

Applied Statistical Methods - Solution 9

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Problem 1: Milk Dataset

Use the dataset `milk` from package `pedigreemm` and fit a sire model to each of the response variables (`milk`, `fat`, `prot` and `scs`) in the data. The dataset can be loaded using the command `pedigreemm::milk`. The other variables like `lact` and `herd` can be used as fixed effects. The `sire` column is used as a random effect. For this analysis, we assume that sires are unrelated.

Your Tasks

- Analyse the `milk` dataset from package `pedigreemm` using the function `lme4::lmer()` for all given response variables. You can use the same model for each of the responses.
- Compute the estimated heritability for each response variable, using the fact that the heritability h^2 can be computed from the variance σ_s^2 of the sire effects and the phenotypic variance σ_p^2 with the formula

$$h^2 = \frac{4 * \sigma_s^2}{\sigma_p^2}$$

- Compute the summary statistic using the function `summary()` of all the predicted sire breeding values. Solutions for the sire breeding values are obtained using the function `ranef()`

Solution

- Assign `milk` dataset to a tibble

```
tbl_milk <- tibble::as_tibble(pedigreemm::milk)
```

- Analyse the data for each of the responses. The responses are pre-defined and must appear as column names

```
vec_resp_milk <- c("milk", "fat", "prot", "scs")
# check
if (!all(is.element(vec_resp_milk, colnames(tbl_milk)))){
  stop(" *** ERROR: Response not in dataset: ",
       vec_resp_milk[!is.element(vec_resp_milk, colnames(tbl_milk))])
}
```

For each of the responses run an analysis

```
vec_fix_fact_milk <- c("lact", "herd")
vec_fix_cov_milk <- c("dim")
s_rand_eff_milk <- "sire"
s_rhs <- paste0(c(paste0(vec_fix_fact_milk, collapse = " + "),
                 paste0(vec_fix_cov_milk, collapse = " + "),
                 paste0("1|", s_rand_eff_milk, "|", collapse = "")),
              collapse = " + ")
```

Convert fixed effects to factors

```
# convert fixed effects to factors
for (f in vec_fix_fact_milk){
  tbl_milk[[f]] <- as.factor(tbl_milk[[f]])
}
```

Construct a function that runs an analysis for a given response

```
run_lmer_single_response <- function(ps_resp, ps_rhs, ptbl_data){
  # check
  # formula
  s_formula <- paste(ps_resp, ps_rhs, sep = " ~ ")
  frma_lmem <- as.formula(s_formula)
  return(lme4::lmer(frma_lmem, data = ptbl_data))
}
```

Let the analysis be done for all responses

```
l_lmer_results <- lapply(vec_resp_milk,
  run_lmer_single_response,
  ps_rhs = s_rhs,
  ptbl_data = tbl_milk)
```

Print all the summaries as results

```
for (l in l_lmer_results){
  print(summary(l))
}
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: milk ~ lact + herd + dim + (1 | sire)
## Data: ptbl_data
##
## REML criterion at convergence: 64682.3
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.3515 -0.5939  0.0471  0.6391  3.0229
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   sire     (Intercept)         436399  660.6
##   Residual                    14323717 3784.7
## Number of obs: 3397, groups:  sire, 38
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 22179.3013   572.6886  38.728
## lact2       -567.0717   160.5548  -3.532
## lact3      -1027.2394   186.3072  -5.514
## lact4       -938.8171   239.1321  -3.926
## lact5      -1149.8552   395.5424  -2.907
## herd2       -405.1815   546.4401  -0.741
## herd4       1795.5114   873.3207   2.056
## herd5       3545.1581   753.3613   4.706
## herd6       -557.2013   706.5353  -0.789
```

