Working with R

A University of Queensland Advanced Workshop

Session 16:
More on Neck Pain:
Analysis

Bill Venables, CSIRO/Data61, Dutton Park

Rhetta Chappell, Griffith University

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Contents

1 Making the data

The script for this section contains the **R** code to reproduce the data, which you should run again.

This is a reminder of the variables names and an assurance that the data appears clean, with no missing values:

```
colSums(is.na(longNeckPain))
```

```
       Ident      Cluster        Group         Time         time
           0            0            0            0            0
       Treat Organisation     Industry         Ergo          Age
           0            0            0            0            0
         BMI          Sex    Education   Occupation  Comorbidity
           0            0            0            0            0
       NPain
           0
```

2   Initial models

- A *longitudinal* study; need to recognize that some readings refer to the *same* participant and some to *different*. $\rightarrow$ random effect models.

- *Sex* will clearly be a dominant fixed effect term, but the study is designed to assess *Treat*.

- Initially we use *Time* and *Group* instead of *Treat* directly, but incorporate the latter, later.

- The strategy will be to build an initial random effect linear model with a fairly large fixed effect component, and to refine the model down to something justified by the data.

- The response, *NPain*, is a discrete variable with possible values $0, 1, 2, \ldots, 9$. It seems to be skewed as well. Nevertheless normal (gaussian) models still prove useful for investigative purposes.

2.1 Neck pain score

```r
suppressPackageStartupMessages(library(lme4))
mod_0 <- lmer(NPain ~ Sex*(Time*Group + Age +
                        BMI + Comorbidity + Ergo + Industry) +
            (1|Ident), data = longNeckPain)
dropterm(mod_0) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
Sex:Time:Group	4	9574.95	1.7598	0.7798
Sex:Industry	4	9576.33	3.1465	0.5336
Sex:BMI	1	9579.24	0.0505	0.8221
Sex:Age	1	9579.87	0.6874	0.4070
Sex:Ergo	1	9580.40	1.2101	0.2713
<none>		9581.19		
Sex:Comorbidity	1	9581.33	2.1470	0.1429

- There are no model refinement tools available in the public packages, but a simple backward elimination tool is provided in WWRCourse.

- It is similar to *MASS::stepAIC* but only provides backward elimination.

- Only *fixed effect* terms are considered for removal; all random effects are retained.

- The function is *step_down()*; at each stage it removes the current (non–marginal) term that *most reduces* the AIC criterion.

- The process stops when removing any remaining term would *increase* AIC.

```
mod_0s <- step_down(mod_0)
dropterm(mod_0s) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
\<none\>		9551.78		
Group	1	9552.16	2.3842	0.1226
BMI	1	9552.91	3.1312	0.0768
Sex:Comorbidity	1	9553.59	3.8158	0.0508
Time	4	9561.97	18.1913	0.0011

- The remaining terms are not all "significant" in the conventional sense, but if any factors are useful for a model they are likely to be included in this set.

