# Contrasting TLS-derived orthogonal stem profiles, in poplar plantations

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## Contents

## General scope

Assessment of poplar profiles sensitivity to competition anisotropy and to plantation density. Three plots have been established in a poplar plantation of 10 years in Viadana (Mantova). Poplar rows are alternated with rows of other valuable (but less fast growing) species, one every two poplar rows. Distances from stem to stem within the plantation rows vary between the plots: 4 m, 4.5 m and 5 m. Distance between the the plantation rows is 9 m. Each plot includes 12 stems from two facing rows. Based on TLS-data, stem profiles from two orthogonal vertical crosssections have been determined: one along the rows direction and the other on the between-rows direction. Profiles have been sampled systematically adopting different segment lengths (Segm_lenght) estimating stem crosssection width (diam_btw_rows and diam_wti_rows) at different heigths along the stem (Sect_height)

[MEMO: credo sia opportuno ricordarsi di guardare Rubio-Cuadrado Á, Bravo-Oviedo A, Mutke S, Del Río M (2018). Climate effects on growth differ according to height and diameter along the stem in Pinus pinaster Ait. iForest 11: 237-242. – doi: 10.3832/ifor2318-011 [online 2018-03-12]]

## Setup and fetch the data

```
library(tidyverse)
library(magrittr)
library(ggplot2)

source("DataWrangling.R")
```

# Data synthesis

```r
library(knitr)

tff %>%
  select(Treat, TreeId, dbh = DBH) %>%
  unique() %>%
  ggplot(aes(y = dbh, x = Treat)) + geom_boxplot(colour = "darkgrey") +
  geom_jitter(width = .1, height = 0.15) +
  ggtitle("Effect of plantation density on brest height diametr (dbh)") +
  ylab("dbh [cm]")
```

## Effect of plantation density on brest height diametr (dbh)
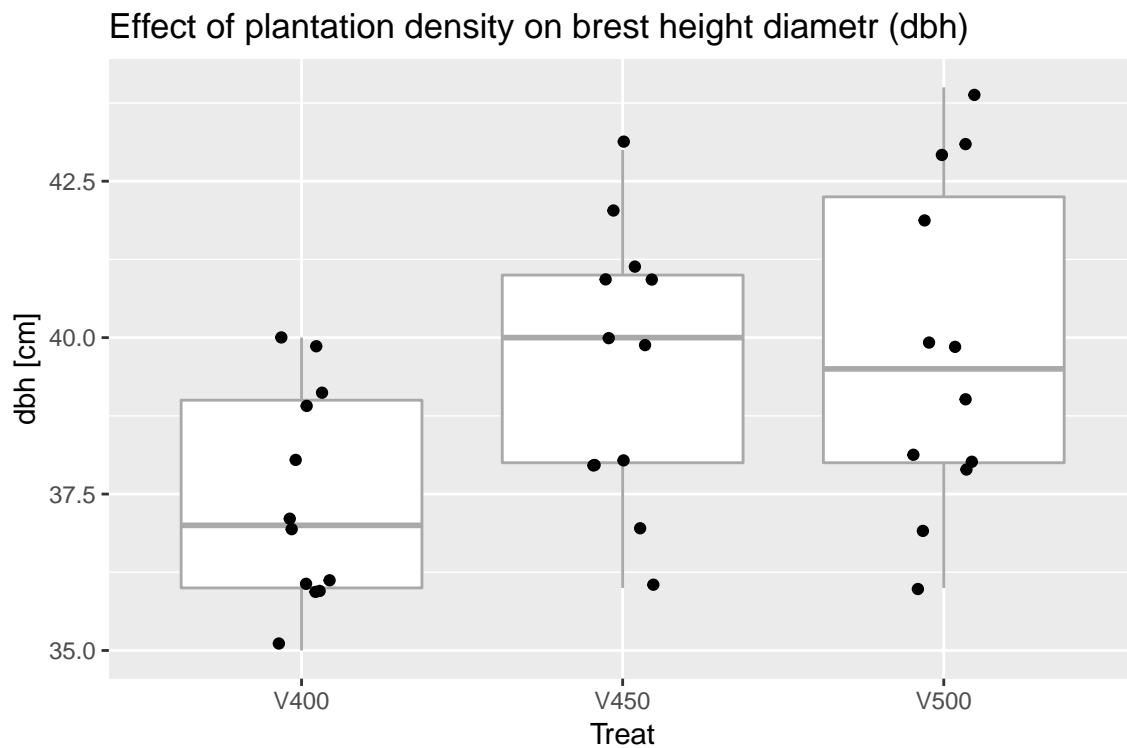


```r
tff %>%
  select(Treat, TreeId, dbh = DBH) %>%
  unique() %>%
  lm(dbh ~ Treat, data = .) %>%
  summary() %>% tidy() %>%
  kable(digits = 3, format.args = list(zero.print = F),
        caption = "Plantation density effect on 'dbh'")
```

Table 1: Plantation density effect on 'dbh'

| term | estimate | std.error | statistic | p.value |
|------|----------|-----------|-----------|---------|
| (Intercept) | 37.417 | 0.635 | 58.957 | |
| TreatV450 | 2.167 | 0.898 | 2.414 | 0.021 |
| TreatV500 | 2.417 | 0.898 | 2.693 | 0.011 |

2

```
TLSdbh_df <- tff %>%
  filter(abs(1.3 - Sect_height)<.0001) %>%
  select(Treat, treid, TreeId, dbh = DBH, starts_with('diam')) %>%
  gather(direction, TLSdbh, starts_with('diam')) %>%
  mutate(TLSdbh = 100 * TLSdbh)

TLSdbh_df %>%
  lm(TLSdbh ~ Treat + direction, data = .) %>%
  summary() %>% tidy() %>%
  kable(digits =c(0, 2, 3, 3, 5),
        caption = "Plantation density and measurement directions effects on TLS estimated dbh")
```

Table 2: Plantation density and measurement directions effects on
TLS estimated dbh

| term | estimate | std.error | statistic | p.value |
|------|----------|-----------|-----------|---------|
| (Intercept) | 37.54 | 0.540 | 69.560 | 0.00000 |
| TreatV450 | 2.09 | 0.661 | 3.158 | 0.00237 |
| TreatV500 | 2.60 | 0.661 | 3.928 | 0.00020 |
| directiondiam_wti_rows | -1.84 | 0.540 | -3.401 | 0.00113 |

In the observed conditions poplar stems display an elliptical crosssection: width measured along the direction
where competiors a nearer (within plantation rows) is almost 2 cm smaller than the orthogonal measure
(between rows, where the competing subjects are relatively further away).
The difference observed at brest height level corresponds to the gross average of the differences measured up
to 5 m along the stem.

