Stat 8931 (Aster Models)
Lecture Slides Deck 3
Using Model Matrices instead of Formulas

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R and License

- The version of R used to make these slides is 3.5.1.
- The version of R package `aster` used to make these slides is 1.0.2.

Example Two

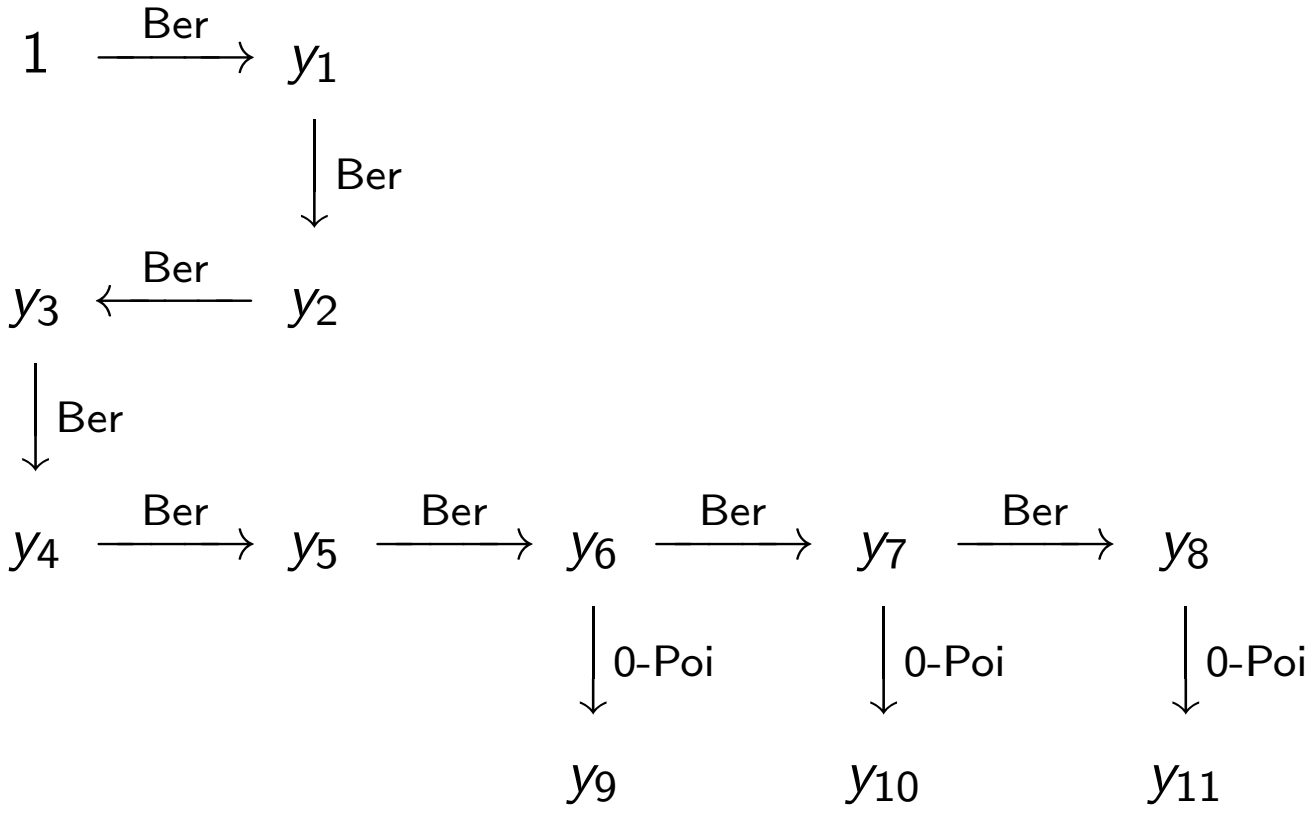
Our second example comes from the second aster paper (Shaw, Geyer, Wagenius, Hangelbroek and Etterson, *American Naturalist*, 2008).

There are three examples in the paper. This is the one involving *Echinacea angustifolia*.

In that paper and the accompanying tech report this example was held up as one where the model was too complicated to use the R formula mini-language and model matrices for different submodels had to be constructed "by hand" (using R but without any helpful R functions).

This example also illustrates some very important points about aster models and hypothesis tests.

Example Two (cont.)



Sorry the graph is snakelike. Otherwise, it would be really small.

Example Two (cont.)

All of the conditionally Bernoulli variables are survival indicators, but they are not all the same. This comes from an experiment in which the individual plants are crosses with parents from different ancestral populations.

The first three survival indicators (y_1 though y_3) are for survival in the growth chamber. Individuals that survived these first three time periods were transplanted into the experimental field. The next five survival indicators (y_5 though y_8) are for annual survival in the field (2001 through 2005). The conditionally zero-truncated Poisson components of the response vector (y_9 though y_{11}) are for rosette (basal leaf cluster) counts. These plants had not lived long enough when these data were analyzed for the 2008 paper to have flowers yet.

Example Two (cont.)

It is not completely clear (to me) why zero-truncated Poisson.

Perhaps the issue is that a plant with rosette count $= 0$ has no leaves and is not long for this world if not dead already.

If it were possible to observe rosette count $= 0$ on surviving plants, then the conditional distribution should have been Poisson rather than zero-truncated Poisson.

We will stick with zero-truncated Poisson, following the paper.

Example Two (cont.)

We take the rosette count for 2005 (the last year in the data) for an individual to be the best surrogate of observed fitness in these data (hereafter just called "fitness").

This is often done — use some measure of size as best surrogate of fitness — when actual fecundity traits are not available. This is justified by size being (in many species) positively correlated with fitness.

