The Tomato example: illustrating the smoothing and extraction of traits (SET) using growthPheno Version 2.x

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This vignette illustrates the use of the two `growthPheno` (Brien, 2025) wrapper functions `traitSmooths` and `traitExtractFeatures` that are key to carrying out the smoothing and extracting traits (SET) method described by Brien et al. (2020). The Tomato example, used here, is the example that Brien et al. (2020) used to illustrate the SET method. More details on the rationale for this method are available in Brien et al. (2020, Methods section).

Here, the process has been modified from that described in the paper to take advantage of the new wrapper functions and other new capabilities that have been built into in Version 2.x of `growthPheno`. In particular, both natural cubic smoothing splines (NCSS) and P-splines (PS) are investigated for smoothing not only the Projected Shoot Area (PSA), but also the Water Use (WU). A segmented smooth, as suggested in Brien et al. (2020), is used to allow for a discontinuity in the growth resulting from unintentional, restricted watering for three days following imaging on DAP 39.

Two different approaches are shown for smoothing the two traits:

PSA: For this trait, we first use `traitSmooths` to compare several smooths using logaritmic smoothing and then automatically choose a P-spline smooth whose `lamda` value is in the middle of the values for which smooths have been obtained. This is then followed by a comparison of two contending smooths. Finally, the chosen smooth is extracted and added to the data.

WU: A more time-efficient approach is taken with this trait. First several direct smooths are compared and stored. Then plots of two contending smooths amongst the stored smooths are compared. Finally the chosen smooth is extracted from the stored smooths.

Initialize

Set up characters for variable names and titles

```
# The responses
responses <- c("PSA", paste("PSA", c("AGR", "RGR"), sep = "."))
responses.smooth <- paste0("s", responses)

# Specify time intervals of homogeneous growth dynamics
DAP.endpts   <- c(18,22,27,33,39,43,51)
nDAP.endpts <- length(DAP.endpts)
DAP.starts <- DAP.endpts[-nDAP.endpts]
DAP.stops   <- DAP.endpts[-1]
DAP.segs <- list(c(DAP.endpts[1]-1, 39),
                 c(40, DAP.endpts[nDAP.endpts]))
```

```
tune.fac <- c("Method","Type","Tuning")
#Functions to label the plot facets
labelAMF <- as_labeller(function(lev) paste(lev, "AMF"))
labelZn <- as_labeller(function(lev) paste("Zn:", lev, "mg/kg"))
vline.water <- list(geom_vline(xintercept=39, linetype="longdash",
                               alpha = 0.3, linewidth=1))
vline.DAP.endpts <- list(geom_vline(xintercept=DAP.starts, linetype="longdash",
                                   colour = "blue", alpha = 0.5, linewidth=0.75))
```

Step I: Import the longitudinal data

In this step, the aim is to produce the data.frame `longi.dat` that contains the imaging variables, covariates and factors for the experiment.

Load the pre-prepared data

```
data(tomato.dat)
```

Copy the data to preserve the original data.frame

```
longi.dat <- tomato.dat
```

Step II: Investigate the smoothing of the PSA and obtain growth rates

The growth rates are the Absolute Growth Rate (AGR) and the Relative Growth Rate (RGR) for the PSA, which must be calculated from the observed data by differencing consecutive observations for a plant. They will also be calculated from the smoothed traits by differencing, although `growthPheno` can also obtain growth rates using the first derivatives of the smooths.

Fit three-parameter logistic curves logistic curves to compare with spline curves

We fit a three-parameter logistic curve, using `nlme` (Pinheiro J., Bates D., and R Core Team, 2023), as an alternative to spline smoothing.