## To be careful about!

```
TLSdbh_df %>%
  spread(direction, TLSdbh) %>%
  mutate( dbh = jitter(dbh, factor = 1)) %>%
  ggplot(aes(x = dbh, color = Treat)) +
  geom_abline(slope=1, color = "grey") +
  geom_errorbar(aes(ymin=diam_wti_rows, ymax=diam_btw_rows),
                width = .2, linetype =2, size = .5) +
  geom_line(aes(y = I((diam_wti_rows + diam_btw_rows)/2))) +
  geom_point(aes(y = I((diam_wti_rows + diam_btw_rows)/2)), shape = 1) +
  scale_x_continuous(breaks = seq(0, 100, 1), minor_breaks = NULL) +
  scale_y_continuous(breaks = seq(0, 100, 1), minor_breaks = NULL) +
  ggtitle("Field measured dbh and corresponding TLS estimates",
          subtitle = "between- and within-rows estiamates by plantation density")
```

Field measured dbh and corresponding TLS estimates

between– and within–rows estiamates by plantation density

I((diam_wti_rows + diam_btw_rows)/2)

dbh

Treat

V400

V450

V500
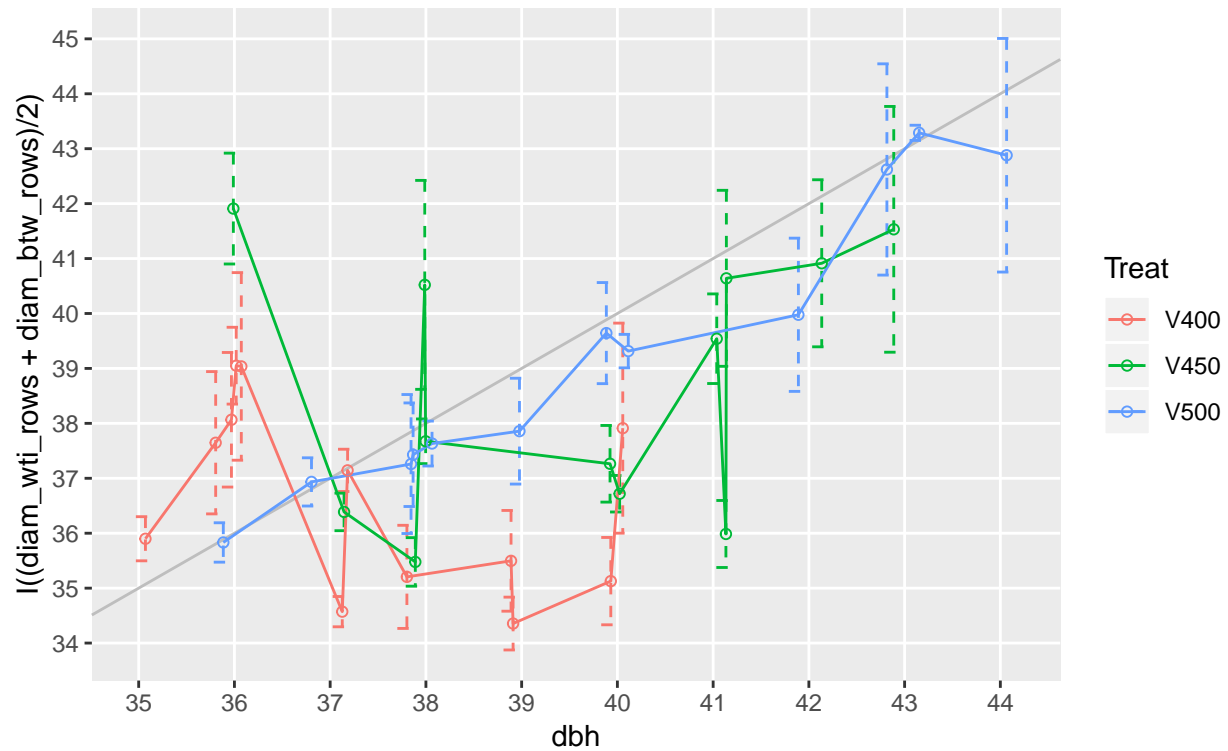
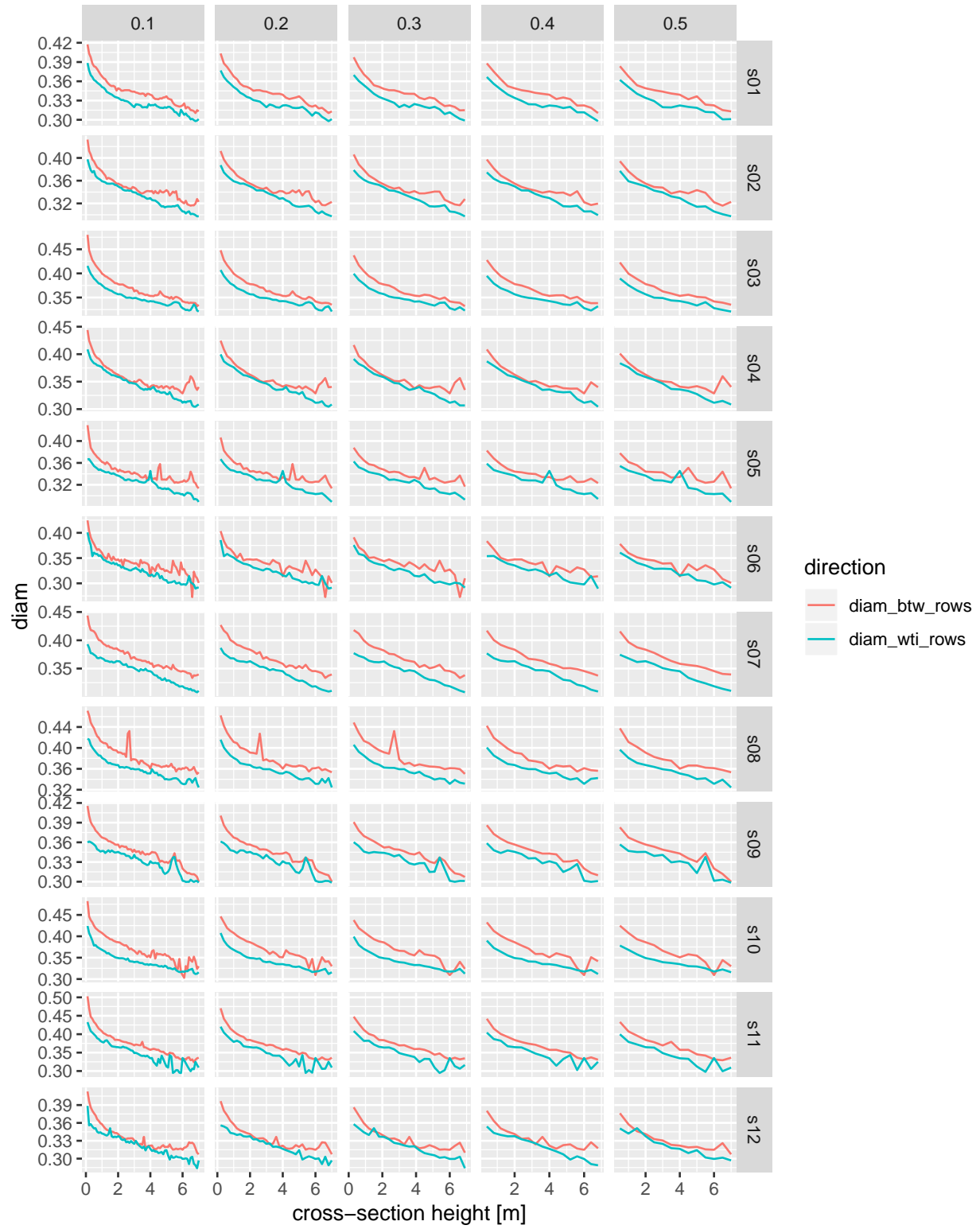## Plot all profiles

```
Diameters <- TLSderivedDiam %>%
  select( -ends_with("centro")) %>%
  filter(complete.cases(.)) %>%
  gather(direction, diam, starts_with("diam"))

gl <- Diameters %$%
  levels(tesi) %>%
  map(
    ~ Diameters %>%
      filter(tesi == .x) %>%
      ggplot(aes(slice, diam)) +
      xlab("cross-section height [m]") +
      geom_line(aes(color = direction)) +
      facet_grid(treid ~ length_toppo, scales = "free") +
      ggtitle(paste0("Tesis: '", .x, "'")) +
      theme(plot.title = element_text(hjust = 0.5))
  )
print(gl)
```
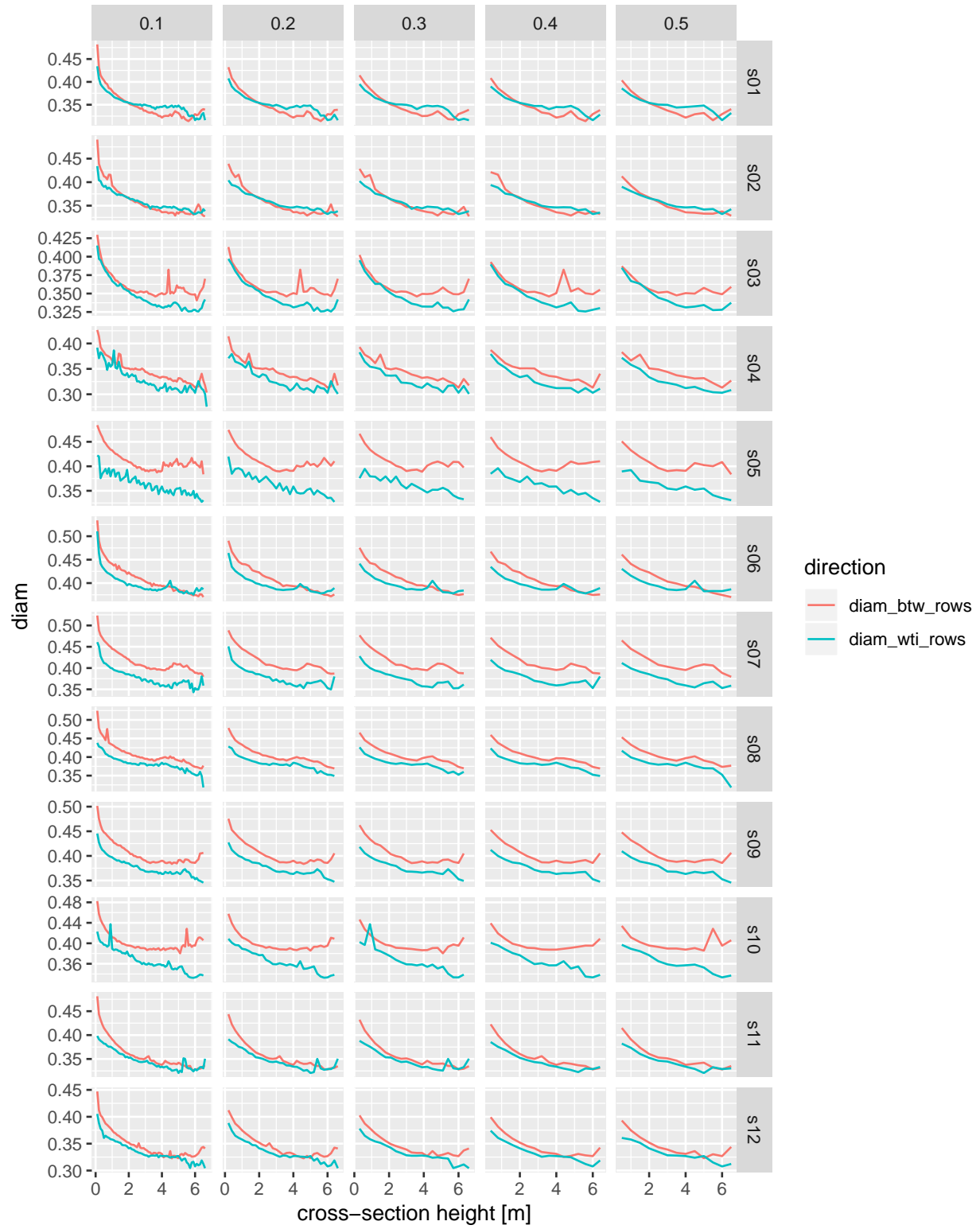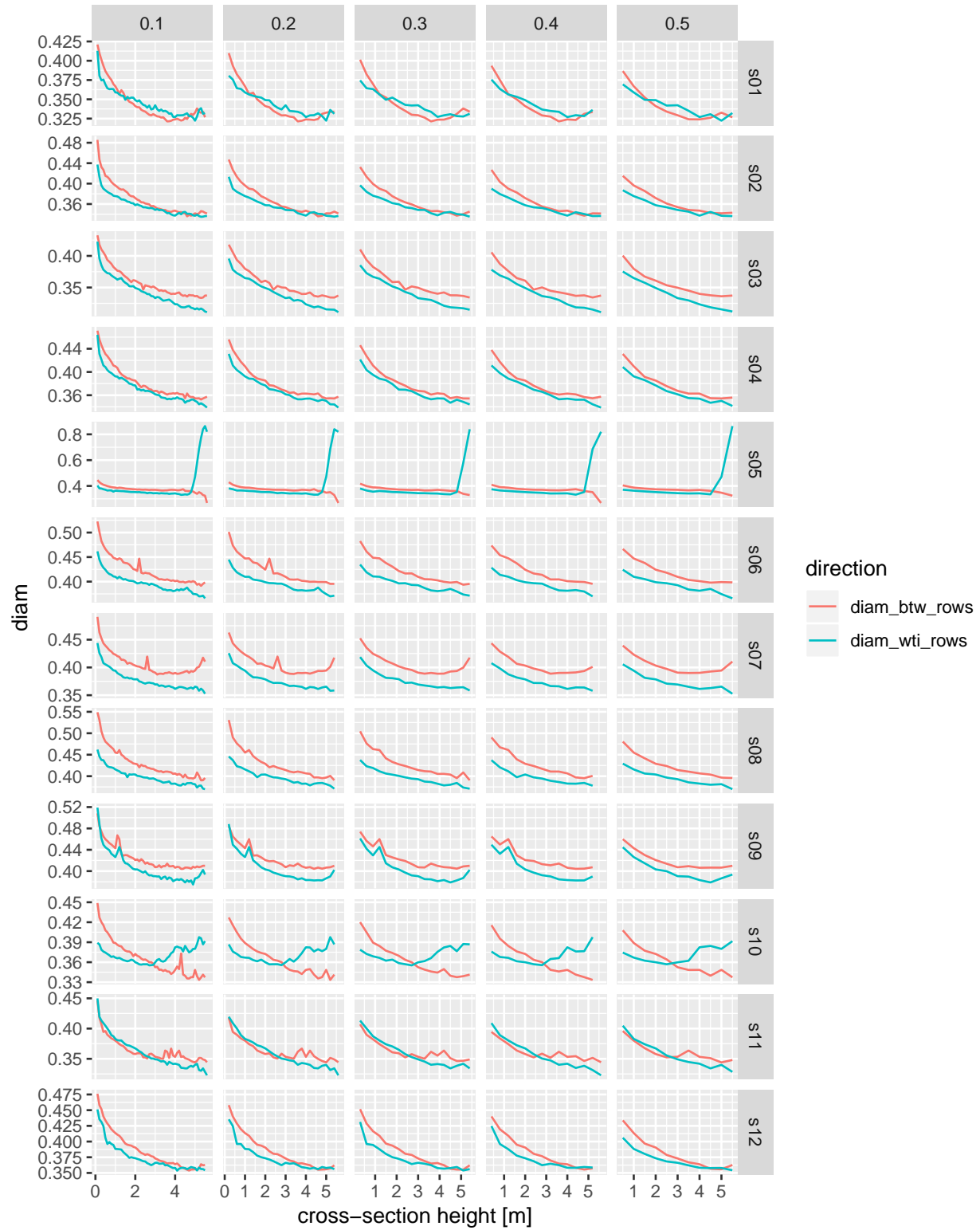
```
## [[1]]
```