- We gain an insight into the implications of the (fixed effect part of) the model by considering it's implications for prediction.

```
pNeckPain <- with(longNeckPain,
                  expand.grid(Time = levels(Time),
                              Group = levels(Group),
                              Sex = levels(Sex),
                              Comorbidity = c(0, 2),
                              BMI = quantile(BMI, c(0.25, 0.75)) %>% round))
pNeckPain$NPain <- predict(mod_0s, pNeckPain, re.form = ~0)
ggplot(pNeckPain) + aes(x = Time, y = NPain, group = Group,
                        linetype = Group, colour = Sex) +
  geom_point() + geom_line() + facet_grid(Sex ~ BMI + Comorbidity) +
  theme(legend.position = "bottom") + ylab("Mean neck pain score") +
  scale_colour_manual(values = c(male = "steelblue",
                                 female = "rosybrown"))
```
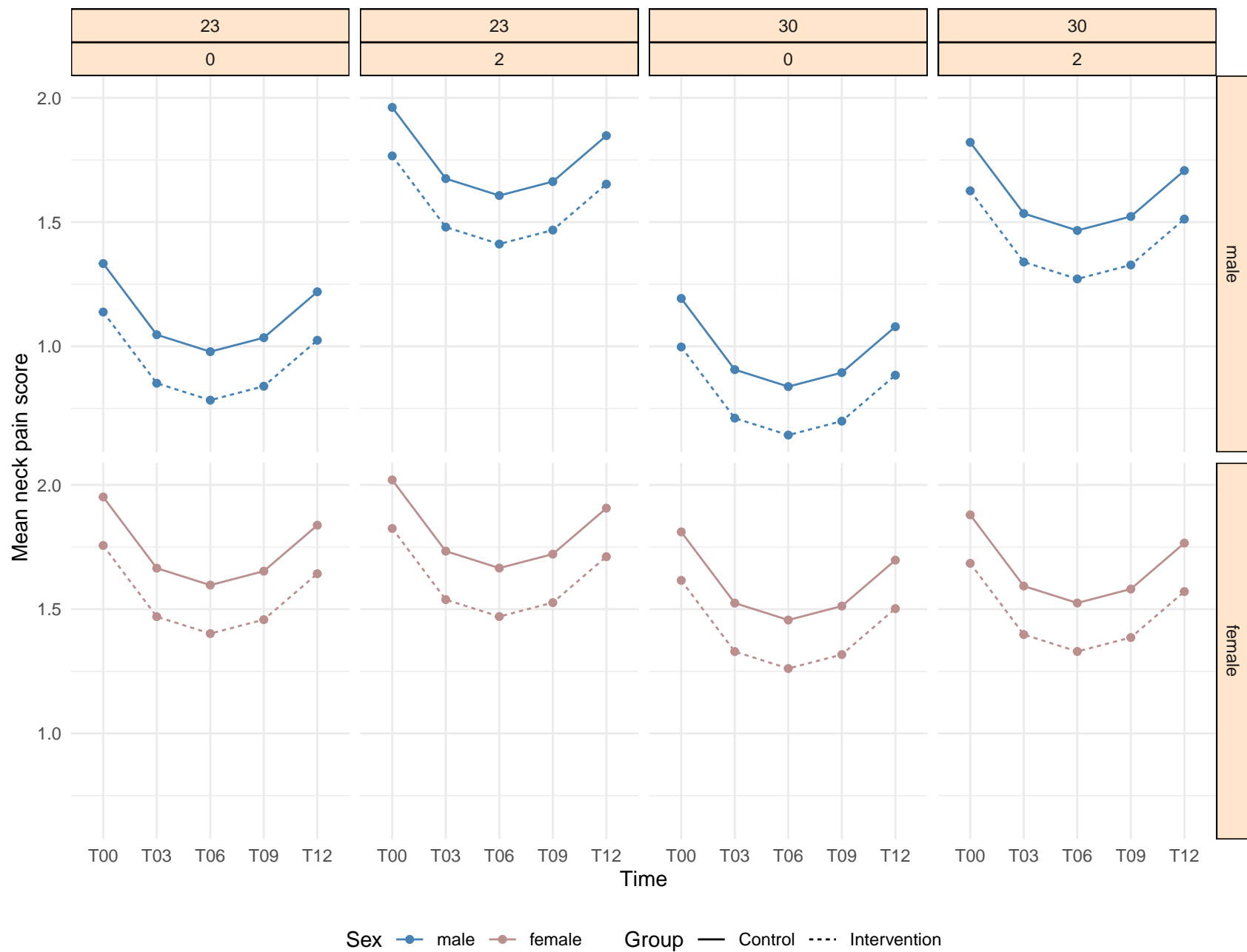
Surprises:

- Females consistently report higher mean neck pain scores than males.

- *Comorbidity* seems to affect males more than females.

- The effect of *Group*, ie exercise or not, modelled as a consistent shift, is minuscule, but at least exercise seems to have a slightly beneficial effect.

- Fatter people (*BMI* of 30.12) have a *lower* neck pain score than thinner people (*BMI* of 22.78), if only very slightly. A first time for everything, it seems!

Notes:

- This is what the model implies *could* be the case for the mean pain score for the various groups.