Organize non-missing data into a grouped object

```
logist.dat<- na.omit(longi.dat)
logist.grp <- nlme::groupedData(PSA ~ cDAP | Snapshot.ID.Tag,
                                data = logist.dat)
```

Fit logistics to individuals and obtain fitted values

```
logist.lis <- nlme::nlsList(SSlogis, logist.grp)
logist.dat$sPSA <- fitted(logist.lis)
logist.dat <- cbind(Tuning = factor("Logistic"), logist.dat)
```

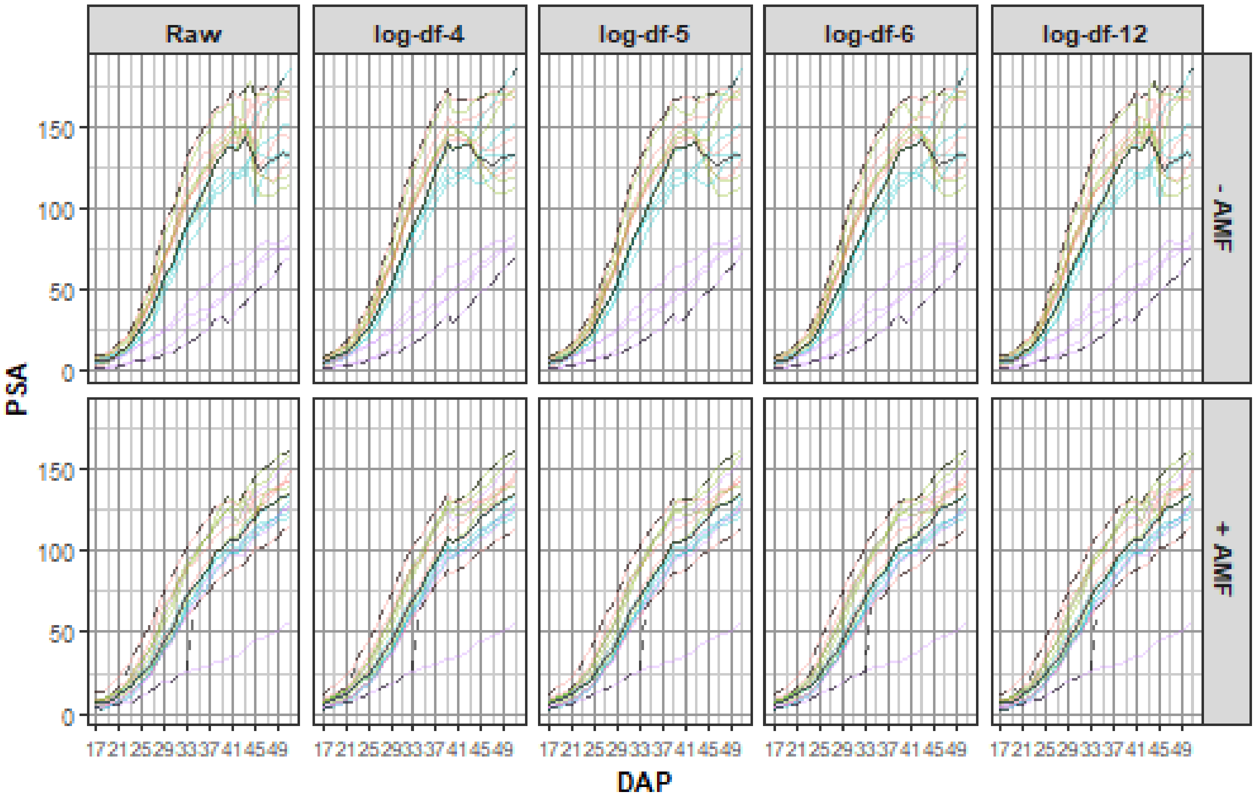
Compute smooths and growth rates of the PSA for a range of smoothing parameters

We begin by using the function `traitSmooth` to investigate a set of smooths for the PSA, employing all five `traitSmooth` steps of (i) Smooth, (ii) Profile plots, (iii) Median deviations plots, (iv) Choose a smooth, and (v) Chosen smooth plot. The only changes to the defaults for these five steps are to the df values that are investigated and to specify segmented smoothing. This includes allowing `traitSmooth` to choose automaticaly a single smooth as the chosen smooth. A segmented smooth involving two segments has also been specified, as suggested by Brien et al. (2020). The breakpoint for the segments is DAP 39, it coinciding with the start of an unintentional, three-day restriction in the watering; thus, the segments consist of DAP 18–39 and DAP 40–51. The growth rates are calculated, by default, from both the unsmoothed trait PSA and the smoothed trait sPSA by difference, rather than from the spline derivatives. Thus, the growth rate calculation for the smoothed data matches that which is obligatory for the observed data. Also, three-parameter logistic curves are fitted to the data using the `R` package `nlme` and growth rates calculated for it. The default layouts of the three sets of plots produced are mdofified using the three arguments `profile.plot.args`, `meddevn.plot.args` and `chosen.plot.args`.

