Selecting Time Predictors

Preselecting Time Predictors

- How does one preselect the time predictors
  - Theoretical justification (most defensible)
  - Statistical selection
    - Graphing (see Unit 4)
      - Random error can make visual detection difficult
      - Scaling, aspect ratio, etc. can distort features of change curves (e.g., nonlinear aspects may be exaggerated/understated depending on axes limits)
    - Statistical analysis
      - Descriptive or inferential
      - Group- or subject-level (inference for group-level analysis only)

Selection of Time Transformations

- Two primary uses of time transformations
  - Anchor intercept at particular point
  - Model nonlinear trends
- Most common method to model nonlinear trends is to use polynomials
  - Polynomials are power transformations of original time predictor

$$\text{power transformation} = \text{base}^{\text{exponent}}$$

  - base = time predictor; exponent = non-negative integer

For the MPLS data

$$\text{grade}^0, \text{grade}^1, \text{grade}^2, \text{grade}^3, \ldots$$

1 grade

- The *order* (degree) of the polynomial is the value of its largest exponent
  - 0th-order polynomial = intercept-only model
  - First-order polynomial = linear model
  - Second-order polynomial = quadratic model

- Polynomials used in LMER to account for nonlinear change
- Assume no static predictors, then expected value is

$$E(y_{ij}) = \beta_0(\texttt{grade}_{ij}^0) + \beta_1(\texttt{grade}_{ij}^1) + \beta_2(\texttt{grade}_{ij}^2) + \ldots + \beta_k(\texttt{grade}_{ij}^k)$$

- Number of polynomials is *k* + 1 (same as number of fixed effects)
- Convention is when higher order polynomials are included in the model, all lower order polynomials are also included
  - For example, if $\texttt{grade}_{ij}^2$ is in the model, so is $\texttt{grade}_{ij}^1$
  - This is regardless of statistical results of the lower order terms

- Desirable to avoid saturated models (no summarization of the data)
- Saturated models have same number of fixed effects (including intercept) as total number of time points
- Only consider models up to order two less than number of time points
    - In MPLS data $max(n_i) = 4$
    - At most, a quadratic (order = 2) model would be considered
- Order of the polynomial determines number of random effects (also the number of static predictor interaction terms)

- Consider linear and quadratic models where `grade` is the time predictor and there is one static predictor, `ethW`

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + \\ \beta_2(\texttt{ethW}_i) + \beta_4(\texttt{grade}_{ij} \cdot \texttt{ethW}_i) + \epsilon_{ij}$$

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + (\beta_2 + b_{02})(\texttt{grade}^2_{ij}) + \\ \beta_3(\texttt{ethW}_i) + \beta_4(\texttt{grade}_{ij} \cdot \texttt{ethW}_i) + \beta_5(\texttt{grade}^2_{ij} \cdot \texttt{ethW}_i) + \epsilon_{ij}$$

- Linear model = 2 random effects and 1 interaction term
- quadratic model = 3 random effects and 2 interaction terms

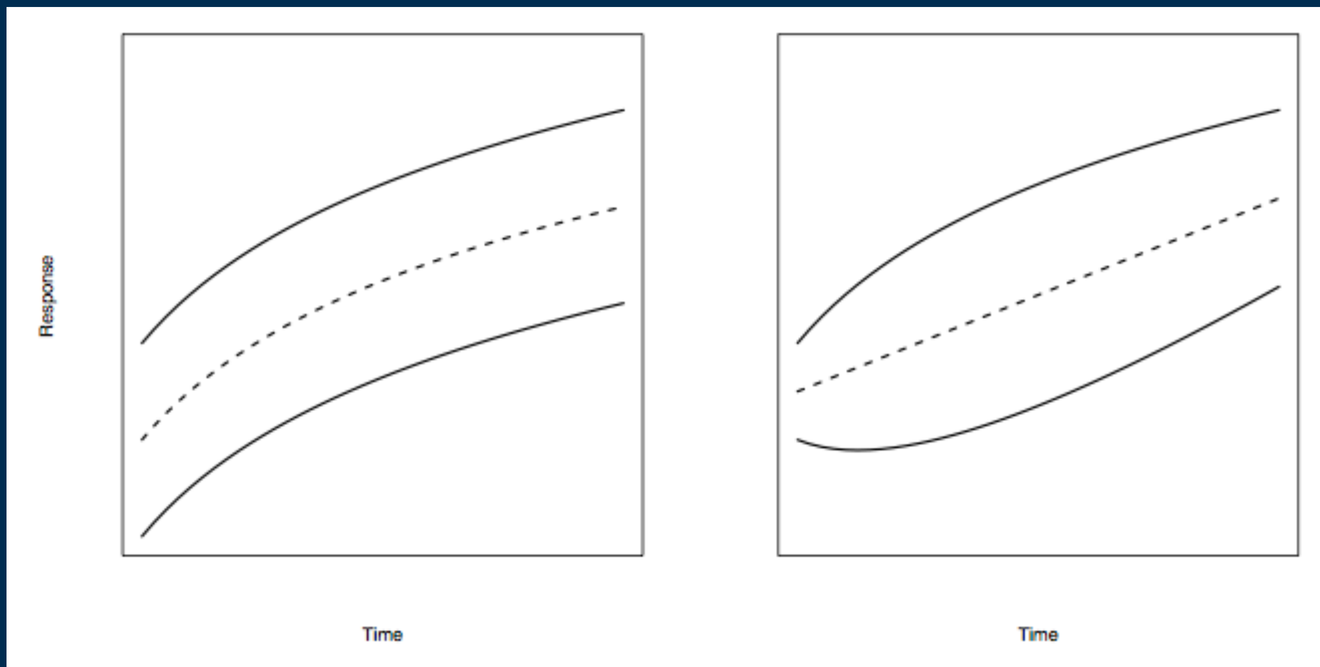
- Linear model has 3 variance components associated with random effects
- Quadratic model has 6 variance components associated with random effects
    - Addition of second-order polynomial term adds 3 VC!
- Time transformations are considered in initial steps of any analysis
    - Also important to consider role of static predictors and random effects
    - As per the previous units, when considering time transformations, number of static predictors and random effects will be held constant among models
        - Only difference in models is number of polynomial terms