Tesis: 'V400'

## 
## [[2]]

Tesis: 'V450'

```
## 
## [[3]]
```

Tesis: 'V500'

```
# install.packages("svglite")
for(i in 1:3) ggsave(paste0("AllProfiles",i,".svg"), gl[[i]], scale = 2)
```

```
## Saving 14 x 18 in image
## Saving 14 x 18 in image
## Saving 14 x 18 in image
```

## Selection of the most convenient segment length level for detailed analysis

```
tff %>%
  filter(complete.cases(.)) %>%
  select(Segm_length, Sect_height) %>%
  unique() %$%
  table(Segm_length) %>% t() %>%
  cbind(t(matrix("freq", dimnames = list("segment length") )), .) %>%
  kable( align = 'c',
         caption = "Number of sections estimated on each tree for each segment-length level")
```

Table 3: Number of sections estimated on each tree for each segment-length level

| segment length | 0.1 | 0.2 | 0.3 | 0.4 | 0.5 |
|:---:|:---:|:---:|:---:|:---:|:---:|
| freq | 55 | 27 | 18 | 13 | 11 |

```
tff %>%
  group_by(Segm_length, Treat) %>%
  summarise(mean_delta = mean(delta_d_cm)) %>%
  ggplot(aes(x = Segm_length, y = mean_delta, colour = Treat)) +
  geom_point() + geom_line() +
  ylab("BetweenRowsDiam - WithinRowsDiameter [cm] Averages") +
  xlab("Lenght of analysis segments [m]") +
  ggtitle("Stem crosssections are significantly wider in the direction with less competition (between pl
```