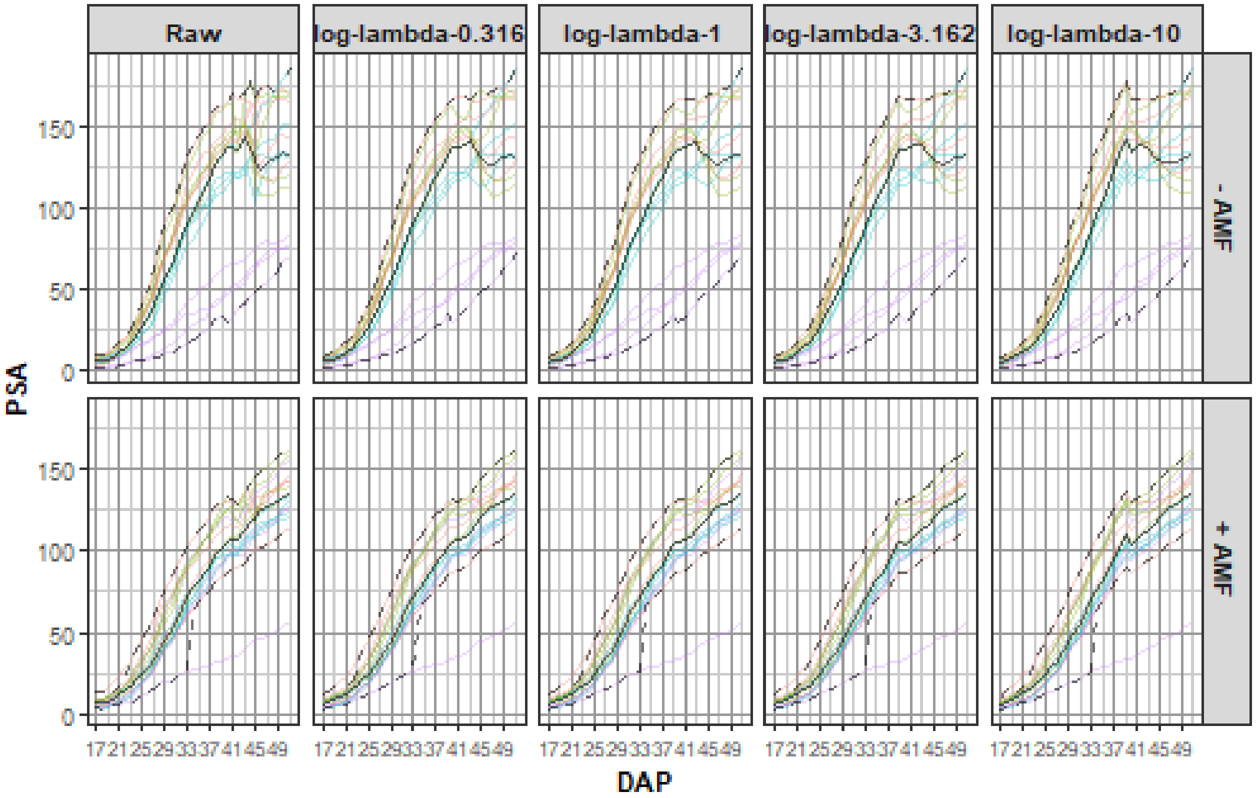
It is noted that the plots that are produced show that the logistic would not be an adequate fit for this data, especially after DAP 42.