Example Two (cont.)

The data for this example are in the dataset `echin2` in the `aster` package.

```
> library(aster)
> data(echin2)
> sapply(echin2, class)
```

```
crosstype yearcross      flat       row      posi
 "factor"  "factor"  "factor"  "factor" "numeric"
     varb      resp        id      root
 "factor" "integer" "integer" "numeric"
```

Since we already have `varb`, `resp`, and `id` as variables, it is clear (as the help page for this dataset says) that this is a "long format" data frame that does not need to be reshaped with the `reshape` function.

Example Two (cont.)

All datasets in the `aster` package except the very first one (the dataset `echinacea` used for example one in decks 1 and 2) are like this: "long format" so that they do not need to be reshaped with the `reshape` function.

The idea is we left one example of how to go from what we guess is a more likely format for users to use (one row of the data for each individual) to the format the `aster` and `reaster` functions need (go from "wide" to "long") with the `reshape` function.

After that one example, we don't need more.

Example Two (cont.)

Set up the graphical model.

```
> levels(echin2$varb)

 [1] "ld01"     "ld02"     "ld03"     "ld04"
 [5] "ld05"     "lds1"     "lds2"     "lds3"
 [9] "roct2003" "roct2004" "roct2005"

> vars <- unique(as.character(echin2$varb))
> vars

 [1] "lds1"     "lds2"     "lds3"     "ld01"
 [5] "ld02"     "ld03"     "roct2003" "ld04"
 [9] "roct2004" "ld05"     "roct2005"

> pred <- c(0, 1, 2, 3, 4, 5, 6, 6, 8, 8, 10)
> fam <- c(1, 1, 1, 1, 1, 1, 3, 1, 3, 1, 3)
```

Example Two (cont.)

```
> foo <- rbind(vars, c("initial", vars)[pred + 1])
> rownames(foo) <- c("successor", "predecessor")
> t(foo)

      successor  predecessor
 [1,] "lds1"     "initial"
 [2,] "lds2"     "lds1"
 [3,] "lds3"     "lds2"
 [4,] "ld01"     "lds3"
 [5,] "ld02"     "ld01"
 [6,] "ld03"     "ld02"
 [7,] "roct2003" "ld03"
 [8,] "ld04"     "ld03"
 [9,] "roct2004" "ld04"
[10,] "ld05"     "ld04"
[11,] "roct2005" "ld05"
```

Example Two (cont.)

```
> cbind(vars, fam)

      vars        fam
 [1,] "lds1"      "1"
 [2,] "lds2"      "1"
 [3,] "lds3"      "1"
 [4,] "ld01"      "1"
 [5,] "ld02"      "1"
 [6,] "ld03"      "1"
 [7,] "roct2003"  "3"
 [8,] "ld04"      "1"
 [9,] "roct2004"  "3"
[10,] "ld05"      "1"
[11,] "roct2005"  "3"
```

Caution

I have to admit the first time I did this slide deck I fouled this up.

I decided another order of the node names in `vars` would look nicer.

Does not work. The R function `aster` is going to use the order in the data frame it is given (we do not feed it the `vars` object, it only has the `varb` variable in that data frame to work with).

`vars` must be defined as above, if we are using a pre-existing "long format" data frame.

Example Two (cont.)

So that takes care of the graphical model, and we know what the variables `varb`, `resp`, `id`, and `root` do.

How about covariates?

```
> sapply(echin2, class)
```

```
crosstype yearcross      flat       row      posi
 "factor"  "factor"  "factor"  "factor" "numeric"
     varb      resp        id      root
 "factor" "integer" "integer" "numeric"
```

Those are `crosstype`, `yearcross`, `flat`, `row`, and `posi`.

Example Two (cont.)

```
> levels(echin2$crosstype)

[1] "Br" "Wi" "Wr"
```

From the legend for Figure 2 in the paper

> The experimentally imposed crossing treatments are between remnant populations ("Br"), within remnant populations ("Wr"), and inbred within remnants ("Wi")

This is the treatment of scientific interest. Does amount of inbreeding affect fitness?

Example Two (cont.)

```
> levels(echin2$yearcross)
```

```
[1] "1999" "2000"
```

The year in which crosses were done.

```
> levels(echin2$flat)
```

```
[1] "1" "2" "3"
```

The planting tray the individual was in while in the growth chamber.

Example Two (cont.)

```
> levels(echin2$row)

[1] "0"  "10" "11" "12" "13"
```

The row of the experimental field in which the individual was planted if the individual survived that long. Individuals that did not survive to be transplanted have level `"0"` of this factor (the four actual rows are levels `"10"`, `"11"`, `"12"`, and `"13"`)

```
> range(echin2$posi)

[1] -0.350  0.365
```

Position along the row. This is meaningless for individuals with `row == "0"`.

Example Two (cont.)

The predictor variables `row` and `posi` giving the outdoor spatial location after transplantation cause all the difficulty in specifying models. These variables are meaningless for individuals that did not survive to be transplanted but R forces us to give them values.

Somehow our model formulas have to do the Right Thing (TRT) despite this complication.

```
> unique(echin2$posi[as.character(echin2$row) == "0"])
```

```
[1] 0
```

At least we know we can ignore this complication for `posi` (multiplying a beta by zero is the same as leaving that term out of a regression equation).

Example Two (cont.)

