|  |  |  |  |
| --- | --- | --- | --- |
| Model | Df | t value | P value |
| LEAN mass Depletion Between Strains |  |  |  |
| * Strain | 10.737 | 2.450 | 0.0328\* |
| * Diapause Day 15 | 16.52 | 0.178 | 0.8610 |
| * Diapause Day 20 | 15.193 | -0.556 | 0.5864 |
| * Diapause Day 30 | 16.004 | -0.683 | 0.5044 |
| Final model:  lme4::lmer(formula = lean\_mass ~ strain + sample\_day + (1 | rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list( strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |
| Model | Df | t value | P value |
| LIPID mass depletion between strains |  |  |  |
| * Strain | 16.655 | 4.735 | 0.000202\* |
| * Diapause Day 15 | 14.117 | -2.377 | 0.03095\* |
| * Diapause Day 20 | 15.759 | -1.085 | 0.294324 |
| * Diapause Day 30 | 15.155 | -1.526 | 0.147622 |
| Final model:  lme4::lmer(formula = lipid\_mass ~ strain + sample\_day + (1 |  rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list(  strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |

Lean UZ x BE W,W15,W20,30

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lean\_mass ~ sample\_day + strain + (1 | rep/cohort)

Data: dataLeDl

REML criterion at convergence: -1066.6

Scaled residuals:

Min 1Q Median 3Q Max

-1.4145 -0.2978 -0.0879 0.1923 8.7759

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 3.970e-06 0.001992

rep (Intercept) 5.264e-05 0.007255

Residual 1.094e-04 0.010461

Number of obs: 182, groups: cohort:rep, 35; rep, 20

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0274068 0.0027013 21.5050000 10.146 1.18e-09 \*\*\*

sample\_dayW15 0.0008192 0.0046063 16.5200000 0.178 0.8610

sample\_dayW20 -0.0034785 0.0062587 15.1930000 -0.556 0.5864

sample\_dayW30 -0.0043285 0.0063386 16.0040000 -0.683 0.5044

strainUZ 0.0046671 0.0019053 10.7370000 2.450 0.0328 \*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) sm\_W15 sm\_W20 sm\_W30

sampl\_dyW15 -0.549

sampl\_dyW20 -0.359 0.224

sampl\_dyW30 -0.356 0.221 0.178

strainUZ -0.303 0.054 -0.107 -0.102

Lipid UZ X BE W,W15,W20,30

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lipid\_mass ~ strain + sample\_day + (1 | rep/cohort)

Data: dataWeDl

REML criterion at convergence: -1915.5

Scaled residuals:

Min 1Q Median 3Q Max

-4.2305 -0.4876 -0.0109 0.4502 2.6547

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 4.249e-07 0.0006519

rep (Intercept) 4.811e-07 0.0006936

Residual 6.975e-06 0.0026411

Number of obs: 221, groups: cohort:rep, 43; rep, 24

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0102745 0.0004052 30.1780000 25.355 < 2e-16 \*\*\*

strainUZ 0.0020915 0.0004418 16.6550000 4.735 0.000202 \*\*\*

sample\_dayW15 -0.0014694 0.0006180 14.1170000 -2.377 0.032095 \*

sample\_dayW20 -0.0008887 0.0008193 15.7590000 -1.085 0.294324

sample\_dayW30 -0.0014078 0.0009226 15.1550000 -1.526 0.147622

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) strnUZ sm\_W15 sm\_W20

strainUZ -0.497

sampl\_dyW15 -0.552 0.117

sampl\_dyW20 -0.330 -0.084 0.234

sampl\_dyW30 -0.258 -0.146 0.200 0.176

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Df | t value | P value |
| UZ LEAN mass depletion during diapause |  |  |  |
| * Diapause Day 15 | 11.713 | 0.182 | 0.859 |
| * Diapause Day 20 | 9.811 | -0.271 | 0.792 |
| * Diapause Day 30 | 10.378 | -0.346 | 0.736 |
| Model | Df | t value | P value |
| BE LEAN mass depletion during diapause |  |  |  |
| * Diapause Day 15 | 14.133 | -0.267 | 0.793 |
| * Diapause Day 20 | 13.621 | -1.095 | 0.292 |
| * Diapause Day 30 | 24.952 | -0.997 | 0.328 |
| Final model:  lme4::lmer(formula = lean\_mass ~ strain + sample\_day + (1 | rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list( strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |

BE Lean W,W15,W20,W30

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lean\_mass ~ sample\_day + (1 | rep/cohort)

Data: dataLeBEE

REML criterion at convergence: -501.3

Scaled residuals:

Min 1Q Median 3Q Max

-2.0067 -0.2256 -0.0440 0.1637 7.6001

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 2.073e-08 0.000144

rep (Intercept) 7.323e-05 0.008558

Residual 1.231e-04 0.011096

Number of obs: 90, groups: cohort:rep, 19; rep, 19

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.028820 0.003151 17.033000 9.145 5.55e-08 \*\*\*

sample\_dayW15 -0.001455 0.005438 14.133000 -0.267 0.793

sample\_dayW20 -0.011154 0.010184 13.621000 -1.095 0.292

sample\_dayW30 -0.008770 0.008794 24.952000 -0.997 0.328

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) sm\_W15 sm\_W20

sampl\_dyW15 -0.580

sampl\_dyW20 -0.309 0.179

sampl\_dyW30 -0.358 0.208 0.111

convergence code: 0

Model is nearly unidentifiable: large eigenvalue ratio

- Rescale variables?