Stem crosssections are significantly wider in the direction with less competi
 Average difference between orthogonal profiles are clearly greather at lowe
Length of analysis segments has little influence, but ... (next graph)
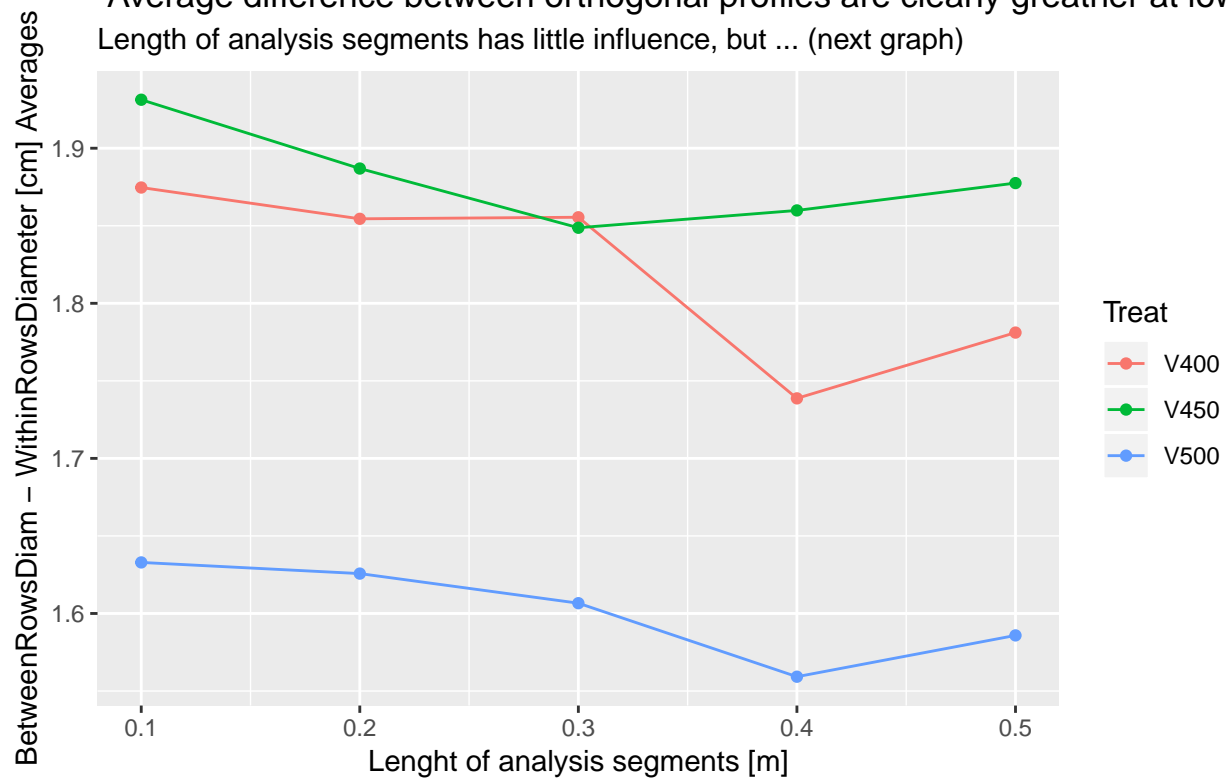


```
tff %>%
  ggplot(aes(x = Treat, y = delta_d_cm, colour = Treat)) +
  geom_boxplot() +
  stat_summary(fun.y = mean, geom = "point", shape = 13, size = 4) +
  facet_grid(~Segm_length, labeller = label_both) +
  ylab("BetweenRowsDiam - WithinRowsDiameter [cm]") +
  ggtitle("The variability of the difference between orthogonal profiles\n hides completely the effect
```

## The variability of the difference between orthogonal profiles
 hides completely the effect of plantation density (means = crossed circles)
Will tree level modelling let the effect emerge?
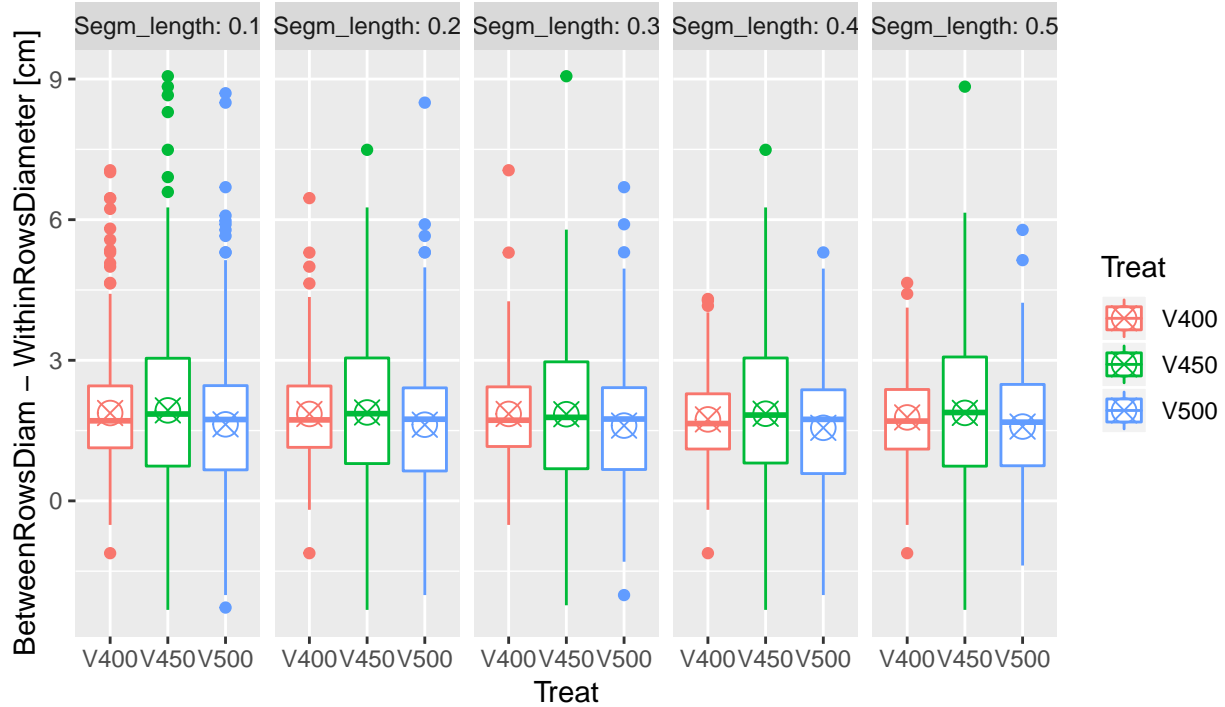


```
tff %>%
  group_by(Segm_length) %>%
  do( fit = tidy(lm(data = ., delta_d ~ Treat * TreeId ))) %>%
  unnest() %>%
  filter(substr(term, 1, 5) %in% c("Treat")) %>%
  select(-c(3:5)) %>%
  spread(term, p.value) %>%
  kable(caption = "ANOVA p.values for Treat by Segm_length from: lm(delta_d ~ Treat * TreeId) ")
```