## herd7	2050.2860	907.0908	2.260
## herd8	-349.0441	681.3300	-0.512
## herd13	2574.4707	735.7602	3.499
## herd14	556.1105	524.9750	1.059
## herd17	4020.2199	782.3927	5.138
## herd18	-1653.5144	703.7817	-2.349
## herd22	-765.3971	731.4518	-1.046
## herd23	-319.5227	605.6600	-0.528
## herd26	3815.7866	1389.9893	2.745
## herd27	-1467.1500	1282.3213	-1.144
## herd29	99.4121	776.3642	0.128
## herd30	4786.8342	831.7947	5.755
## herd34	299.2986	670.9064	0.446
## herd36	-992.0130	795.9012	-1.246
## herd37	3052.8175	707.6809	4.314
## herd38	2486.6492	638.8885	3.892
## herd41	1845.6266	721.4234	2.558
## herd45	595.2089	635.5650	0.937
## herd46	1957.0566	728.7574	2.685
## herd48	5747.5087	746.2061	7.702
## herd49	-533.7808	1034.2567	-0.516
## herd52	3836.7977	657.4239	5.836
## herd53	1155.4060	861.6142	1.341
## herd54	306.0101	803.6259	0.381
## herd55	-3168.1618	854.3604	-3.708
## herd59	1500.7075	605.7404	2.477
## herd60	-93.1071	620.9171	-0.150
## herd62	2867.7655	889.6308	3.224
## herd64	4488.2422	666.6853	6.732
## herd66	1568.2347	745.6632	2.103
## herd68	-318.6871	629.6671	-0.506
## herd69	-720.5528	610.7063	-1.180
## herd70	-2762.9034	673.9141	-4.100
## herd75	2527.1950	638.5451	3.958
## herd77	-1456.3385	1088.3172	-1.338
## herd89	-4164.5413	906.5904	-4.594
## herd90	835.3527	704.7541	1.185
## herd95	1898.5536	2749.3678	0.691
## herd96	2840.0896	2751.8931	1.032
## herd97	6006.9118	3836.3784	1.566
## herd98	-1589.8130	1550.0904	-1.026
## herd99	-2145.5194	2756.7237	-0.778
## herd100	1125.4711	2754.7748	0.409
## herd101	476.9742	2751.7144	0.173
## herd103	-6296.3744	2751.0073	-2.289
## herd104	-3698.2979	2273.0843	-1.627
## herd105	-3281.2862	3839.2518	-0.855
## herd106	593.8344	2785.4041	0.213
## herd107	-4731.4899	3840.2745	-1.232
## herd108	3288.2457	3841.1488	0.856
## herd109	-1315.0161	1027.7215	-1.280
## herd110	3993.4835	2749.6515	1.452
## dim	9.1286	0.6194	14.737

```

##
## Correlation matrix not shown by default, as p = 62 > 12.
## Use print(summary(l), correlation=TRUE) or
##     vcov(summary(l))         if you need it
## Linear mixed model fit by REML ['lmerMod']
## Formula: fat ~ lact + herd + dim + (1 | sire)
##   Data: ptbl_data
##
## REML criterion at convergence: 42711.5
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.4455 -0.6047 -0.0047  0.6297  5.0727
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   sire     (Intercept)  675.7    25.99
##   Residual                    19705.0  140.37
## Number of obs: 3397, groups: sire, 38
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  913.64827   21.34689  42.800
## lact2        -3.12756    5.95520  -0.525
## lact3       -17.84204    6.91054  -2.582
## lact4       -18.58159    8.87041  -2.095
## lact5       -45.92505   14.67266  -3.130
## herd2       -123.27145   20.29486  -6.074
## herd4         67.40094   33.03755   2.040
## herd5         19.32710   28.09209   0.688
## herd6        -93.34786   26.27480  -3.553
## herd7        -92.45223   33.70998  -2.743
## herd8       -107.52354   25.35701  -4.240
## herd13        -0.98249   27.37090  -0.036
## herd14        25.97963   19.48136   1.334
## herd17       -29.33251   29.10324  -1.008
## herd18       -173.18362   26.17006  -6.618
## herd22       -155.14524   27.20152  -5.704
## herd23       -100.03718   22.54883  -4.436
## herd26        -44.84622   51.63849  -0.868
## herd27       -143.50703   47.65044  -3.012
## herd29        -28.14249   28.89087  -0.974
## herd30         19.73302   31.17323   0.633
## herd34        -53.04222   24.97092  -2.124
## herd36        -69.43396   29.60786  -2.345
## herd37        -38.01074   26.33616  -1.443
## herd38        -26.91082   23.74423  -1.133
## herd41        -11.92557   26.88505  -0.444
## herd45        -44.91041   23.66587  -1.898
## herd46         -6.06832   27.10444  -0.224
## herd48         68.73228   27.74948   2.477
## herd49        -54.19039   38.39780  -1.411
## herd52         83.47301   24.45448   3.413