We need to set up some more "predictor variables" which are indicator variables for parts of the graph.

```
> indoors <- grepl("lds", as.character(echin2$varb))
> indoors <- as.numeric(indoors)
> outdoors <- 1 - indoors
> fit <- grepl("roct2005", as.character(echin2$varb))
> fit <- as.numeric(fit)
> echin2 <- data.frame(echin2, indoors = indoors,
+     outdoors = outdoors, fit = fit)
> names(echin2)

 [1] "crosstype" "yearcross" "flat"      "row"
 [5] "posi"      "varb"      "resp"      "id"
 [9] "root"      "indoors"   "outdoors"  "fit"
```

Example Two (cont.)

And we check that our understanding of `row == "0"` is correct.

```
> is.lds3 <- as.character(echin2$varb) == "lds3"
> is.dead <- is.lds3 & echin2$resp == 0
> is.norow <- as.character(echin2$row) == "0"
> with(echin2, identical(id[is.dead],
+     unique(id[is.norow])))
```

```
[1] TRUE
```

An individual has `row == "0"` if and only if that individual died in the growth chamber (`lds3 == 0`).

Example Two (cont.)

Our formula starts (as always) with `resp ~ varb`.

The next term is `fit : crosstype`. This is the most important term for scientific inference. What is the effect of inbreeding on fitness?

Example Two (cont.)

The next term is just `yearcross`. At least that is what was done in the paper.

But does it make sense that the year of crossing has the same effect (numerically) on different kinds of variables? Our slogan **no naked predictors** says this should be something like `layer : yearcross` with `layer` defined as follows

```
> layer <- gsub("[0-9]", "", as.character(echin2$varb))
> layer <- as.factor(layer)
> levels(layer)

[1] "ld"   "lds"  "roct"

> echin2 <- data.frame(echin2, layer = layer)
```

(the two kinds of survival variables are for different lengths of time, weeks or years, and so need to be distinguished).

Example Two (cont.)

As we shall see, `yearcross` isn't statistically significant anyway, so if we hadn't fussed about this it wouldn't have mattered for these data.

An alternative way to deal with `yearcross` would be to have it affect only the first survival node and no other (the term would be `lds01 : yearcross` with the definition of `lds01` left as an exercise for the reader).

Exactly how `yearcross` should go in is a scientific question not a statistical one.

Example Two (cont.)

The next term is `indoors : flat` because, presumably, what flat an individual was in is no longer relevant after it has been transplanted and is no longer in that flat.

The next term is `outdoors : (row + posi)` because, presumably, the location where an individual will be transplanted does not matter before the transplantation occurs.

It might be a problem that the interpreter for the R formula mini-language is going to make a dummy variable named `outdoors:row0` that will just be the zero vector (every individual who survives to be transplanted outdoors goes in a real row not in the fake row `"0"`). Since such a predictor variable can never be in a full rank matrix R will drop it (we hope, let's see).

Example Two (cont.)

```
> aout <- aster(resp ~ varb + layer : yearcross + indoors :
+     outdoors : (row + posi) + fit : crosstype,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout), silent = TRUE)

apparent null eigenvectors of information matrix
directions of recession or constancy of log likelihood
 [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
```

Example Two (cont.)

Well that's annoying. What is that? What is a direction of recession or constancy?

Too complicated to explain here (much more on this when we get to the subject).

Example Two (cont.)

```
> names(aout$coefficients)

 [1] "(Intercept)"
 [2] "varbld02"
 [3] "varbld03"
 [4] "varbld04"
 [5] "varbld05"
 [6] "varblds1"
 [7] "varblds2"
 [8] "varblds3"
 [9] "varbroct2003"
[10] "varbroct2004"
[11] "varbroct2005"
[12] "layerld:yearcross1999"
[13] "layerlds:yearcross1999"
[14] "layerroct:yearcross1999"
[15] "indoors:flat1"
[16] "indoors:flat2"
[17] "outdoors:row0"
[18] "outdoors:row10"
[19] "outdoors:row11"
[20] "outdoors:row12"
[21] "outdoors:posi"
[22] "fit:crosstypeBr"
[23] "fit:crosstypeWi"
```

Example Two (cont.)

So our reasoning about `outdoors:row0` was wrong (isn't it funny how I say "our" reasoning as if the mistake was not entirely mine).

The individuals that died in the growth chamber are outdoors as far as the `aster` function is concerned. They have values for all the nodes. It's just that those values are zero for node `"lds3"` and all later nodes and perhaps some earlier nodes.

So now are we stuck? Do we have to construct model matrices by hand?

Example Two (cont.)

Dealing with this example would be a lot easier if we could use different graphs for different individuals. Don't have "outdoors" nodes for individuals that weren't transplanted.

Actually, that would be possible. We would tell `aster` that there is just one individual but the graph has a lot of nodes.

Nothing in the `aster` function requires that the graph be connected. In our "big graph" every maximal connected component (all the nodes downstream from one initial node) would correspond to one real individual (which the `aster` function wouldn't know about or care). But it would be an enormous pain to specify a model this way. (The `aster2` packages makes this easier in some cases, but isn't ready for use yet.)

Example Two (cont.)

But there is an easier idea. We didn't define `outdoors` correctly. We should have excluded the "outdoors" nodes for individuals who were not transplanted.

```
> id.transplant <- with(echin2,
+     id[as.character(varb) == "lds3" & resp > 0])
> transplant <- with(echin2, id %in% id.transplant)
> transplant <- as.numeric(transplant)
> echin2 <- data.frame(echin2, transplant = transplant)
```

Now does it work?