Table 4: ANOVA p.values for Treat by Segm_length from: lm(delta_d ~ Treat * TreeId)

| Segm_length | TreatV450 | TreatV500 |
|---|---|---|
| 0.1 | 0.0017793 | 0.0069014 |
| 0.2 | 0.0088386 | 0.0245643 |
| 0.3 | 0.0430879 | 0.0825336 |
| 0.4 | 0.0962377 | 0.0698999 |
| 0.5 | 0.1407219 | 0.1240557 |

```
oll <- 0.1 # optimal Log Length for profiles discrimination
# Segm_length ottimale: compromesso tra min lag correlation e conservazione del dettaglio della forma
stff <- tff %>%
  filter(Segm_length == oll)
```

# Profile's difference analysed by Hierarchical Linear Modeling (HLM)

Tree level modelling has been developed based on crossesctions estimated dividing the stem in segments of 0.1 meters.

```r
library(lme4)
library(HLMdiag)
```

```
##
## Attaching package: 'HLMdiag'

## The following object is masked from 'package:stats':
##
##     covratio
```

```r
mc <- function(frml, main = paste0(as.expression(frml)), ...) {
# evaluate the model (specified as formula) and produce the residulas control plot
  fm <- stff %>%  lmer(data = ., frml, ... )
  p <- qplot(x = stff$Sect_height, y = residuals(fm),
        geom = c("point", "smooth")) +
    xlab("cross-section height [m]") +
    ylab("level-1 residuals") +
    ggtitle(main)
  print(p)
return(fm)
}

# prova CON Sect_height, al cubo (con RML=T, non converge!)
fm13 <- mc(delta_d_cm ~ Treat + (1 | TreeId)
          + Sect_height *(1 | TreeId)
          + I(Sect_height^2)* (1 | TreeId)
          + I(Sect_height^3)* (1 | TreeId)
          , REML = F
          , main = "delta_d ~ Treat + (poly(Sect_height, 3)| TreeId)")
```

```
## `geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```

## delta_d ~ Treat + (poly(Sect_height, 3)| TreeId)
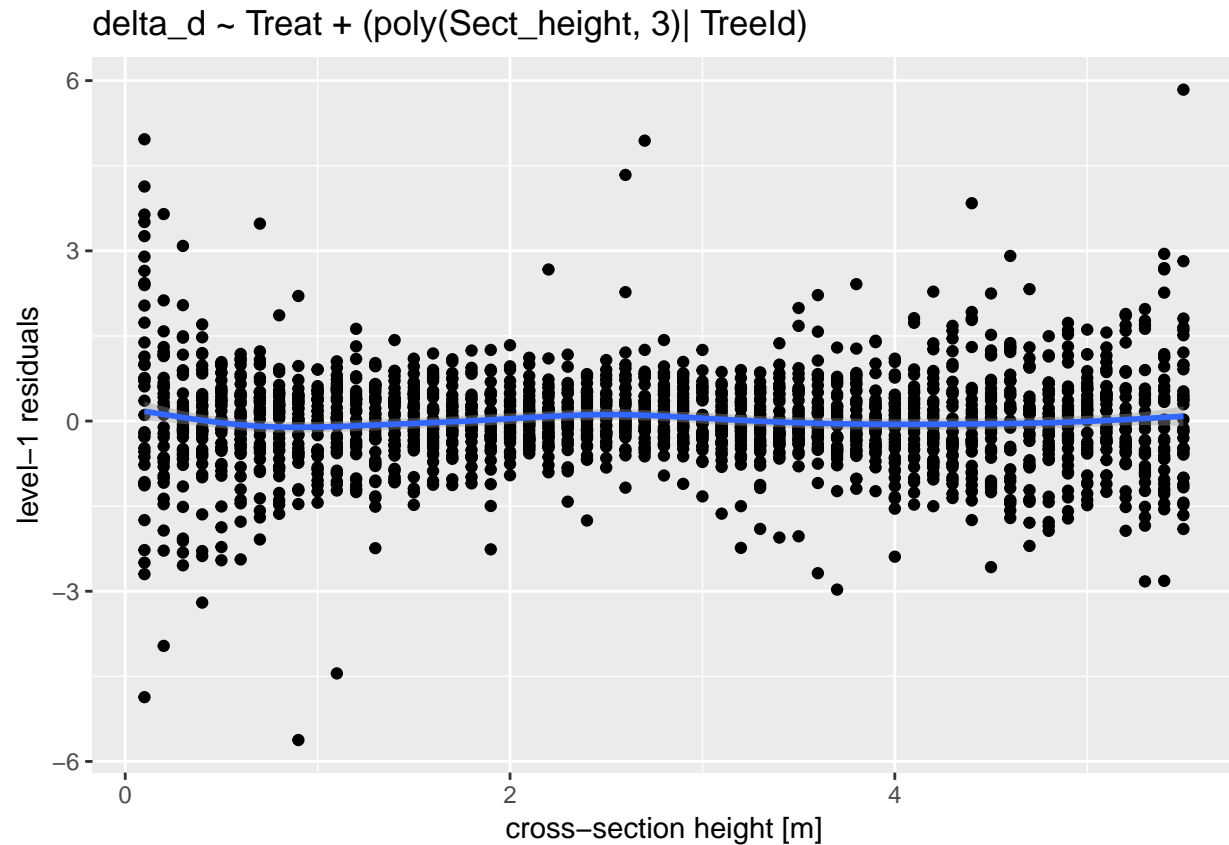


```
stff %>% ggplot() +
  geom_point(aes(x = Sect_height, y = delta_d_cm)) +
  geom_smooth(aes(x = Sect_height, y = delta_d_cm)) +
  geom_line(aes(x = Sect_height, y = fitted(fm13)), color = "yellow", size = 1) +
  facet_wrap(~TreeId) +
  ggtitle("Nested models fitting profile differences by tree")
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