- Unfortunately, the effects of any of the fixed effect terms is, in practical terms, almost negligible.

- One feature of the situation not accommodated by the data is the at time 0 no group had received any treatment; allocation to the two groups was random, so there is no reason for their mean pain level, within each group, to be the same for *Control* and *Intervention* at time 0.

- We re-fit a model that uses *Treat* instead of *Time* and *Group*, and check what the differences are.

```r
mod_1s <- update(mod_0s, . ~ . - Time - Group + Treat) %>% step_down
pNeckPain <- pNeckPain %>%
  within({
    Treat <- ifelse(Time == "T00", "Base",
                    paste0(substring(Group, 0, 1),
                           substring(Time, 2)))
  })
pNeckPain$NPainT <- predict(mod_1s, pNeckPain, re.form = ~0)
ggplot(pNeckPain) + aes(x = Time, y = NPainT, group = Group,
                        linetype = Group, colour = Sex) +
  geom_point() + geom_line() + facet_grid(Sex ~ BMI + Comorbidity) +
  theme(legend.position = "bottom")  + ylab("Mean neck pain score") +
  scale_colour_manual(values = c(male = "steelblue",
                                 female = "rosybrown"))
```
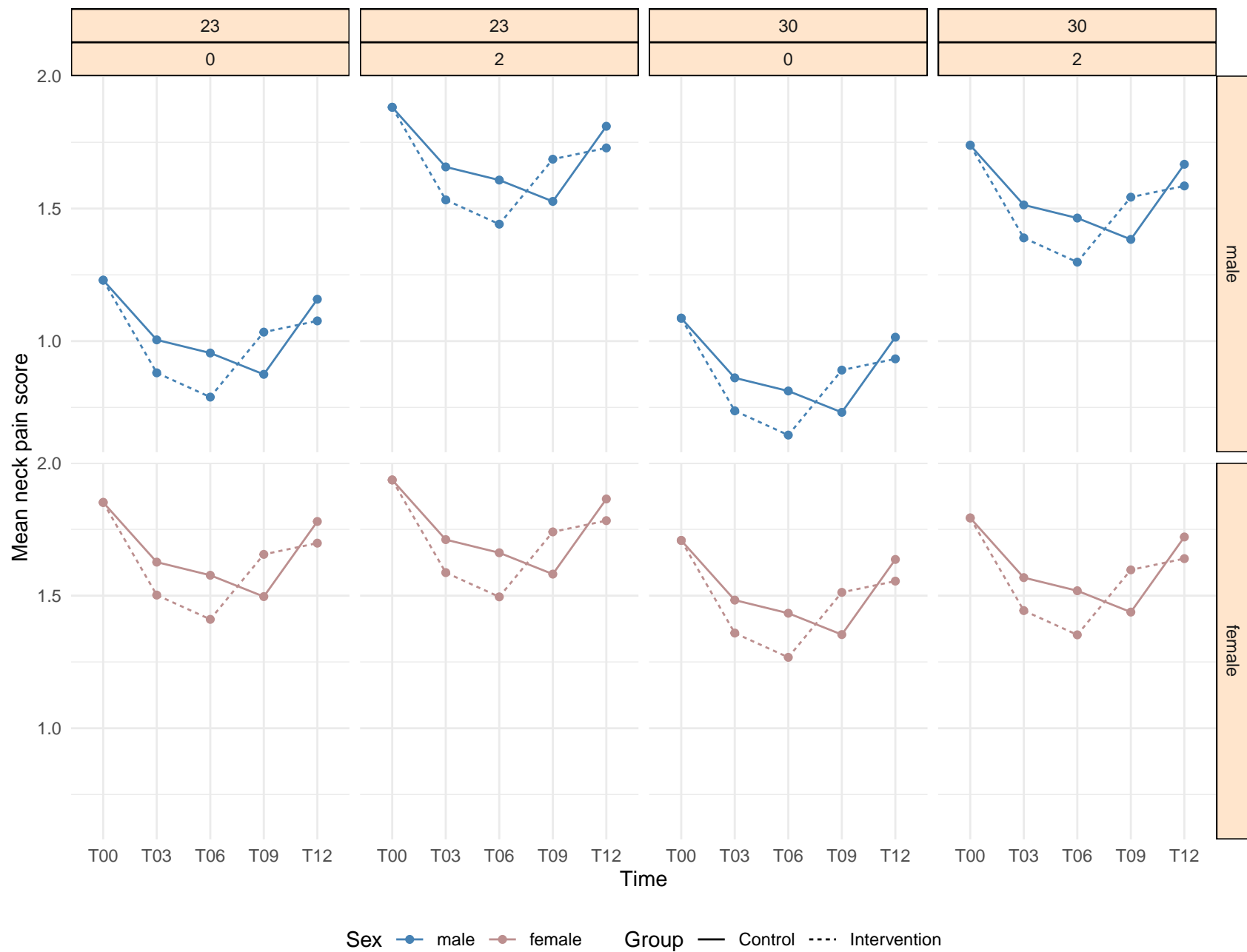
Cold water:

```
dropterm(mod_1s) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
<none>		9557.82		
BMI	1	9559.07	3.2516	0.0714
Sex:Comorbidity	1	9559.73	3.9151	0.0479
Treat	8	9562.05	20.2330	0.0095

- The `AIC` has gone *up* from 9551.78 to 9557.82, implying this is a less well supported model than the simpler one produced earlier.

- The next step would be to explore simpler models than the latest which nevertheless respect the constraint that at time 0 there is, in reality, only one group. But — it looks not to be all that useful an enterprise: the effects, however assessed, are tiny.

2.2　Neck pain severity

- The researchers were more interested in the *upper tail* of the pain score distribution than the mean.

  - A pain score less than 3, (strictly), is considered clinically fairly normal.

  - A pain score of 3 or more is considered clinically debilitating.

  Note that all the fixed effect mean scores coming out of the model, as displayed in out visualisation, were well within the clinically normal region.

- We now consider modelling the *probability* that a participant will register a pain score of 3 or more, i.e. within the clinically debilitating range.