```

```

## herd53      -34.28559   32.09108  -1.068
## herd54      -56.27583   29.88240  -1.883
## herd55     -197.87715   31.77086  -6.228
## herd59      -21.23528   22.56866  -0.941
## herd60     -105.62412   23.08122  -4.576
## herd62      -34.51391   33.05735  -1.044
## herd64       36.61065   24.83194   1.474
## herd66     -90.63616   27.73316  -3.268
## herd68     -53.87295   23.42433  -2.300
## herd69    -128.47790   22.72433  -5.654
## herd70    -245.93829   25.11742  -9.792
## herd75     -76.06256   23.75975  -3.201
## herd77    -140.65586   40.41529  -3.480
## herd89    -219.06039   34.79154  -6.296
## herd90    -122.09286   26.20182  -4.660
## herd95     160.31707  102.01316   1.572
## herd96     121.54513  102.10996   1.190
## herd97     228.93906  142.31594   1.609
## herd98     -87.30903   57.56693  -1.517
## herd99    -108.06358  102.30015  -1.056
## herd100     94.16122  102.23388   0.921
## herd101    -45.31427  102.10462  -0.444
## herd103   -351.44585  102.08486  -3.443
## herd104   -132.35824   84.36061  -1.569
## herd105   -194.04205  142.43226  -1.362
## herd106   -110.85591  103.52642  -1.071
## herd107   -95.48285  142.47691  -0.670
## herd108  -111.05764  142.50439  -0.779
## herd109  -106.74405   38.17333  -2.796
## herd110    97.05187  102.02807   0.951
## dim         0.27360    0.02298  11.907

##
## Correlation matrix not shown by default, as p = 62 > 12.
## Use print(summary(l), correlation=TRUE) or
##   vcov(summary(l))           if you need it

## Linear mixed model fit by REML ['lmerMod']
## Formula: prot ~ lact + herd + dim + (1 | sire)
##   Data: ptbl_data
##
## REML criterion at convergence: 40474.4
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -4.6737 -0.6009  0.0550  0.6335  3.0182
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   sire     (Intercept)  239.4   15.47
##   Residual                10101.1  100.50
## Number of obs: 3397, groups: sire, 38
##
## Fixed effects:
##               Estimate Std. Error t value