- Number of random effects held constant by including one greater than the lowest order polynomial in every model
  - For example, considering linear (k_1=1) and quadratic (k_2=2) and cubic (k_3=3) models all three would include only 2 random effects (b_{0i} and b_{1i})
  - Addition/removal of random effects occurs in later parts of the analysis (e.g., after static predictors have been chosen)
- Consideration of static predictors also is important
  - Subgroups may have different change curves
  - Graph your data first!!!
  - In exploratory analyses, consider not including static predictors–especially in nascent areas of research

Group-Level Selection of Time Transformations

- Focus is on selection of appropriate polynomial in fixed effects structure of LMER model
  - At group-level methods such as AIC and LRT can be used
- Confirmatory analysis
  - Linear model hypothesized
  - Both first- and second-order models estimated and the latter used to confirm linear model (quadratic term not needed?)
- Exploratory analysis
  - Selection of polynomials may be focus of analysis

- Static predictors
  - Change curve is expected to be similar for subgroups, static predictor can be ignored in selection of time transformation
  - If not, static predictor interactions need to be included (aggregate curve distorted)



Multimodal Inference

- When static predictors are not included, set of models can be evaluated using AIC and AICc
    - In this situation models only differ by number of polynomial terms
- When static predictors are included this approach is not recommended

Analysis Without Static Predictors

- Recall these are referred to as unconditional models
- Number of random effects forced to be the same across models
- Consider exploratory analysis for MPLS data set

Model I: Intercept-only model (flat line)

Model L: Linear model with single predictor, `grade5`

Model Q Quadratic model with two predictors, `grade5` and `grade5`^{2}

- Cubic model not considered (saturated model)
- Number of random effects will be one (b_{0i})

```r
## Fit models
> model.i <- lmer(read ~ 1 + (1 | subid), data = mpls.l,
                  REML = FALSE)

> model.l <- lmer(read ~ 1 + grade5 + (1 | subid),
                  data = mpls.l, REML = FALSE)

> model.q <- lmer(read ~ 1 + grade5 + I(grade5 ^ 2) +
                  (1 | subid), data = mpls.l, REML = FALSE)

## AICc results
> myaicc <- as.data.frame(aictab(
    cand.set = list(model.i, model.l, model.q),
    modnames = c("I", "L", "Q"),
    sort = FALSE) )

## Evidence ratio
> myaicc$eratio <- max(myaicc$AICcWt) / myaicc$AICcWt

## Print results
> myaicc
```

Intercept model is implausible–low weight of evidence and extremely large evidence ratio

	Modnames	K	AICc	Delta_AICc	AICcWt	eratio
1	I	3	632.8	44.999	0.0000000001179	5906380283.244
2	L	4	587.8	0.000	0.6965765431840	1.000
3	Q	5	589.5	1.662	0.3034234566980	2.296

Quadratic model has weight of evidence 1/2 size of linear model. Its evidence ratio is not too large indicating it is a plausible model as well

Linear model is most plausible model

- How plausible is the quadratic model?
  - Examine coefficients

```
> summary(model.q)@coefs

             Estimate Std. Error t value
(Intercept) 205.2475     4.0547 50.6194
grade5        6.3634     1.8466  3.4461
I(grade5^2)  -0.4898     0.6229 -0.7863
```

Negative quadratic term (not 0) indicates concavity with respect to grade axis...slowing down or deceleration for later grades

t-value is close to 0, confirming results from model comparison

t-ratios should not be used to examine lower order effects

- How plausible is the linear model?
  - Examine coefficients

```
> summary(model.l)@coefs

             Estimate Std. Error t value
(Intercept)  205.677      4.022  51.140
grade5         4.985      0.582   8.564
```

t-value is relatively large

Multimodal analysis suggests that best approximating change curve is linear. This should be tempered by small sample size (*N*=22) and small grade range (5-8).