```
longNeckPain <- within(longNeckPain, {
  Severe <- (NPain >= 3) + 0 ## coerce logical to binary
})
bin_0 <- glmer(Severe ~ Sex*(Time*Group + Age + BMI + Comorbidity +
                        Ergo + Industry) + (1|Ident),
          family = binomial, data = longNeckPain, nAGQ = 0)
dropterm(bin_0) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
Sex:Time:Group	4	2300.58	3.5942	0.4637
Sex:Industry	4	2301.69	4.7131	0.3180
Sex:BMI	1	2303.03	0.0530	0.8179
Sex:Ergo	1	2303.29	0.3140	0.5752
Sex:Age	1	2303.83	0.8512	0.3562
<none>		2304.98		
Sex:Comorbidity	1	2305.71	2.7313	0.0984

The model looks to be grossly over-fitted. Try an automatic step down to see how things simplify:

```
bin_0s <- step_down(bin_0)
dropterm(bin_0s) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
<none>		2277.41		
Sex:Group	1	2277.57	2.1567	0.1420
BMI	1	2277.84	2.4323	0.1189
Sex:Time	4	2278.03	8.6140	0.0715
Sex:Comorbidity	1	2279.38	3.9667	0.0464

- A slightly more complicated model, but the same suite of predictors turn up as *possibly* influential.

- The significances look even less impressive!

- Visualise the implications in the now standard way.