Example Two (cont.)

```
> aout <- aster(resp ~ varb + layer : yearcross + indoors :
+     transplant : (row + posi) + fit : crosstype,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout), silent = TRUE)

apparent null eigenvectors of information matrix
directions of recession or constancy of log likelihood
             [,1]       [,2]
 [1,]  0.0675840  0.3718730
 [2,]  0.0000000  0.0000000
 [3,]  0.0000000  0.0000000
 [4,]  0.0000000  0.0000000
 [5,]  0.0000000  0.0000000
 [6,] -0.0675840 -0.3718730
 [7,] -0.0675840 -0.3718730
 [8,]  0.9838835 -0.1788105
 [9,]  0.0000000  0.0000000
[10,]  0.0000000  0.0000000
```

Example Two (cont.)

```
> names(aout$coefficients)

 [1] "(Intercept)"
 [2] "varbld02"
 [3] "varbld03"
 [4] "varbld04"
 [5] "varbld05"
 [6] "varblds1"
 [7] "varblds2"
 [8] "varblds3"
 [9] "varbroct2003"
[10] "varbroct2004"
[11] "varbroct2005"
[12] "layerld:yearcross1999"
[13] "layerlds:yearcross1999"
[14] "layerroct:yearcross1999"
[15] "indoors:flat1"
[16] "indoors:flat2"
[17] "transplant:row10"
[18] "transplant:row11"
[19] "transplant:row12"
[20] "transplant:row13"
[21] "transplant:posi"
[22] "fit:crosstypeBr"
[23] "fit:crosstypeWi"
```

Example Two (cont.)

We don't have `row0` any more, but we still have a problem.

It is still complaining about directions of recession (DOR) or constancy (DOC).

And I will tell you that when there are a lot of zeros and repeated values in the "apparent" DOR or DOC, they probably really are one or the other.

That is, we appear to have a real problem. But we don't want to delve into that can of worms yet.

Example Two (cont.)

```
> aout.no.yearcross <- aster(resp ~ varb + indoors : flat +
+     transplant : (row + posi) + fit : crosstype,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout), silent = TRUE)

apparent null eigenvectors of information matrix
directions of recession or constancy of log likelihood
             [,1]       [,2]
 [1,]  0.0675840  0.3718730
 [2,]  0.0000000  0.0000000
 [3,]  0.0000000  0.0000000
 [4,]  0.0000000  0.0000000
 [5,]  0.0000000  0.0000000
 [6,] -0.0675840 -0.3718730
 [7,] -0.0675840 -0.3718730
 [8,]  0.9838835 -0.1788105
 [9,]  0.0000000  0.0000000
[10,]  0.0000000  0.0000000
```

Example Two (cont.)

```
> names(aout.no.yearcross$coefficients)

 [1] "(Intercept)"      "varbld02"
 [3] "varbld03"         "varbld04"
 [5] "varbld05"         "varblds1"
 [7] "varblds2"         "varblds3"
 [9] "varbroct2003"     "varbroct2004"
[11] "varbroct2005"     "indoors:flat1"
[13] "indoors:flat2"    "transplant:row10"
[15] "transplant:row11" "transplant:row12"
[17] "transplant:row13" "transplant:posi"
[19] "fit:crosstypeBr"  "fit:crosstypeWi"
```

Example Two (cont.)

Looks like we are stuck. We need at least a little bit of info about DOR and DOC to get going.

A **direction of constancy** (DOC) is a direction in the parameter space (where β lives) in which the log likelihood is constant (moving along lines in that direction does not change the log likelihood).

A **direction of recession** (DOR) is a direction in the parameter space (where β lives) in which the log likelihood is nondecreasing (moving along lines in that direction the log likelihood increases or stays the same).

Whenever there is a DOR that is not a DOC, the MLE does not exist (the log likelihood goes up hill in that direction all the way to infinity).

Example Two (cont.)

Theory of exponential families (which we will eventually get to, but for now leave vague) says the MLE does not exist when the canonical statistic vector $M^T y$ is on the boundary of its range.

In general, that is hard to check.

We can only hope it is easy in the case at hand.

Example Two (cont.)

If we look inside the R function `summary.aster`, here is how it makes these "apparent" DOR or DOC.

```
> info.tol <- sqrt(.Machine$double.eps)
> info.tol
```

```
[1] 1.490116e-08
```

```
> infomat <- aout$fisher
> fred <- eigen(infomat, symmetric = TRUE)
> sally <- fred$values < max(fred$values) * info.tol
> apparent <- zapsmall(fred$vectors[ , sally])
> rownames(apparent) <- names(aout$coefficients)
> apparent
```

```
                          [,1]        [,2]
(Intercept)          0.0675840  0.3718730
varbld02             0.0000000  0.0000000
varbld03             0.0000000  0.0000000
varbld04             0.0000000  0.0000000
```

Example Two (cont.)

Computationally, these are apparent null eigenvectors of the Fisher information matrix (and we don't yet know what that is either).

Since lengths of direction vectors do not matter, we can try to make them look nicer by changing the length.

We can also just drop all the zero rows. Those are the components of the submodel canonical parameter and statistic that are not involved in the DOR/DOC.

```
> zero.rows <- apply(apparent == 0, 1, all)
> apparent <- apparent[! zero.rows, ]
```

Example Two (cont.)

```
> apparent
```

	[,1]	[,2]
(Intercept)	0.0675840	0.3718730
varblds1	-0.0675840	-0.3718730
varblds2	-0.0675840	-0.3718730
varblds3	0.9838835	-0.1788105
transplant:row10	-0.0675840	-0.3718730
transplant:row11	-0.0675840	-0.3718730
transplant:row12	-0.0675840	-0.3718730
transplant:row13	-0.0675840	-0.3718730

We see a pattern. Lots of the same numbers in each column.