Analysis with Static Predictors

- Approach with static predictors is not clear cut
- Possible to use multimodal approach
  - Results are vulnerable to misinterpretation
- To illustrate, consider the following models

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + \beta_2(\texttt{dadv}_i) + \epsilon_{ij}$$

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + \beta_2(\texttt{dadv}_i) + \beta_3(\texttt{ethW}_i) + \epsilon_{ij}$$

Suppose goal is to choose time transformations and there is suspicion that quadratic term is necessary

Models are

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + \beta_2(\texttt{grade}_{ij}^2) + \beta_3(\texttt{dadv}_i) + \epsilon_{ij}$$

and

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade}_{ij}) + \beta_2(\texttt{grade}_{ij}^2) + \beta_3(\texttt{dadv}_i) + \beta_4(\texttt{ethW}_i) + \epsilon_{ij}$$

The second model has one additional quadratic term.

	Modnames	K	AICc	Delta_AICc	AICcWt	eratio
1	1L	7	579.5	3.8907	0.07594	6.996
2	1Q	8	580.3	4.7414	0.04963	10.705
3	2L	8	575.6	0.0000	0.53131	1.000
4	2Q	9	576.4	0.8746	0.34311	1.549

- Model 2L is best fitting; model 2Q second best
- Because of this you might say that the best approximating model may include a quadratic change curve
  - 2Q is fitting well because it shares static predictors with 2L not because of the quadratic term
  - Comparing 1Q to 1L it is seen that the quadratic also fits worse
- With respect to the change curve, model 1L fits better then 2Q

- When change curves of static predictor subgroups are not parallel then the order of polynomial should be selected with the interactions in the model
- Suppose intention is to evaluate models that differ in ethnicity and risk effects
    - Three polynomial models are examined (I, L, and Q)
        - Two static predictors as single effects and all possible interactions

Intercept-only model

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\mathtt{grade5}_{ij}) + \\ \beta_2(\mathtt{dadv}_i) + \beta_3(\mathtt{ethW}_i) + \epsilon_{ij}$$

Linear model

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade5}_{ij}) +$$
$$\beta_2(\texttt{dadv}_i) + \beta_3(\texttt{ethW}_i) +$$
$$\beta_4(\texttt{grade5}_{ij} \cdot \texttt{dadv}_i) +$$
$$\beta_5(\texttt{grade5}_{ij} \cdot \texttt{ethW}_i) + \epsilon_{ij}$$

Quadratic model

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i})(\texttt{grade5}_{ij}) + \beta_2(\texttt{grade5}^2_{ij}) +$$
$$\beta_3(\texttt{dadv}_i) + \beta_4(\texttt{ethW}_i) +$$
$$\beta_5(\texttt{grade5}_{ij} \cdot \texttt{dadv}_i) +$$
$$\beta_6(\texttt{grade5}_{ij} \cdot \texttt{ethW}_i) +$$
$$\beta_7(\texttt{grade5}^2_{ij} \cdot \texttt{dadv}_i) +$$
$$\beta_8(\texttt{grade5}^2_{ij} \cdot \texttt{ethW}_i) + \epsilon_{ij}$$

```
## Estimate models
> model.i <- lmer(read ~ dadv + ethW + (1 | subid), mpls.l,
    REML = FALSE)
> model.l <- lmer(read ~ grade5 * dadv + grade5 * ethW + (1 | subid),
    data = mpls.l, REML = FALSE)
> model.q <- lmer(read ~ grade5 * dadv + grade5 * ethW +
    I(grade5 ^ 2) * dadv + I(grade5 ^ 2) * ethW + (1 | subid),
    data = mpls.l, REML = FALSE)

## Compute AIC
> myaicc <- as.data.frame(aictab(
    cand.set = list(model.i, model.l, model.q),
    modnames = c("I", "L", "Q"), sort = FALSE))[ , -c(5,7)]

## Compute evidence ratio
> myaicc$eratio <- max(myaicc$AICcWt) / myaicc$AICcWt

> myaicc
```

	Modnames	K	AICc	Delta_AICc	AICcWt	eratio
1	I	5	622.5	42.011	0.0000000007294	1325838559.08
2	L	8	580.5	0.000	0.9670361058595	1.00
3	Q	11	587.2	6.758	0.0329638934111	29.34

- Linear model has large weight of evidence

Likelihood Ratio Test: Analysis Without Static Predictors

- Analysis with polynomial terms can be performed in a step-up or top-down approach
  - Step-up approach compares initial (simpler) model to a more complex model that adds polynomial terms
  - Top-down approach compares initial (more complex) model to a simpler model that removes polynomial terms
- Recall that both approaches compare nested models (reduced model has fewer parameters)
- Emphasis when selecting polynomial terms is on accept/reject decision making
  - Testing typically terminates with the first non-significant result
  - Sometimes a rule of two consecutive non-significant results is used