```r
pNeckPain$pSevere <- predict(bin_0s, pNeckPain,
                             type = "response", re.form = ~0)
ggplot(pNeckPain) + aes(x = Time, y = pSevere, group = Group,
                        linetype = Group, colour = Sex) +
  geom_point() + geom_line() + facet_grid(Sex ~ BMI + Comorbidity) +
  theme(legend.position = "bottom")  + ylab("Pr(severe neck pain)") +
  scale_colour_manual(values = c(male = "steelblue",
                                 female = "rosybrown"))
```
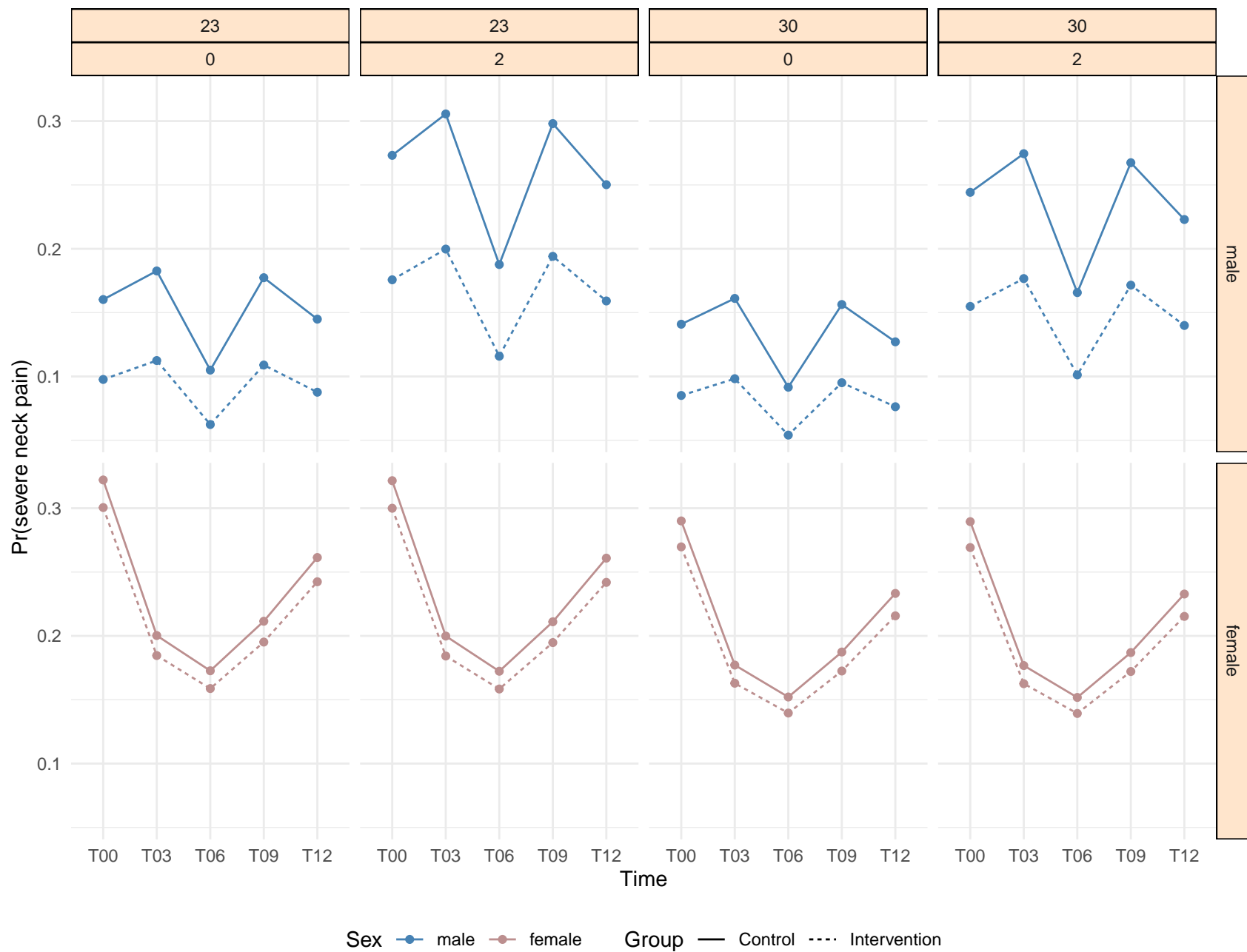
Notes:

- From our initial visualisation (previous session) we saw that, fortuitously, the `Intervention` group had a much lower incidence of severe neck pain than the `Control` group. This appears to have been seized upon by the modelling process as a real effect.

- Females have higher incidence of severe neck pain, not surprisingly, but there gap between `Control` and `Intervention` is much smaller. *Time* affects both sexes but for females, nothing else seems to have any effect.

Now check what results when both groups are forced to have the same incidence at time 0:

```r
bin_1s <- glmer(Severe ~ Sex*(Treat + Comorbidity) + (1|Ident),
                family = binomial, data = longNeckPain, nAGQ = 0) %>%
  step_down()
dropterm(bin_1s, test = "Chisq", sorted = TRUE) %>%
  booktabs(digits=c(0, 0, 2, 4, 4))
```

	Df	AIC	LRT	Pr(Chi)
<none>		2285.41		
Treat	8	2288.42	19.0166	0.0148
Sex:Comorbidity	1	2289.05	5.6400	0.0176

```r
pNeckPain$pSevereT <- predict(bin_1s, pNeckPain,
                              type = "response", re.form = ~0)
ggplot(pNeckPain) + aes(x = Time, y = pSevereT, group = Group,
                        linetype = Group, colour = Sex) + ylim(0, 0.3) +
  geom_point() + geom_line() + facet_grid(Sex ~ Comorbidity) +  ## BMI is gone!
  theme(legend.position = "bottom")  + ylab("Pr(severe neck pain)") +
  scale_colour_manual(values = c(male = "steelblue", female = "rosybrown"))
```

21
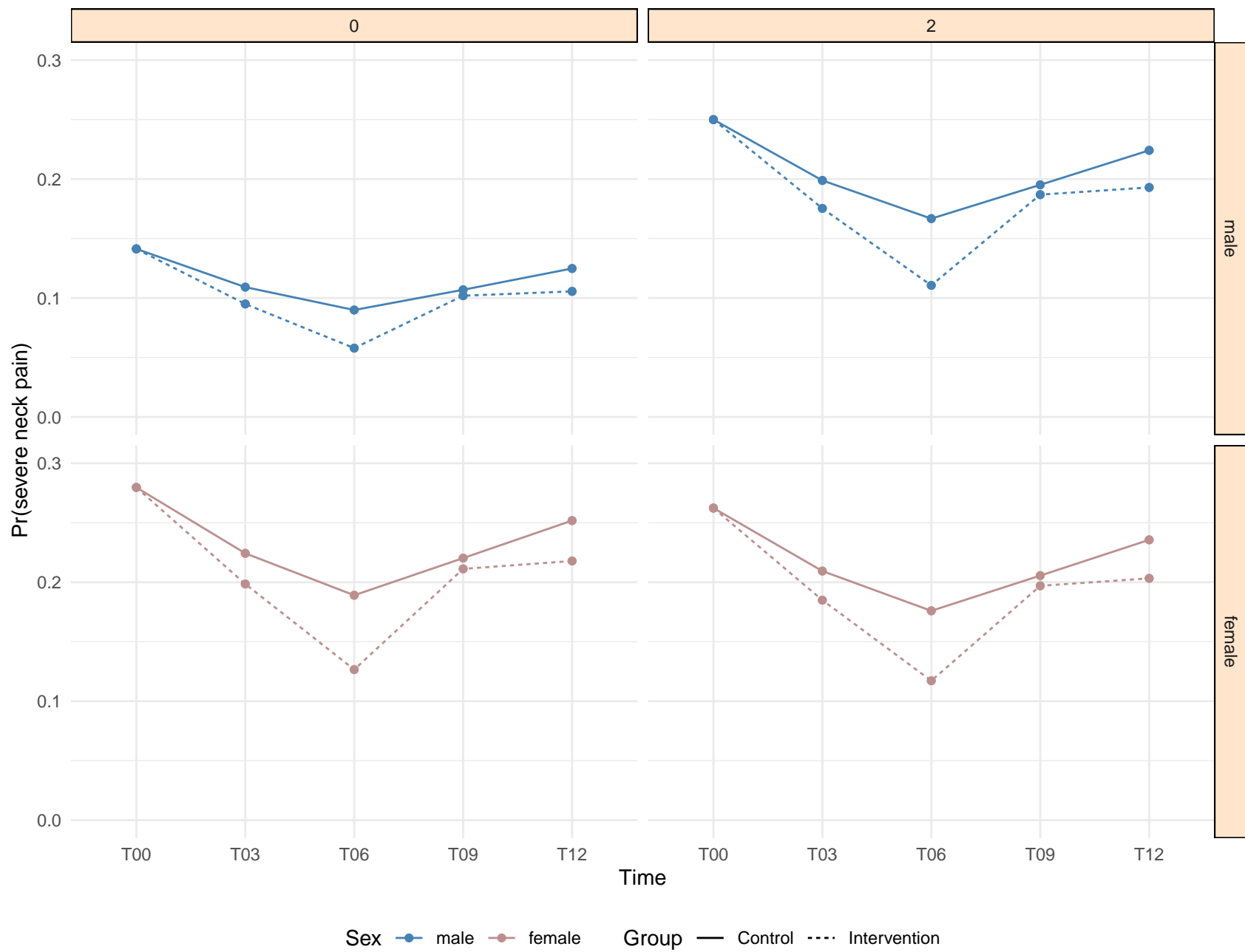
Final comments:

- Always keep in mind these visualisations are of the model, not of the data. The results generate questions, primarily, not answer them.

- It is interesting that the ultimate models, for mean neck pain and probability of severe neck pain respectively, have similar features to them. This is suggestive (only!).

- This eclectic glimpse of the model building process and visualisation of the results has ignored many important features that you should follow-up upon, in particular:

  - Look at the variance component estimates: what do you conclude?

  - Look at the implications of the model for a much wider range of cases: two *Comorbidity* coupled with two *BMI* values do not cover the field very well.

  - Compare the model suggestions with the initial visualisations to see how realistic they might be.