Nested models fitting profile differences by tree
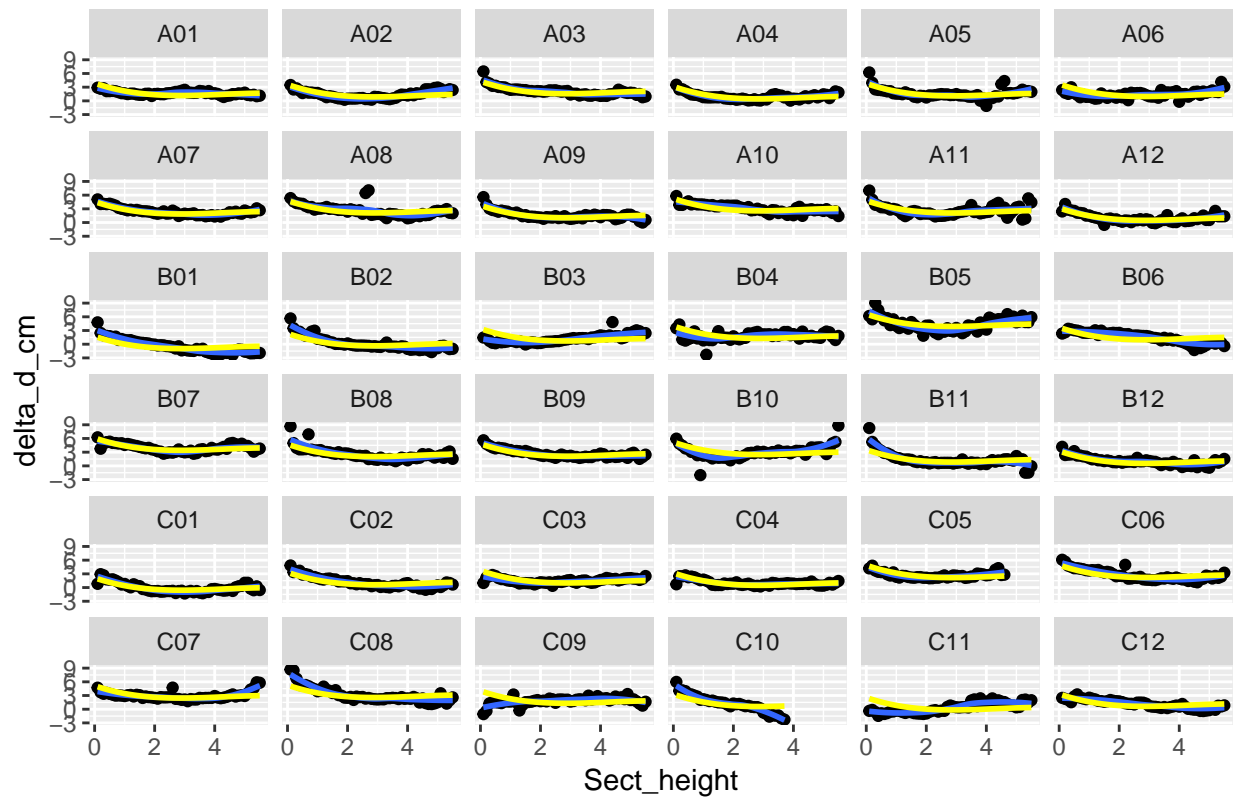


```
resid2_fm13 <- HLMresid(object = fm13, level = "TreeId")
names(resid2_fm13) <- paste0("pw",0:3,"coeff")
# head(resid2_fm13)

stff %>%
  select(Treat, TreeId) %>%
  unique() %>%
  inner_join(mutate(resid2_fm13, TreeId = row.names(resid2_fm13))) %>%
  gather(param, value,  3:6) %>%
  ggplot(aes(x = Treat, y = value)) +
  geom_boxplot(color = "darkgrey") +
  geom_jitter(width = .15, height = 0) +
  geom_hline(yintercept = 0) +
  facet_wrap(~param, scales = "free") +
  ggtitle("Level 2 (Treat = plantation distance) residuals")
```

```
## Joining, by = "TreeId"
```