- Again consider the 3 models with no static predictors fitted earlier (I, L, and Q)

```
## Fit models
> model.i <- lmer(read ~ 1 + (1 | subid), data = mpls.l,
                  REML = FALSE)

> model.l <- lmer(read ~ 1 + grade5 + (1 | subid),
                  data = mpls.l, REML = FALSE)

> model.q <- lmer(read ~ 1 + grade5 + I(grade5 ^ 2) +
                  (1 | subid), data = mpls.l, REML = FALSE)

## LRT
> anova(model.i, model.l, model.q)
```

```
Data: mpls.l
Models:
model.i: read ~ 1 + (1 | subid)
model.l: read ~ 1 + grade5 + (1 | subid)
model.q: read ~ 1 + grade5 + I(grade5^2) + (1 | subid)
        Df AIC BIC logLik Chisq Chi Df      Pr(>Chisq)
model.i  3 633 640   -313
model.l  4 587 597   -290 47.22      1 0.0000000000064 ***
model.q  5 589 601   -289  0.62      1            0.43
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

- Step-up approach
    - Begin with model.i compared to model.l (linear term is needed)
    - Model.l compared to model.q (quadratic term does not add anything...it is not needed)
- Top-down approach – begin with model.q compared to model.l (non-significance suggests more parsimonious model is accepted)

LRT with Static Predictors

- Use same modeling techniques as with AICc
- All polynomials should be fitted with interaction terms included in the model

Subject-Level Selection of Time Predictors

- Goal is to use individual change curves to suggest polynomial effects to be included in model
- Goodness-of-fit index computed for each subject to quantify adequacy of model
    - These indices are then summarized in plots or pooled to create a single descriptive measure
- When subgroups differ in curve shape, highest order polynomial should be fitted for all subjects
    - For subgroups with simpler curve, parameter estimates of higher order terms will be close to zero
- Disadvantage to subject-level selection is that it is only descriptive
    - Statistical theory cannot be used to judge sample effects
- Missing data may not allow the same model to be fitted to all subjects

Level 1 Polynomial Model

- Change curves are either connected observed values or connected fitted values
- Observed change curves are not model based
- Fitted change curves use the subject-specific Level 1 model
- Consider the following Level 1 model

$$
\begin{aligned}
y_{ij} &= \beta^*_{0i} + \beta^*_{1i}(\texttt{grade5}_{ij}) \\
&\quad + \beta^*_{2i}(\texttt{grade5}^2_{ij}) + \ldots + \beta_{ki}(\texttt{grade5}^k_{ij}) + \epsilon_{ij}
\end{aligned}
$$

where each β^* is a subject-specific regression weight

- Since i = 1, ..., N, there are N Level 1 equations
- There are no static predictors (those are level 2 predictors)
- For subject-level analysis, the correlation among repeated measures is ignored and OLS estimation is used. This is justified since the concern is only with description.

Missing Data

- The requirement that the number of time points > k + 1 limits the polynomial for subjects with missing data
- Useful to create a new variable that indexes the number of missing points
- This can be used to exclude some subjects from the analysis

The `ddply()` function from the **plyr** library evaluates an expression/ function a given number of times and then stores the result in a data frame.

```
## load plyr library

> library( plyr )


## Create a vector of 0/1 that indicates missingness of read
## for each row

> mpls.l$miss <- as.numeric(is.na(mpls.l$read))


## Compute the number of missing values for each subject

> mysel <- ddply(.data = data.frame(mpls.l$miss),
    .variables = .(mpls.l$subid), .fun = sum)
```

```
## Change variable names

> colnames(mysel) <- c("subid", "totmiss")
```

```
## Merge the number of missing values with the original data
## frame

> mpls.l2 <- merge(mpls.l, mysel, by = "subid")
```

```
> head(mpls.l2)

  subid risk gen eth ell sped  att grade read grade5 dadv ethW miss totmiss
1     1  HHM   F Afr   0    N 0.94     5  172      0 DADV   NW    0       0
2     1  HHM   F Afr   0    N 0.94     6  185      1 DADV   NW    0       0
3     1  HHM   F Afr   0    N 0.94     7  179      2 DADV   NW    0       0
4     1  HHM   F Afr   0    N 0.94     8  194      3 DADV   NW    0       0
5     2  HHM   F Afr   0    N 0.91     5  200      0 DADV   NW    0       1
6     2  HHM   F Afr   0    N 0.91     6  210      1 DADV   NW    0       1
```

Subject-Level Fits

- Examine the subject-specific fitted curves
  - For small *n*, graphing works well
  - For large *n* graphs are generally cumbersome and it works better to examine summary measure(s) from the fitted model (e.g., R^2)

1) Fit a linear model to each subject using the `lm()` function
2) Extract the summary measures of interest from each fitted model (e.g., coefficients, R^2, etc.)
3) Plot or summarize (e.g., through a mean) the summary measures that were extracted

```
## Function to fit lm

> fit.linear <- function(x) {
    lm(read ~ grade5, data = x)
    }



## Fit lm to each subject's data

> mylm.1 <- dlply(.data = mpls.l,
     .variables = .(mpls.l$subid), .fun = fit.linear)

> mylm.1

$`1`

Call:
lm(formula = read ~ grade5, data = x)

Coefficients:
(Intercept)       grade5
        174            6
                ⋮
```

The `dlply()` function fits the `fit.linear()` function to each subject's data and outputs the results in a list

```
## Function to obtain coefficients

> get.coef <- function(x) {
    x$coefficients
    }



## Obtain coefficients from each subject's model

> ldply(.data = mylm.1, .fun = get.coef)
```

The `ldply()` function fits the `get.coef()` function to each model stored in the list and then outputs the results as a data frame.