Session information

Date: 2021-01-29

- R version 4.0.3 (2020-10-10), `x86_64-pc-linux-gnu`

- Running under: `Ubuntu 20.04.1 LTS`

- Matrix products: default

- BLAS: `/usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0`

- LAPACK: `/usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0`

- Base packages: base, datasets, graphics, grDevices, methods, stats, utils

- Other packages: dplyr 1.0.3, english 1.2-5, forcats 0.5.1, ggplot2 3.3.3, ggthemes 4.2.4, gridExtra 2.3, haven 2.3.1, knitr 1.31, lattice 0.20-41, lme4 1.1-26, Matrix 1.3-2, patchwork 1.1.1, purrr 0.3.4, readr 1.4.0, scales 1.1.1, stringr 1.4.0, tibble 3.0.5, tidyr 1.1.2, tidyverse 1.3.0, WWRCourse 0.2.3, WWRData 0.1.0, WWRGraphics 0.1.2, WWRUtilities 0.1.2, xtable 1.8-4

- Loaded via a namespace (and not attached): assertthat 0.2.1, backports 1.2.1, boot 1.3-26, broom 0.7.3, cellranger 1.1.0, cli 2.2.0, colorspace 2.0-0, compiler 4.0.3, crayon 1.3.4, DBI 1.1.1, dbplyr 2.0.0, digest 0.6.27, ellipsis 0.3.1, evaluate 0.14, fansi 0.4.2, farver 2.0.3, fractional 0.1.3, fs 1.5.0, generics 0.1.0, glue 1.4.2, grid 4.0.3, gtable 0.3.0, highr 0.8, hms 1.0.0, httr 1.4.2, iterators 1.0.13, jsonlite 1.7.2, labeling 0.4.2, lazyData 1.1.0, lifecycle 0.2.0, lubridate 1.7.9.2, magrittr 2.0.1, MASS 7.3-53, minqa 1.2.4, modelr 0.1.8, munsell 0.5.0, nlme 3.1-151, nloptr 1.2.2.2, parallel 4.0.3, PBSmapping 2.73.0, pillar 1.4.7, pkgconfig 2.0.3, R6 2.5.0, randomForest 4.6-14, Rcpp 1.0.6, readxl 1.3.1, reprex 1.0.0, rlang 0.4.10, rpart 4.1-15, rstudioapi 0.13, rvest 0.3.6, SOAR 0.99-11, splines 4.0.3, statmod 1.4.35, stringi 1.5.3, tidyselect 1.1.0, tools 4.0.3, vctrs 0.3.6, withr 2.4.1, xfun 0.20, xml2 1.3.2