Example Two (cont.)

```
> apparent <- sweep(apparent, 2, apparent[1, ], "/")
> apparent
```

```
                          [,1]       [,2]
(Intercept)            1.00000  1.0000000
varblds1              -1.00000 -1.0000000
varblds2              -1.00000 -1.0000000
varblds3              14.55794 -0.4808375
transplant:row10      -1.00000 -1.0000000
transplant:row11      -1.00000 -1.0000000
transplant:row12      -1.00000 -1.0000000
transplant:row13      -1.00000 -1.0000000
```

Example Two (cont.)

I think I see what's happening.

The (pseudo) predictor `transplant` perfectly predicts the `lds3` node of the graph. That's DOR.

I am not clear why there are two DOR/DOC instead of one.

But I am out of ideas. Looks like we do have to do model matrices "by hand" for this one.

Example Two (cont.)

```
> m <- model.matrix(resp ~ varb + layer : yearcross +
+     indoors : flat + outdoors : (row + posi) +
+     fit : crosstype, data = echin2)
> dim(m)

[1] 6127   29

> m <- m[ , colnames(m) != "outdoors:row0"]
> dim(m)

[1] 6127   28
```

Example Two (cont.)

```
> aout <- aster(resp ~ 0 + m,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout), silent = TRUE)

apparent null eigenvectors of information matrix
directions of recession or constancy of log likelihood
 [1]  0.3535534  0.0000000  0.0000000  0.0000000
 [5]  0.0000000 -0.3535534 -0.3535534 -0.3535534
 [9]  0.0000000  0.0000000  0.0000000  0.0000000
[13]  0.0000000  0.0000000  0.0000000  0.0000000
[17] -0.3535534 -0.3535534 -0.3535534 -0.3535534
[21]  0.0000000  0.0000000  0.0000000
```

Example Two (cont.)

This is hard to see without extracting the eigenvectors as we did before and putting labels on the components of the DOR or DOC. If we do that (for once not shown) we see that it is a problem with `lds` nodes and `outdoors` nodes.

And the answer is obvious if we add up all the `outdoor:row1`x dummy variables we just get `outdoor`, which is the same as the sum of the of the `varbldsx` dummy variables.

Have to drop something. R would have dropped the `"row10"` level of the `row` factor if we hadn't had the bogus `"row0"` level to confuse it.

Example Two (cont.)

```
> dim(m)

[1] 6127   28

> grep("row", colnames(m), value = TRUE)

[1] "outdoors:row10" "outdoors:row11" "outdoors:row12"
[4] "outdoors:row13"

> m <- m[ , ! grepl("row10", colnames(m))]
> dim(m)

[1] 6127   27
```

Example Two (cont.)

```
> aout <- aster(resp ~ 0 + m,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout))

Call:
aster.formula(formula = resp ~ 0 + m, pred = pred, fam = fa
    varvar = varb, idvar = id, root = root, data = echin2)

                          Estimate Std. Error z value
m(Intercept)               0.74649    0.27173   2.747
mvarbld02                  0.18029    0.44949   0.401
mvarbld03                  1.54701    0.46449   3.331
mvarbld04                  1.44860    0.47435   3.054
mvarbld05                  2.90222    0.38842   7.472
mvarblds1                 -1.13189    0.50667  -2.234
mvarblds2                  0.32434    0.57666   0.562
mvarblds3                  1.21221    0.56491   2.146
mvarbroct2003             -3.01924    0.34267  -8.811
```

Example Two (cont.)

	Estimate	Std. Error	z value	Pr(>|z|)
m(Intercept)	0.746488	0.271726	2.7472	0.0060105
mvarbld02	0.180287	0.449488	0.4011	0.6883513
mvarbld03	1.547012	0.464487	3.3306	0.0008667
mvarbld04	1.448602	0.474349	3.0539	0.0022590
mvarbld05	2.902224	0.388415	7.4720	7.901e-14
mvarblds1	-1.131885	0.506668	-2.2340	0.0254845
mvarblds2	0.324339	0.576658	0.5624	0.5738117
mvarblds3	1.212208	0.564913	2.1458	0.0318863
mvarbroct2003	-3.019236	0.342669	-8.8109	< 2.2e-16
mvarbroct2004	-1.910658	0.299234	-6.3852	1.712e-10
mvarbroct2005	-1.141527	0.309447	-3.6889	0.0002252
mlayerld:yearcross1999	0.025827	0.128321	0.2013	0.8404856
mlayerlds:yearcross1999	0.311623	0.226641	1.3750	0.1691433
mlayerroct:yearcross1999	-0.028953	0.121738	-0.2378	0.8120099
mindoors:flat1	-0.245502	0.186994	-1.3129	0.1892203
mindoors:flat2	-0.491118	0.172267	-2.8509	0.0043594
moutdoors:row11	0.145657	0.036319	4.0105	6.060e-05
moutdoors:row12	0.121987	0.035296	3.4561	0.0005481
moutdoors:row13	0.118659	0.034554	3.4340	0.0005947
moutdoors:posi	-0.322929	0.069919	-4.6186	3.863e-06
mfit:crosstypeBr	0.101693	0.139439	0.7293	0.4658167
mfit:crosstypeWi	-0.562843	0.181571	-3.0999	0.0019361

Example Two (cont.)

Hooray! It worked!

What a struggle!

But maybe it will go faster now that we have a clue.

Example Two (cont.)

But another issue occurred to me while the struggle was going on.

We are not really following the dictum about "naked" predictors.

The `row` and `posi` predictors do not make sense for different kinds of variables. As in example one, where we had `nsloc` and `ewloc` "interacted with" `layer`, we should have the same for `row` and `posi` here.

So we start over.

There will be a problem that any of these `outside : layer : row` dummy variables that involve `ldsx` nodes are bogus, since such nodes aren't outside. We will have to remove them too.