```
   mpls.l$subid (Intercept) grade5
1             1       173.5    6.0
2             2       201.8    4.5
3             3       190.6    7.6
4             4       199.3   -3.0
5             5       208.7    1.7
6             6       190.9    2.9
7             7       200.2    6.2
8             8       191.5    1.5
9             9       147.9   10.4
10           10       201.8    6.5
11           11       220.5    6.5
12           12       228.0    7.0
13           13       229.0    2.5
14           14       198.8   12.3
15           15       216.7    9.0
16           16       228.0    0.5
17           17       201.7    5.2
18           18       218.1    0.6
19           19       214.3    3.0
20           20       207.9    3.4
21           21       237.3    3.0
22           22       220.8    8.5
```

Subject 4 has a negative slope, but all the rest are positive

Repeat this Process for a Quadratic Model

```
## Function to fit quadratic

> fit.quad <- function(x) {
    lm(read ~ grade5 + I(grade5 ^ 2), data = x)
    }



## Fit lm to each subject’s data

> mylm.1 <- dlply(.data = mpls.l,
     .variables = .(mpls.l$subid), .fun = fit.linear)



## Obtain coefficients from each subject's model

> ldply(.data = mylm.1, .fun = get.coef)
```

```
   mpls.l$subid (Intercept) grade5 I(grade5^2)
1             1       174.0   4.50        0.50
2             2       200.0  15.50       -5.50
3             3       191.6   4.60        1.00
4             4       200.0  -7.00        2.00
5             5       207.4   5.45       -1.25
6             6       188.7   9.65       -2.25
7             7       199.2   9.20       -1.00
8             8       191.0   4.50       -1.50
9             9       147.4  11.90       -0.50
10           10       200.0  17.50       -5.50
11           11       218.7  11.75       -1.75
12           12       226.5  11.50       -1.50
13           13       229.8   0.25        0.75
14           14       198.5  13.05       -0.25
15           15       218.0   1.00        4.00
16           16       226.8   4.25       -1.25
17           17       202.2   3.70        0.50
18           18       218.6  -0.90        0.50
19           19       215.0  -1.00        2.00
20           20       203.9  15.40       -4.00
21           21       237.0   5.00       -1.00
22           22       219.0  19.50       -5.50
```

Most subjects have a negative effect for the quadratic term.

The signs represent shape differences.

A negative sign is *concave* to the *x*-axis (∩).

A positive sign is *convex* to the *x*-axis (∪).

```
## Function to extract R2

> get.R2 <- function(x) {
    summary(x)$r.squared
    }


## Extract R2 from each subject's model

> linear.r2 <- ldply(.data = mylm.1, .fun = get.R2)


## Change column names

> colnames(linear.r2) <- c("subid", "Rsq")


## Merge missingness and R2

> Rsq1 <- merge(mysel, linear.r2, by = "subid")
```

```
> Rsq1
   subid totmiss     Rsq
1      1       0 0.68966
2      2       1 0.66758
3      3       0 0.96267
4      4       1 0.87097
5      5       0 0.58384
6      6       0 0.24342
7      7       0 0.97563
8      8       1 0.75000
9      9       0 0.91197
10    10       1 0.80732
11    11       0 0.89989
12    12       0 0.81940
13    13       0 0.32982
14    14       0 0.99435
15    15       1 0.93822
16    16       0 0.03226
17    17       0 0.81939
18    18       0 0.18000
19    19       1 0.87097
20    20       0 0.47377
21    21       1 0.96429
22    22       1 0.87753
```

Repeat this Process for a Quadratic Model

```
> quad.r2 <- ldply(.data = mylm.2, .fun = get.R2)

> colnames(quad.r2) <- c("subid", "Rsq")

> Rsq2 <- merge(mysel, quad.r2, by = "subid")

