIdent(form=~1|Genotype), na.action="na.omit", method="REML") |
| ✓ | X | model=do.call("gls", args = list(formula, dataset, weights=varIdent(form=~1|Genotype), na.action="na.omit") |
| ✓ | ✓ | model =do.call("gls", args = list(formula, dataset, na.action="na.omit") |

F8 – table length concept

# Table will include intercept, 1 or 2 rows for genotype depending on number of genotypes being compared, and the fixed effects (i.e. gender, genotype, weight)

# Relates to the differences in formula and hence information assembled in F4

# Consider weight:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| scenarios | Gender | Interaction  ? | Formula | Table length  #2 genotypes | Table length  #3 genotypes |
| 1 | X | X | ~ genotype | 2 | 3 |
| 2 | X | ✓ | ~ genotype + gender + gender\*genotype | 4 | 5 |
| 3 | ✓ | X | ~ genotype + gender | 3 | 4 |
| 4 | ✓ | ✓ | ~ genotype + gender + gender\*genotype | 4 | 5 |

#consider any other dependent variable:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Possible scenarios | Gender  Significant? | Interaction  Significant? | Weight  Significant? | Formula | Table length  #2 genotypes | Table length  #3 genotypes |
| 1 | X | X | X | ~ genotype | 2 | 3 |
| 2 | X | ✓ | X | ~ genotype + gender + gender\*genotype | 4 | 5 |
| 3 | ✓ | X | X | ~ genotype + gender | 3 | 4 |
| 4 | ✓ | ✓ | X | ~ genotype + gender + gender\*genotype | 4 | 5 |
| 5 | X | X | ✓ | ~ genotype + weight | 3 | 4 |
| 6 | X | ✓ | ✓ | ~ genotype + gender +weight + gender\*genotype | 5 | 6 |
| 7 | ✓ | X | ✓ | ~ genotype + gender +weight | 4 | 5 |
| 8 | ✓ | ✓ | ✓ | ~ genotype + gender + weight+ gender\*genotype | 5 | 6 |

#the output is based on having 2 genotype and in F9 we assess how many genotypes and if three add one to the output to adjust for the additional row.