```

## (Intercept)	687.84915	15.05458	45.690
## lact2	-5.22348	4.26338	-1.225
## lact3	-13.56882	4.94697	-2.743
## lact4	-14.32312	6.34887	-2.256
## lact5	-21.14774	10.50091	-2.014
## herd2	-15.49471	14.46642	-1.071
## herd4	80.44214	22.26248	3.613
## herd5	101.42674	19.77209	5.130
## herd6	-49.97128	18.65285	-2.679
## herd7	53.85117	23.98051	2.246
## herd8	-24.85331	17.95591	-1.384
## herd13	66.03249	19.41086	3.402
## herd14	9.70295	13.92509	0.697
## herd17	109.89813	20.64402	5.323
## herd18	-74.94346	18.58298	-4.033
## herd22	-43.73434	19.31041	-2.265
## herd23	-11.58183	15.94946	-0.726
## herd26	20.61570	36.78421	0.560
## herd27	-48.33932	33.91609	-1.425
## herd29	-32.98307	20.46449	-1.612
## herd30	129.62836	21.60393	6.000
## herd34	1.63952	17.67893	0.093
## herd36	-19.36150	20.99663	-0.922
## herd37	74.19203	18.65291	3.978
## herd38	55.01220	16.88826	3.257
## herd41	20.74571	18.95723	1.094
## herd45	-10.91260	16.73092	-0.652
## herd46	48.82779	19.23558	2.538
## herd48	146.24036	19.70026	7.423
## herd49	-4.67361	27.40547	-0.171
## herd52	92.37518	17.34591	5.325
## herd53	25.79652	22.66968	1.138
## herd54	-18.60610	21.21973	-0.877
## herd55	-109.31983	22.55610	-4.847
## herd59	-3.59154	15.92558	-0.226
## herd60	-13.91199	16.40581	-0.848
## herd62	67.84174	23.52892	2.883
## herd64	112.02522	17.53687	6.388
## herd66	30.25665	19.68037	1.537
## herd68	-10.80834	16.61041	-0.651
## herd69	-7.17148	16.10200	-0.445
## herd70	-81.03427	17.70222	-4.578
## herd75	51.84225	16.83448	3.080
## herd77	-62.40786	28.82230	-2.165
## herd89	-136.54329	22.51005	-6.066
## herd90	9.09527	18.61498	0.489
## herd95	57.54430	72.94915	0.789
## herd96	18.32784	73.01133	0.251
## herd97	155.07864	101.83915	1.523
## herd98	-40.59226	41.04723	-0.989
## herd99	-79.08308	73.12301	-1.082
## herd100	-0.36401	73.06205	-0.005
## herd101	7.31608	73.00460	0.100
## herd103	-192.35676	72.97616	-2.636

```

## herd104      -144.28294   60.28039  -2.394
## herd105      -102.10287  101.90064  -1.002
## herd106         5.44255   73.66756   0.074
## herd107     -132.35566  101.91766  -1.299
## herd108       115.50101  101.94846   1.133
## herd109       -48.20625   27.20305  -1.772
## herd110       -57.81409   72.94988  -0.793
## dim           0.24386    0.01644  14.831

##
## Correlation matrix not shown by default, as p = 62 > 12.
## Use print(summary(l), correlation=TRUE) or
##   vcov(summary(l))           if you need it

## Linear mixed model fit by REML ['lmerMod']
## Formula: scs ~ lact + herd + dim + (1 | sire)
##   Data: ptbl_data
##
## REML criterion at convergence: 11023.1
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.0849 -0.7031 -0.1689  0.5332  5.1888
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   sire     (Intercept)  0.02892  0.1701
##   Residual                    1.47787  1.2157
## Number of obs: 3397, groups: sire, 38
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  2.9028929  0.1807507  16.060
## lact2        -0.0068241  0.0515663  -0.132
## lact3         0.1015210  0.0598323   1.697
## lact4        -0.0161535  0.0767806  -0.210
## lact5         0.1372396  0.1269878   1.081
## herd2         0.2219766  0.1745385   1.272
## herd4        -0.5058221  0.2613789  -1.935
## herd5        -0.4795203  0.2369695  -2.024
## herd6        -0.4903804  0.2245745  -2.184
## herd7        -0.0414502  0.2889896  -0.143
## herd8        -0.2019707  0.2158770  -0.936
## herd13       -0.6138834  0.2335827  -2.628
## herd14        0.0024948  0.1682780   0.015
## herd17       -0.1710233  0.2484421  -0.688
## herd18        0.3150843  0.2237503   1.408
## herd22        0.2507096  0.2324894   1.078
## herd23       -0.1154279  0.1916420  -0.602
## herd26       -0.7957806  0.4437595  -1.793
## herd27       -0.2174592  0.4089785  -0.532
## herd29       -0.1476948  0.2460665  -0.600
## herd30        1.3440147  0.2569701   5.230
## herd34        0.5248772  0.2125322   2.470
## herd36        0.4901778  0.2526440   1.940