> Rsq2
```

```
   subid totmiss    Rsq
1      1       0 0.6935
2      2       1 1.0000
3      3       0 0.9760
4      4       1 1.0000
5      5       0 0.8364
6      6       0 0.3606
7      7       0 0.9959
8      8       1 1.0000
9      9       0 0.9137
10    10       1 1.0000
11    11       0 0.9521
12    12       0 0.8495
13    13       0 0.3536
14    14       0 0.9947
15    15       1 1.0000
16    16       0 0.1935
17    17       0 0.8255
18    18       0 0.2800
19    19       1 1.0000
20    20       0 0.9984
21    21       1 1.0000
22    22       1 1.0000
```

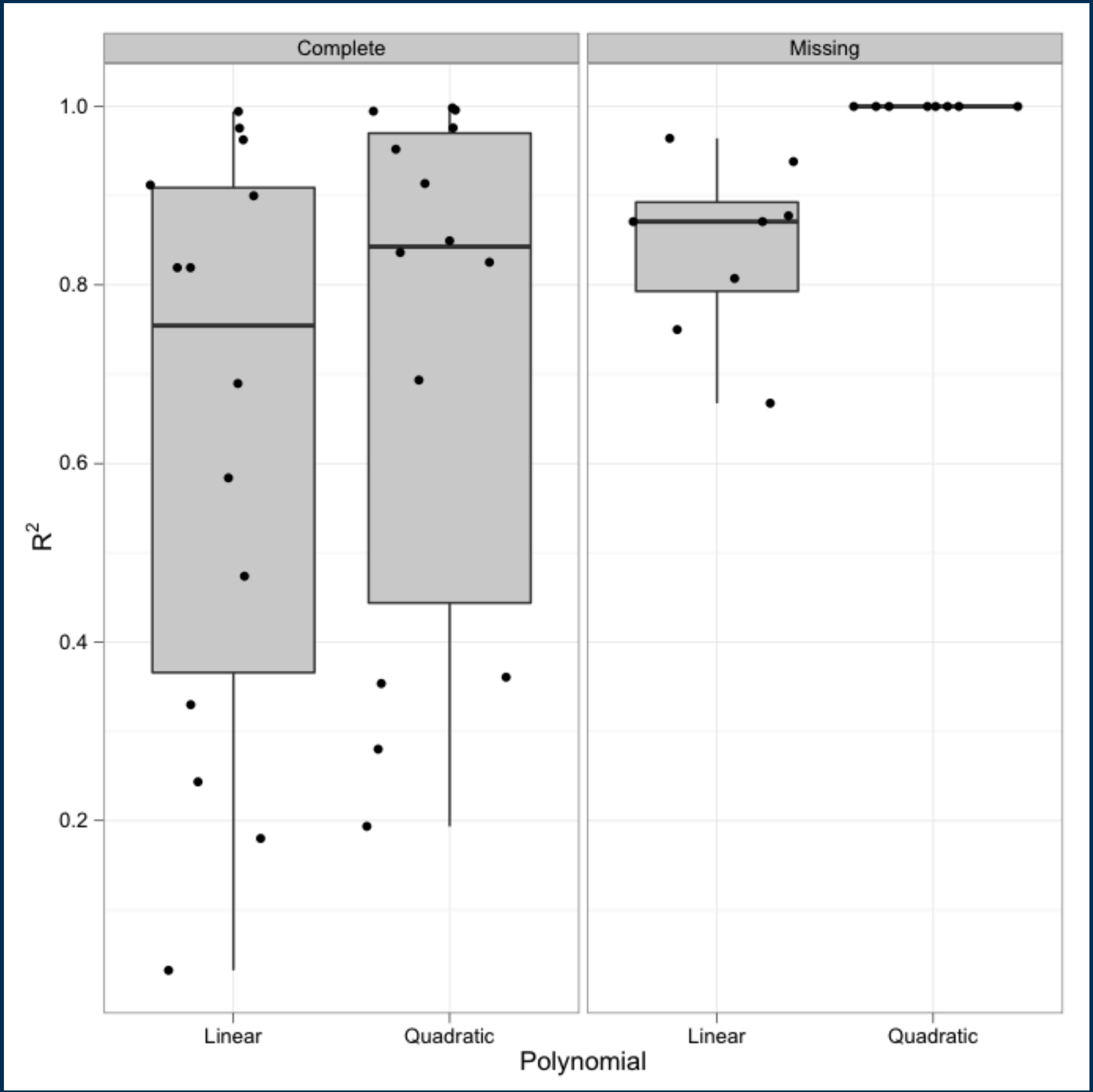
Quadratic polynomial fits perfectly for subjects with missing data (saturated model)

Plot the R^2 values Conditional on Missingness

```
## Get number of rows
> N <- nrow(Rsq1)

## Combine the two data frames into a new data frame
> plotdata <- data.frame(rbind(Rsq1, Rsq2), c(rep(1, N),
    rep(2, N)))

## Change 4th column name to poly
> colnames(plotdata)[4] <- "poly"

## Add variable to indicate polynomial term
> plotdata$poly.f <- factor(plotdata$poly,
    labels = c("Linear", "Quadratic"))

## Add variable to indicate degree of missingness
> plotdata$missing.f <- factor(plotdata$totmiss,
    labels = c("Complete", "Missing"))
```

```
   subid totmiss     Rsq poly poly.f missing.f
1      1       0 0.68966    1 Linear  Complete
2      2       1 0.66758    1 Linear   Missing
3      3       0 0.96267    1 Linear  Complete
4      4       1 0.87097    1 Linear   Missing
5      5       0 0.58384    1 Linear  Complete
6      6       0 0.24342    1 Linear  Complete
7      7       0 0.97563    1 Linear  Complete
8      8       1 0.75000    1 Linear   Missing
9      9       0 0.91197    1 Linear  Complete
10    10       1 0.80732    1 Linear   Missing
11    11       0 0.89989    1 Linear  Complete
12    12       0 0.81940    1 Linear  Complete
13    13       0 0.32982    1 Linear  Complete
14    14       0 0.99435    1 Linear  Complete
15    15       1 0.93822    1 Linear   Missing
16    16       0 0.03226    1 Linear  Complete
17    17       0 0.81939    1 Linear  Complete
18    18       0 0.18000    1 Linear  Complete
19    19       1 0.87097    1 Linear   Missing
20    20       0 0.47377    1 Linear  Complete
21    21       1 0.96429    1 Linear   Missing
22    22       1 0.87753    1 Linear   Missing
```