Example Two (cont.)

```
> m <- model.matrix(resp ~ varb + layer : yearcross +
+     indoors : flat + outdoors : layer : (row + posi) +
+     fit : crosstype, data = echin2)
> outies <- grepl("row0|layerlds:outdoors|row10",
+     colnames(m))
```

Example Two (cont.)

```
> colnames(m)[outies]

 [1] "layerld:outdoors:row0"
 [2] "layerlds:outdoors:row0"
 [3] "layerroct:outdoors:row0"
 [4] "layerld:outdoors:row10"
 [5] "layerlds:outdoors:row10"
 [6] "layerroct:outdoors:row10"
 [7] "layerlds:outdoors:row11"
 [8] "layerlds:outdoors:row12"
 [9] "layerlds:outdoors:row13"
[10] "layerlds:outdoors:posi"
```

Example Two (cont.)

```
> dim(m)

[1] 6127   41

> m <- m[ , ! outies]
> dim(m)

[1] 6127   31
```

Example Two (cont.)

```
> aout <- aster(resp ~ 0 + m,
+     pred, fam, varb, id, root, data = echin2)
> try(summary(aout))

Call:
aster.formula(formula = resp ~ 0 + m, pred = pred, fam = fa
    varvar = varb, idvar = id, root = root, data = echin2)

                          Estimate Std. Error z value
m(Intercept)               0.56195    0.27577   2.038
mvarbld02                  0.08454    0.45061   0.188
mvarbld03                  1.63006    0.46838   3.480
mvarbld04                  1.54872    0.47826   3.238
mvarbld05                  3.00295    0.39238   7.653
mvarblds1                 -0.94874    0.50882  -1.865
mvarblds2                  0.51148    0.57856   0.884
mvarblds3                  1.40328    0.56666   2.476
mvarbroct2003             -2.67680    0.36469  -7.340
```

Example Two (cont.)

	Estimate	Std. Error	z value	Pr(>|z|)
m(Intercept)	0.561948	0.275769	2.0378	0.0415747
mvarbld02	0.084537	0.450606	0.1876	0.8511847
mvarbld03	1.630055	0.468384	3.4802	0.0005011
mvarbld04	1.548720	0.478261	3.2382	0.0012027
mvarbld05	3.002947	0.392378	7.6532	1.960e-14
mvarblds1	-0.948737	0.508824	-1.8646	0.0622421
mvarblds2	0.511475	0.578562	0.8840	0.3766717
mvarblds3	1.403275	0.566664	2.4764	0.0132723
mvarbroct2003	-2.676800	0.364688	-7.3400	2.136e-13
mvarbroct2004	-1.576635	0.324294	-4.8617	1.164e-06
mvarbroct2005	-0.800018	0.334819	-2.3894	0.0168756
mlayerld:yearcross1999	0.069508	0.128345	0.5416	0.5881161
mlayerlds:yearcross1999	0.287124	0.226411	1.2682	0.2047433
mlayerroct:yearcross1999	-0.081130	0.122418	-0.6627	0.5075034
mindoors:flat1	-0.258737	0.187393	-1.3807	0.1673669
mindoors:flat2	-0.476028	0.172587	-2.7582	0.0058123
mfit:crosstypeBr	0.086439	0.140414	0.6156	0.5381578
mfit:crosstypeWi	-0.588787	0.181631	-3.2417	0.0011883
mlayerld:outdoors:row11	0.158092	0.128729	1.2281	0.2194098
mlayerroct:outdoors:row11	0.103061	0.137350	0.7504	0.4530415
mlayerld:outdoors:row12	0.704913	0.148235	4.7554	1.981e-06
mlayerroct:outdoors:row12	-0.523367	0.160789	-3.2550	0.0011339
mlayerld:outdoors:row13	0.374546	0.132670	2.8231	0.0047555
mlayerroct:outdoors:row13	-0.179594	0.144162	-1.2458	0.2128475

Example Two (cont.)

Doesn't all fit on a slide, but it can be looked at outside of the slides.

Anyway, we aren't primarily or even secondarily interested in these "meaningless" parameter estimates.

Example Two (cont.)

Now what about yearcross?

```
> outies <- grepl("yearcross", colnames(m))
> colnames(m)[outies]

[1] "layerId:yearcross1999"   "layerIds:yearcross1999"
[3] "layerroct:yearcross1999" "layerId:yearcross2000"
[5] "layerIds:yearcross2000"  "layerroct:yearcross2000"

> m2 <- m[ , ! outies]
> dim(m)

[1] 6127   31

> dim(m2)

[1] 6127   25
```

Example Two (cont.)

```
> aout2 <- aster(resp ~ 0 + m2,
+     pred, fam, varb, id, root, data = echin2)
> anova(aout2, aout)

Analysis of Deviance Table

Model 1: resp ~ 0 + m2
Model 2: resp ~ 0 + m
  Model Df Model Dev Df Deviance P(>|Chi|)
1       23   -2082.5
2       26   -2079.0  3   3.4784    0.3236
```

Example Two (cont.)

`yearcross` is not statistically significant. Not even close.

Why only 3 degrees of freedom, when we dropped 6 variables?

```
> ncol(m)

[1] 31

> length(aout$coefficients)

[1] 26

> aout$dropped

[1] "mlayerld:yearcross2000"
[2] "mlayerlds:yearcross2000"
[3] "mlayerroct:yearcross2000"
[4] "mindoors:flat3"
[5] "mfit:crosstypeWr"
```

Example Two (cont.)

```
> ncol(m2)

[1] 25

> length(aout2$coefficients)

[1] 23

> aout2$dropped

[1] "m2indoors:flat3"   "m2fit:crosstypeWr"
```

Example Two (cont.)