UZ Lean W,W15,W20,W30

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lean\_mass ~ sample\_day + (1 | rep/cohort)

Data: dataLeUZZ

REML criterion at convergence: -538.5

Scaled residuals:

Min 1Q Median 3Q Max

-1.3208 -0.4016 -0.0889 0.2585 7.5940

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 1.455e-05 0.003814

rep (Intercept) 3.349e-05 0.005787

Residual 9.472e-05 0.009733

Number of obs: 92, groups: cohort:rep, 16; rep, 16

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0309841 0.0028545 14.3750000 10.855 2.58e-08 \*\*\*

sample\_dayW15 0.0009876 0.0054292 11.7130000 0.182 0.859

sample\_dayW20 -0.0016443 0.0060780 9.8110000 -0.271 0.792

sample\_dayW30 -0.0021395 0.0061878 10.3780000 -0.346 0.736

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) sm\_W15 sm\_W20

sampl\_dyW15 -0.526

sampl\_dyW20 -0.470 0.247

sampl\_dyW30 -0.461 0.243 0.217

convergence code: 0

Model is nearly unidentifiable: large eigenvalue ratio

- Rescale variables?

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Df | t value | P value |
| BE LIPID mass depletion during diapause |  |  |  |
| * Diapause Day 15 | 111.4 | -3.877 | 0.000179\* |
| * Diapause Day 20 | 111.4 | 0.752 | 0.453665 |
| * Diapause Day 30 | 111.4 | -1.012 | 0.313505 |
| Model | Df | t value | P value |
| UZ LIPID mass depletion during diapause |  |  |  |
| * Diapause Day 15 | 11.87 | -0.376 | 0.714 |
| * Diapause Day 20 | 9.366 | -0.902 | 0.389 |
| * Diapause Day 30 | 9.851 | -0.740 | 0.476 |
| Final model:  lme4::lmer(formula = lipid\_mass ~ strain + sample\_day + (1 |  rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list(  strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |

Lipid BE Lipid W,W15,W20,30

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lipid\_mass ~ sample\_day + (1 | rep/cohort)

Data: dataLiDBE

REML criterion at convergence: -1003.5

Scaled residuals:

Min 1Q Median 3Q Max

-4.1521 -0.3776 0.0857 0.4855 2.4844

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 0.000e+00 0.000000

rep (Intercept) 0.000e+00 0.000000

Residual 6.257e-06 0.002501

Number of obs: 115, groups: cohort:rep, 24; rep, 23

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 1.039e-02 3.343e-04 1.114e+02 31.071 < 2e-16 \*\*\*

sample\_dayW15 -1.941e-03 5.008e-04 1.114e+02 -3.877 0.000179 \*\*\*

sample\_dayW20 -6.457e-04 8.587e-04 1.114e+02 -0.752 0.453665

sample\_dayW30 -1.311e-03 1.295e-03 1.114e+02 -1.012 0.313505

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) sm\_W15 sm\_W20

sampl\_dyW15 -0.667

sampl\_dyW20 -0.389 0.260

sampl\_dyW30 -0.258 0.172 0.101

Lipid UZ Lipid W,W15,W20,30

Linear mixed model fit by REML

t-tests use Satterthwaite approximations to degrees of freedom ['lmerMod']

Formula: lipid\_mass ~ sample\_day + (1 | rep/cohort)

Data: dataWeUZ

REML criterion at convergence: -886.3

Scaled residuals:

Min 1Q Median 3Q Max

-3.5484 -0.4790 -0.0665 0.4551 2.3316

Random effects:

Groups Name Variance Std.Dev.

cohort:rep (Intercept) 1.384e-06 0.0011765

rep (Intercept) 8.895e-07 0.0009432

Residual 7.653e-06 0.0027664

Number of obs: 106, groups: cohort:rep, 19; rep, 19

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.0121776 0.0005973 16.6340000 20.388 3.36e-13 \*\*\*

sample\_dayW15 -0.0004636 0.0012338 11.8700000 -0.376 0.714

sample\_dayW20 -0.0012370 0.0013708 9.3660000 -0.902 0.389

sample\_dayW30 -0.0010377 0.0014015 9.8510000 -0.740 0.476

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) sm\_W15 sm\_W20

sampl\_dyW15 -0.484

sampl\_dyW20 -0.436 0.211

sampl\_dyW30 -0.426 0.206 0.186

convergence code: 0

unable to evaluate scaled gradient

Model failed to converge: degenerate Hessian with 1 negative eigenvalues