```
## Plot the R2 values

> ggplot(data = plotdata, aes(x = poly.f, y = Rsq)) +
    geom_boxplot(fill = "grey80") +
    geom_point(position = "jitter") +
    facet_grid(. ~ missing.f) +
    theme_bw() +
    xlab("Polynomial") +
    ylab(expression(R ^ 2))



## Obtain median values

> tapply(plotdata$Rsq, list(plotdata$missing.f, plotdata$poly.f),
     median)

         Linear Quadratic
Complete 0.7545    0.8429
Missing  0.8710    1.0000
```



Complete
Missing
1.0
0.8
0.6
0.4
0.2
R2
Linear
Quadratic
Linear
Quadratic
Polynomial

Adjusted R^2

- Drawback of R^2 is that it increases as more predictors are add into the model (even if they are worthless)
- Alternative is to use the penalized measure, *adj.* R^2

$$\bar{R}_i^2 = 1 - (1 - R_i^2)\left(\frac{n_i - 1}{n_i - k - 1}\right)$$

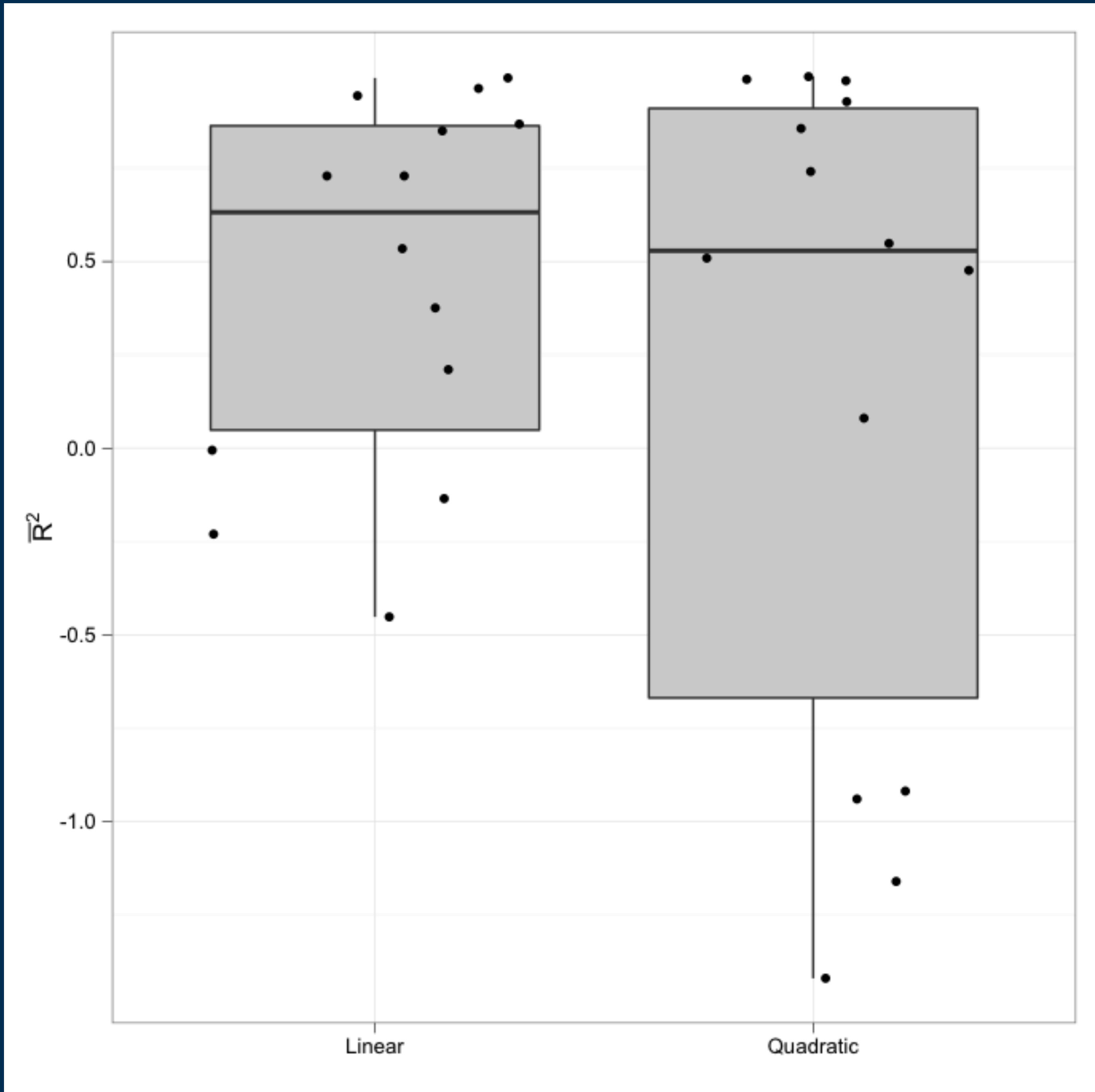
where k is the number of polynomial terms bigger than degree 0 (number of predictors)

$\bar{R}_i^2$ is not defined for saturated models

$\bar{R}_i^2$ can be extracted from the `summary()` object using `$adj.r.squared`