Now what about crosstype?

```
> outies <- grepl("crosstype", colnames(m2))
> colnames(m2)[outies]

[1] "fit:crosstypeBr" "fit:crosstypeWi"
[3] "fit:crosstypeWr"

> m3 <- m2[ , ! outies]
> dim(m2)

[1] 6127   25

> dim(m3)

[1] 6127   22
```

Example Two (cont.)

```
> aout3 <- aster(resp ~ 0 + m3,
+     pred, fam, varb, id, root, data = echin2)
> anova(aout3, aout2)

Analysis of Deviance Table

Model 1: resp ~ 0 + m3
Model 2: resp ~ 0 + m2
  Model Df Model Dev Df Deviance P(>|Chi|)
1      21   -2108.7
2      23   -2082.5  2   26.197 2.048e-06 ***
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example Two (cont.)

`crosstype` is highly statistically significant.

Summary: `aout2` is the best model (looked at so far).

Once we got on the right track, it wasn't too hard.

However, we have not yet addressed another issue of scientific interest. Now that we are on the right track, perhaps it will be straightforward. (Actually, it is far from straightforward because there are interesting theoretical issues, more than one of them.)

Example Two (cont.)

One of the authors on the paper asked the question about whether differential survival in the growth chamber or differential survival and growth (fecundity wasn't really measured) outdoors was more responsible for the statistical significance of `crosstype`.

To examine that, we have to add a term `indoors : crosstype`

Example Two (cont.)

```
> m4 <- model.matrix(resp ~ varb +
+     indoors : flat + outdoors : layer : (row + posi) +
+     fit : crosstype + indoors : crosstype, data = echin2)
> outies <- grepl("row0|layerlds:outdoors|row10", colnames(
> colnames(m4)[outies]

[1] "outdoors:layerld:row0"
[2] "outdoors:layerlds:row0"
[3] "outdoors:layerroct:row0"
[4] "outdoors:layerld:row10"
[5] "outdoors:layerlds:row10"
[6] "outdoors:layerroct:row10"
```

Example Two (cont.)

```
> dim(m4)

[1] 6127   37

> m4 <- m4[ , ! outies]
> dim(m4)

[1] 6127   31
```

Example Two (cont.)

```
> aout4 <- aster(resp ~ 0 + m4,
+     pred, fam, varb, id, root, data = echin2)
> anova(aout3, aout2, aout4)

Analysis of Deviance Table

Model 1: resp ~ 0 + m3
Model 2: resp ~ 0 + m2
Model 3: resp ~ 0 + m4
  Model Df Model Dev Df Deviance P(>|Chi|)
1       21   -2108.7
2       23   -2082.5  2  26.1971 2.048e-06 ***
3       25   -2082.1  2   0.3571    0.8365
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example Two (cont.)

One of these P-values we have seen before (`aout3` versus `aout2`). The other is new.

Since the new one is not statistically significant (not even close), it is clear that model `aout4` fits no better than `aout2`. There is no evidence that we need the `indoors : crosstype` term in the model.

Example Two (cont.)

But there is another way to ask this question. Might it not be that a model with just `indoors : crosstype` instead of `fit : crosstype` would also fit the data?

But we cannot compare those models directly because they are not nested (and nested models are required for validity of the tests done by the `anova` function).

So we have to compare them indirectly by comparing each directly to `aout3` and `aout4`

Example Two (cont.)

```
> outies <- grepl("fit:crosstype", colnames(m4))
> colnames(m4)[outies]

[1] "fit:crosstypeBr" "fit:crosstypeWi"
[3] "fit:crosstypeWr"

> m5 <- m4[ , ! outies]
> dim(m4)

[1] 6127   31

> dim(m5)

[1] 6127   28
```

Example Two (cont.)

```
> aout5 <- aster(resp ~ 0 + m5,
+     pred, fam, varb, id, root, data = echin2)
> anova(aout3, aout5, aout4)

Analysis of Deviance Table

Model 1: resp ~ 0 + m3
Model 2: resp ~ 0 + m5
Model 3: resp ~ 0 + m4
  Model Df Model Dev Df Deviance P(>|Chi|)
1       21   -2108.7
2       23   -2103.4  2   5.2469   0.07255 .
3       25   -2082.1  2  21.3073 2.361e-05 ***
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Example Two (cont.)

The comparison of `aout5` with `aout2` is not statistically significant (although there is some weak indication).

The comparison of `aout5` with `aout4` is highly statistically significant.

Thus `aout5` fits no better than the smallest model under consideration (`aout2`) and much worse than the largest (`aout4`). Thus there is no (or very, very weak) evidence in favor of `aout5`.

This is just the opposite of the situation with `aout2`. Since `aout2` fits as well as `aout4` and is the smaller, more parsimonious model, we choose it.

Example Two (cont.)

So our scientific conclusion is that differential survival in the growth chamber has no effect on fitness. Right? Wrong!

That forgets the aster transform. Recall that its inverse is given by

$$\theta_k = \varphi_k + \sum_{\substack{j \in J \\ p(j) = k}} c_j(\theta_j)$$

where we calculate successors before predecessors.

This implies that the components of φ for all successors, successors of successors, and so forth influence the component of θ for that node and consequently the component of ξ for that node.

Said another way, changing the component of φ for one node changes the components of θ and ξ for all predecessors, predecessors of predecessors, and so forth of that node.

Example Two (cont.)

So the term `fit : crosstype` propagates backwards in the graph to influence conditional mean values for survival in the growth chamber.

How much does it influence it? What the maximum entropy principle makes it do.

Which way does it influence it?

Differentiating the Aster Transform

The derivative of the aster transform is given by

$$\begin{aligned} \Delta\varphi_k &= \Delta\theta_k - \sum_{\substack{j \in J \\ p(j)=k}} c_j'(\theta_j) \Delta\theta_j \\ &= \Delta\theta_k - \sum_{\substack{j \in J \\ p(j)=k}} \xi_j \Delta\theta_j \end{aligned}$$

and the derivative of the inverse aster transform is given by

$$\Delta\theta_k = \Delta\varphi_k + \sum_{\substack{j \in J \\ p(j)=k}} \xi_j \Delta\theta_j$$

which calculates components of $\Delta\theta$ from components of $\Delta\varphi$ in any order that does successors before predecessors.

Example Two (cont.)

Using

$$\Delta\theta_k = \Delta\varphi_k + \sum_{\substack{j \in J \\ p(j)=k}} \xi_j \Delta\theta_j$$

on our example or on any aster model in which the ξ_j are always nonnegative (because the corresponding components of the response vector are always nonnegative), we see that increasing one component of $\Delta\varphi$ also increases the corresponding component of $\Delta\theta$ and then also increases the the components of $\Delta\theta$ for predecessor nodes and predecessor of predecessor nodes and so forth.

In short, increasing fitness at terminal nodes ("fitness nodes") of the graph also increases survival at earlier nodes of the graph, and in particular survival in the growth chamber.

Example Two (cont.)

But exactly how much? For that we need numbers.

Again we need to use the `newdata` argument to the `predict.aster` function, but we do not need to use the `amat`, because we are only interested in one node (`lds3`) rather than a sum of nodes.

Since we are using formulas but useless ones we will have to use the function `predict.aster.default` rather than `predict.aster.formula`.

Example Two (cont.)

First we subset `m2` to have one individual for each cross type.