## Level 2 (Treat = plantation distance) residuals
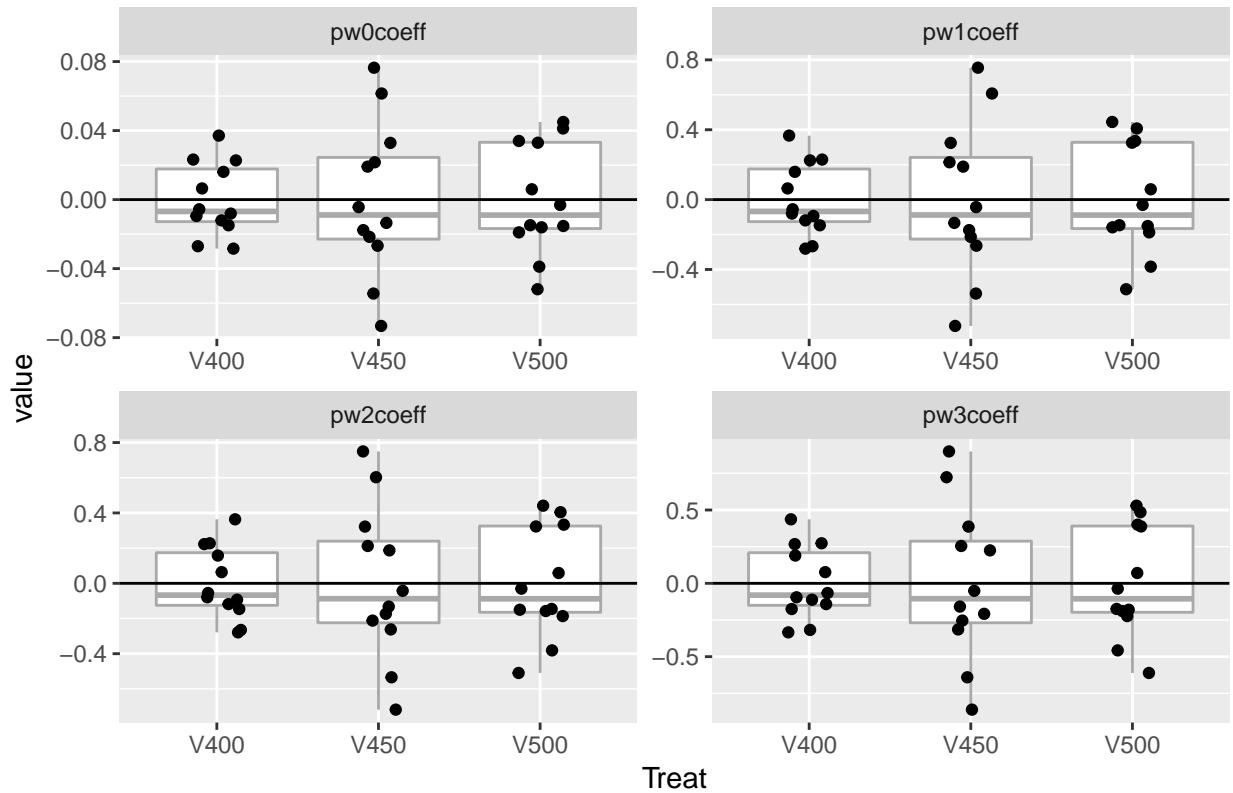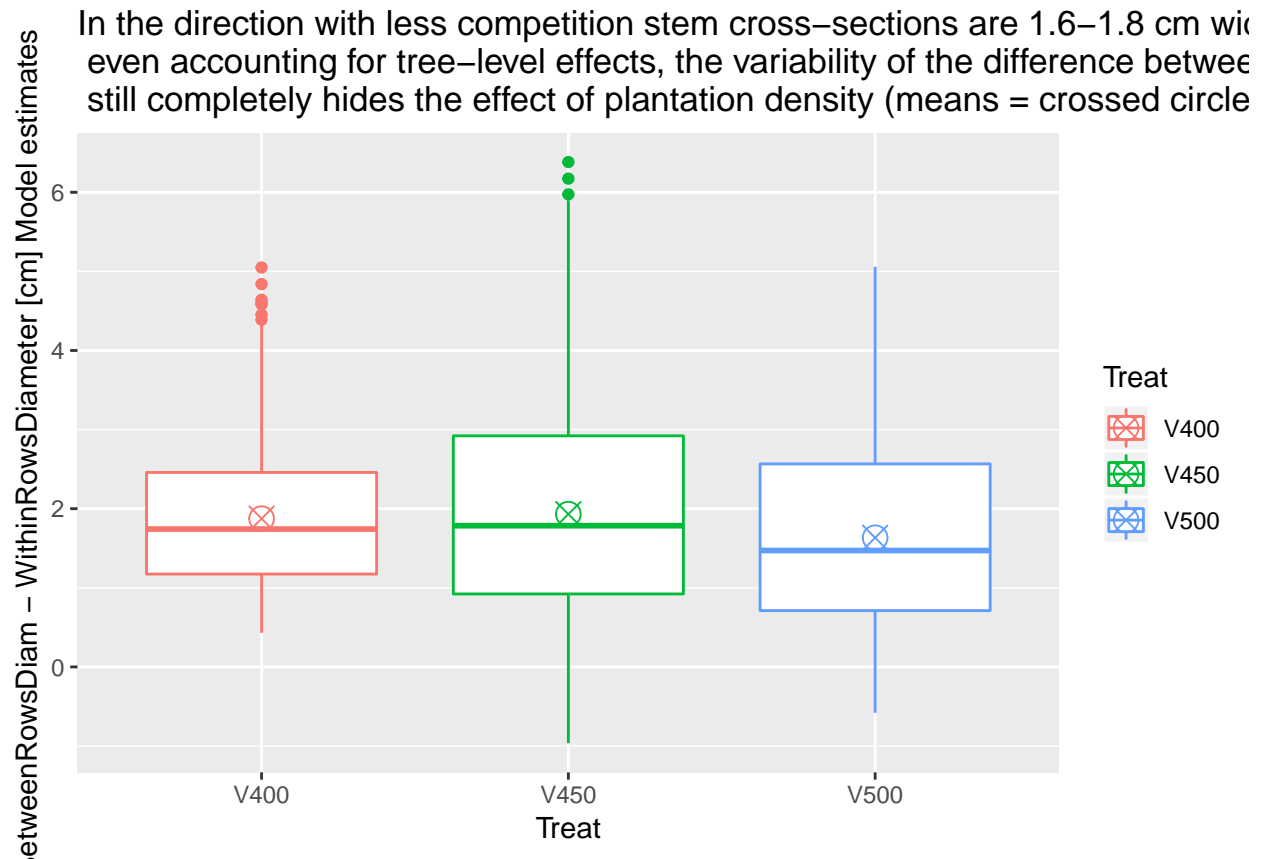


```
Treat_anova <- stff %>%
  lmer(data = ., delta_d_cm ~
             1 * (1 | TreeId)
         + Sect_height *(1 | TreeId)
         + I(Sect_height^2)* (1 | TreeId)
         + I(Sect_height^3)* (1 | TreeId)
         , REML = F) %>%
  anova(fm13)

Treat_anova %>%
  mutate_all(funs(ifelse(is.na(.), 0, .))) %>%
  kable(digits = c(0, 2, 2, 2, 2, 4, 0, 4), format.args = list(zero.print = F),
    caption = cat(paste("Contribution of plantation distance (Treat) to profiles differences variance e
```

```
## Contribution of plantation distance (Treat) to profiles differences variance explaination Models:
## .: delta_d_cm ~ 1 * (1 | TreeId) + Sect_height * (1 | TreeId) +
## .:     I(Sect_height^2) * (1 | TreeId) + I(Sect_height^3) * (1 |
## .:     TreeId)
## fm13: delta_d_cm ~ Treat + (1 | TreeId) + Sect_height * (1 | TreeId) +
## fm13:     I(Sect_height^2) * (1 | TreeId) + I(Sect_height^3) * (1 |
## fm13:     TreeId)
```

| Df | AIC | BIC | logLik | deviance | Chisq | Chi Df | Pr(>Chisq) |
|----|-----|-----|--------|----------|-------|--------|------------|
| 9 | 5150.99 | 5201.19 | -2566.50 | 5132.99 | | | |
| 11 | 5154.44 | 5215.79 | -2566.22 | 5132.44 | 0.5501 | 2 | 0.7595 |

```
fm13 %>%
  augment() %>%
  ggplot(aes(x = Treat, y = .fitted, colour = Treat)) +
  geom_boxplot() +
  stat_summary(fun.y = mean, geom = "point", shape = 13, size = 4) +
  ylab("BetweenRowsDiam - WithinRowsDiameter [cm] Model estimates") +
  ggtitle("In the direction with less competition stem cross-sections are 1.6-1.8 cm wider but,\n even a
```



In the direction with less competition stem cross−sections are 1.6−1.8 cm wid
even accounting for tree−level effects, the variability of the difference betwee
still completely hides the effect of plantation density (means = crossed circle

[rmarkdown::render("AnalysisOfTLSbasedOrthogonalStemProfiles_inArectangulalySpacedPoplarPlantation.Rmd", encoding="UTF-8")]