```r
> mysub <- subset(mpls.l2, totmiss == 0)

> mylm.1 <- dlply(.data = mysub,
    .variables = .(mysub$subid), .fun = fit.linear)

> mylm.2 <- dlply(.data = mysub,
    .variables = .(mysub$subid), .fun = fit.quad)


## Get adjusted R2

> get.adj.R2 <- function(x){
   summary(x)$adj.r.squared
   }


> adjRsq1 <- ldply(.data = mylm.1, .fun = get.adj.R2)

> colnames(adjRsq1) <- c("subid", "adjRsq")

> adjRsq2 <- ldply(.data = mylm.2, .fun = get.adj.R2)

> colnames(adjRsq2) <- c("subid", "adjRsq")
```

```
## Create data frame

> N <- nrow(adjRsq1)

> plotdata <- data.frame(rbind(adjRsq1, adjRsq2),
    c(rep(1, N), rep(2, N)))

> colnames(plotdata)[3] <- "poly"

> plotdata$poly.f <- factor(plotdata$poly,
    labels = c("Linear", "Quadratic"))


## Plot adjusted R2

> ggplot(data = plotdata, aes(x = poly.f, y = adjRsq)) +
   geom_boxplot(fill = "grey80") +
   geom_point(position = "jitter") +
   theme_bw() +
   xlab("") +
   ylab(expression(bar(R)^2))
```



0.5
0.0
-0.5
-1.0
$\overline{R}^2$
Linear
Quadratic

Pooled Measures of Fit

- Another alternative is to pool information from all subjects into a single statistic
- We will combine the subject-level sums of squares (foundation for R^2)

$$R_i^2 = 1 - \left(\frac{SSR_i}{SST_i}\right)$$

where *SSR* is the sum of squares residuals and *SST* is the sum of squares total. A pooled version can be created by replacing each of the sum of squares by the sum among all subjects

$$R_{meta}^2 = 1 - \left(\frac{\sum_{i=1}^{N} SSR_i}{\sum_{i=1}^{N} SST_i}\right)$$

- The meta-R^2 will always increase as predictors are added (just like R^2)
- Better to use penalized fit index
  - Meta-*RSE* (residual standard error)
  - Meta-*R*^{2} *adjusted*

Subject-level RSE

$$RSE_i = \sqrt{\frac{SSR_i}{n_i - k_i - 1}}$$

Pooled meta-RSE

$$RSE_{meta} = \sqrt{\frac{\sum_{i=1}^{N} SSR_i}{\sum_{i=1}^{N} (n_i - k_i - 1)}}$$

Compute Meta-RSE

```
## Estimate coefficients

> my1 <- dlply(.data = mpls.l,
    .variables = .(mpls.l$subid), .fun = fit.linear)

> my2 <- dlply(.data = mpls.l,
    .variables = .(mpls.l$subid), .fun = fit.quad)


## Sum of squares residuals

> ssResid <- function(x){
   sum(resid(x) ^ 2)
   }

> sse1 <- sum(ldply(.data = my1, .fun = ssResid)[ ,2])

> sse2 <- sum(ldply(.data = my2, .fun = ssResid)[ ,2])
```

```r
## Residual df

> dfResid <- function(x){
    x$df.residual
    }

> df1 <- sum(ldply(.data = my1, .fun = dfResid)[, 2])

> df2 <- sum(ldply(.data = my2, .fun = dfResid)[, 2])


## Compute RSE meta

> RSEmeta.1 <- sqrt(sse1/df1)

> RSEmeta.2 <- sqrt(sse2/df2)
```

```
> RSEmeta.1
[1] 4.262

> RSEmeta.2
[1] 5.623
```

Since the meta-RSE value is smaller for the linear model, it is evidence that the linear model is sufficient

Meta-R^2 *Adjusted*

- Obtained by dividing meta-R^2 numerator and denominator by *df*
- We will combine the subject-level sums of squares (foundation for R^2)

$$R^2_{meta} = 1 - \left(\frac{\dfrac{\sum_{i=1}^{N} SSR_i}{\sum_{i=1}^{N} (n_i - k_i - 1)}}{\dfrac{\sum_{i=1}^{N} SST_i}{\sum_{i=1}^{N} (n_i - k_i - 1)}} \right)$$

```
## Use function in script file
## Only change the first 3 lines (if need be)

> Rsq.meta

  lm.objects Rsqmeta
1     mylm.1  0.8298
2     mylm.2  0.8848


> adjRsq.meta

  lm.objects adjRsqmeta
1     mylm.1     0.6432
2     mylm.2     0.2962
```

These values are closer together than the medians computed before.

Although the quadratic model has a higher meta-R^2, the increase is not amazing.

After penalization, the linear model has a meta-R^2 that is more than twice that of the quadratic model.