```
> inies <- match(levels(echin2$crosstype),
+     as.character(echin2$crosstype))
> inies <- echin2$id[inies]
> inies

[1]  5 21  1

> newmodmat <- m2[echin2$id %in% inies, ]
> dim(newmodmat)

[1] 33 25
```

Example Two (cont.)

And then we "fix it up"

```
> grep("flat", colnames(newmodmat), value = TRUE)

[1] "indoors:flat1" "indoors:flat2" "indoors:flat3"

> newmodmat[ , "indoors:flat1"] <-
+     as.numeric(grepl("lds", rownames(newmodmat)))
> newmodmat[ , "indoors:flat2"] <- 0
> newmodmat[ , "indoors:flat3"] <- 0
```

Example Two (cont.)

```
> grep("row", colnames(newmodmat), value = TRUE)

[1] "layerld:outdoors:row11"
[2] "layerroct:outdoors:row11"
[3] "layerld:outdoors:row12"
[4] "layerroct:outdoors:row12"
[5] "layerld:outdoors:row13"
[6] "layerroct:outdoors:row13"
```

Put everyone in row 10.

```
> newmodmat[ , grep("row", colnames(newmodmat))] <- 0
```

Example Two (cont.)

```
> grep("posi", colnames(newmodmat), value = TRUE)

[1] "layerld:outdoors:posi"   "layerroct:outdoors:posi"
```

Put everyone at position zero.

```
> newmodmat[ , grep("posi", colnames(newmodmat))] <- 0
```

Example Two (cont.)

Now more bad design of R package `aster`. We have to make `newmodmat` a 3-way array and supply `root` as a 2-way array.

```
> nind <- nlevels(echin2$crosstype)
> nparm <- ncol(newmodmat)
> nnode <- length(newmodmat) / (nind * nparm)
> all.equal(nnode, as.integer(nnode))

[1] TRUE

> newmodmat <- array(as.vector(newmodmat),
+     c(nind, nnode, nparm))
> newroot <- array(1, c(nind, nnode))
```

Example Two (cont.)

```
> try(pout <- predict(aout2, root = newroot,
+     modmat = newmodmat, se.fit = TRUE), silent = TRUE)
> dim(newmodmat)

[1]  3 11 25

> dim(aout2$modmat)

[1] 557  11  23

> aout2$dropped

[1] "m2indoors:flat3"   "m2fit:crosstypeWr"
```

doesn't work. We have to remove the "dropped columns" from `newmodmat`.

Example Two (cont.)

```
> droppies <- gsub("m2", "", aout2$dropped)
> droppies

[1] "indoors:flat3"   "fit:crosstypeWr"

> outies <- match(droppies, colnames(m2))
> outies

[1] 14 17

> newmodmat <- newmodmat[ , , - outies]
> dim(newmodmat)

[1]  3 11 23
```

Example Two (cont.)

Try 2.

```
> pout <- predict(aout2, root = newroot,
+     modmat = newmodmat, se.fit = TRUE)
> pout.fit <- matrix(pout$fit, nrow = nind)
> pout.se <- matrix(pout$se.fit, nrow = nind)
> rownames(pout.fit) <- levels(echin2$crosstype)
> rownames(pout.se) <- levels(echin2$crosstype)
> colnames(pout.fit) <- vars
> colnames(pout.se) <- vars
```

Example Two (cont.)

```
> foo <- cbind(pout.fit[ , "lds3"],
+     pout.se[ , "lds3"])
> colnames(foo) <- c("fit", "se")
> foo

          fit          se
Br 0.8592819 0.03802385
Wi 0.8694220 0.03340710
Wr 0.7920395 0.04824145
```

Example Two (cont.)

At this point we give up (even though the paper had more confidence intervals).

Enough has been done to show that

- aster modeling when the R formula mini-language is inadequate to express the models is very difficult,
- but not impossible.