```

```

## herd37      0.6412569  0.2242814  2.859
## herd38     -0.5857264  0.2035064 -2.878
## herd41     -0.0321614  0.2274032 -0.141
## herd45      0.1408516  0.2009714  0.701
## herd46     -0.4831023  0.2315651 -2.086
## herd48     -0.4692556  0.2371760 -1.979
## herd49      0.4456772  0.3309014  1.347
## herd52      0.5490433  0.2087311  2.630
## herd53      0.0028894  0.2721992  0.011
## herd54     -0.6486718  0.2555015 -2.539
## herd55      1.1224558  0.2715587  4.133
## herd59     -0.0913609  0.1911135 -0.478
## herd60     -0.3185984  0.1976264 -1.612
## herd62      0.2421185  0.2836912  0.853
## herd64      0.0290572  0.2105039  0.138
## herd66      0.1926726  0.2368906  0.813
## herd68      0.0980277  0.1998564  0.490
## herd69      0.1578356  0.1936641  0.815
## herd70      0.9185132  0.2122622  4.327
## herd75      0.4677678  0.2024318  2.311
## herd77      0.6308696  0.3478703  1.814
## herd89     -0.0945232  0.2599028 -0.364
## herd90      0.6427054  0.2241886  2.867
## herd95      0.6639766  0.8817645  0.753
## herd96      0.2651099  0.8824714  0.300
## herd97      1.4345314  1.2314394  1.165
## herd98     -0.7483216  0.4953909 -1.511
## herd99      1.0221822  0.8836747  1.157
## herd100    -1.3204170  0.8828543 -1.496
## herd101     0.4115713  0.8823720  0.466
## herd103    -0.0370665  0.8819429 -0.042
## herd104     0.6027929  0.7283269  0.828
## herd105     1.8565615  1.2320502  1.507
## herd106    -0.4571387  0.8885900 -0.514
## herd107     1.6780828  1.2321659  1.362
## herd108     0.0589352  1.2326072  0.048
## herd109     0.6751412  0.3281733  2.057
## herd110    -0.7010447  0.8817106 -0.795
## dim        -0.0005187  0.0001988 -2.609

##
## Correlation matrix not shown by default, as p = 62 > 12.
## Use print(summary(l), correlation=TRUE) or
##     vcov(summary(l))           if you need it

```

- Compute estimated heritability. For the sire model, the heritability h^2 is defined as

$$h^2 = \frac{4 * \sigma_s^2}{\sigma_s^2 + \sigma_e^2}$$

The estimates for the sire variance σ_s^2 and σ_e^2 can be extracted from the summary of the lmer result.

```

for (l in l_lmer_results){
  smry_l <- summary(l)
  # getting sire std. dev
  n_sire_var <- attr(smry_l$varcor[[1]], "stddev")[[1]]
}

```



```

n_res_var <- smry_l$sigma
n_h2 <- 4*n_sire_var / (n_sire_var+n_res_var)
s_trait <- unlist(strsplit(as.character(smry_l$call)[2], split = " ~ ", fixed = TRUE))[1]
cat("Heritability for trait: ", s_trait, ": ", n_h2, "\n")
}

```

```

## Heritability for trait: milk : 0.5944334
## Heritability for trait: fat : 0.624975
## Heritability for trait: prot : 0.533636
## Heritability for trait: scs : 0.4908639

```

- Obtain summary statistics for predicted sire breeding values. The breeding values can be obtained by the function `ranef()`

```

for (l in l_lmer_results){
  smry_l <- summary(l)
  s_trait <- unlist(strsplit(as.character(smry_l$call)[2], split = " ~ ", fixed = TRUE))[1]
  cat("Summary statistics of breeding values for trait: ", s_trait, "\n")
  print(summary(lme4::ranef(l)$sire[[1]]))
}

```

```

## Summary statistics of breeding values for trait: milk
##   Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
## -1168.09 -304.68  25.59    0.00  275.90 1218.04
## Summary statistics of breeding values for trait: fat
##   Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
## -37.375 -13.799 -3.095  0.000  14.730  51.130
## Summary statistics of breeding values for trait: prot
##   Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
## -24.7325 -4.2736  0.8155  0.0000  6.1330  28.8272
## Summary statistics of breeding values for trait: scs
##   Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
## -0.324984 -0.078694 -0.006315  0.000000  0.081455  0.241742

```