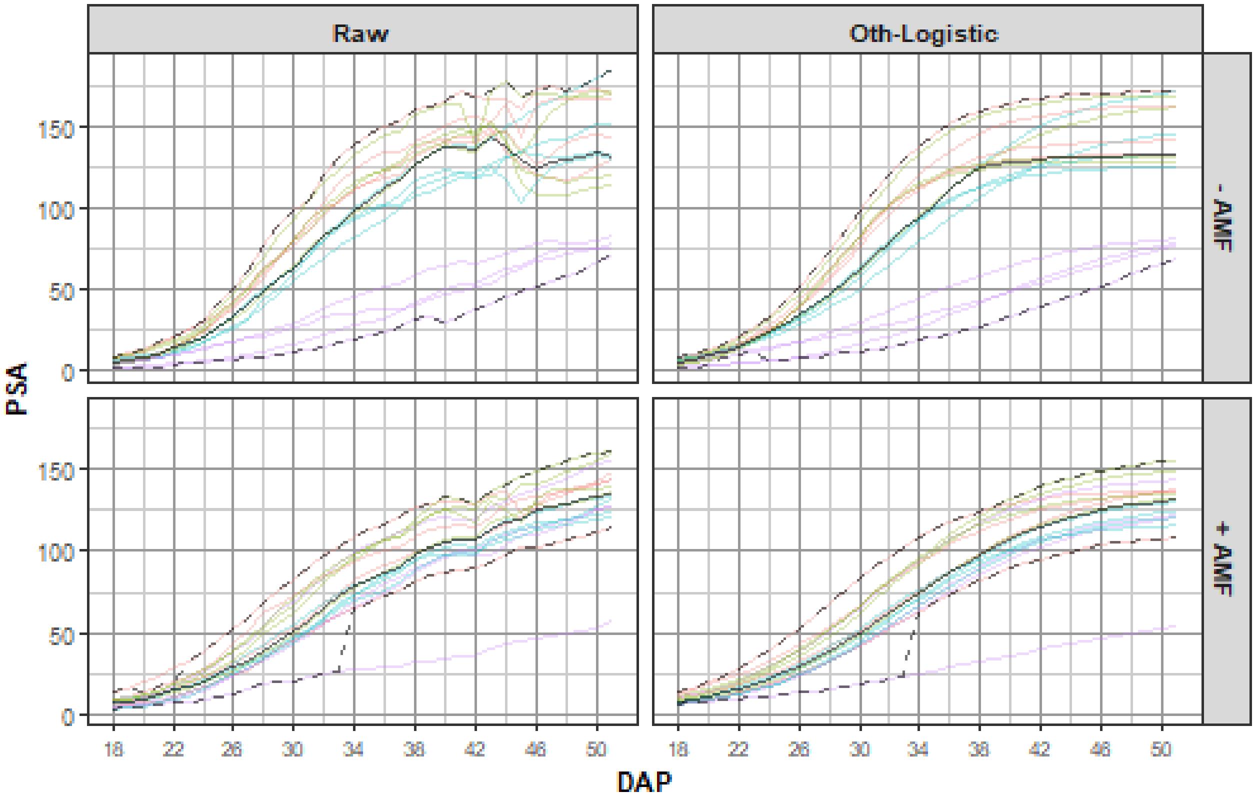
```
suppressWarnings(
  longi.dat <- traitSmooth(data = tomato.dat,
                           response = "PSA", response.smoothed = "sPSA",
                           individuals = "Snapshot.ID.Tag", times = "DAP",
                           keep.columns = c("AMF","Zn"),
                           smoothing.args = args4smoothing(df = c(4:6,12),
                                                           smoothing.segments = DAP.segs,
                                                           external.smooths = logist.dat),
                           profile.plot.args =
                             args4profile_plot(facet.y = "AMF",
                                               colour.column = "Zn",
                                               facet.labeller = labeller(AMF = labelAMF)),
                           meddevn.plot.args =
                             args4meddevn_plot(facet.y = "AMF",
                                               facet.labeller = labeller(AMF = labelAMF)),
                           chosen.plot.args =
                             args4chosen_plot(facet.y = "AMF",
                                              facet.labeller = labeller(AMF = labelAMF),
                                              colour.column = "Zn",
                                              ggplotFuncs = vline.DAP.endpts),
                           mergedata = tomato.dat))
```

Plot for NCSS

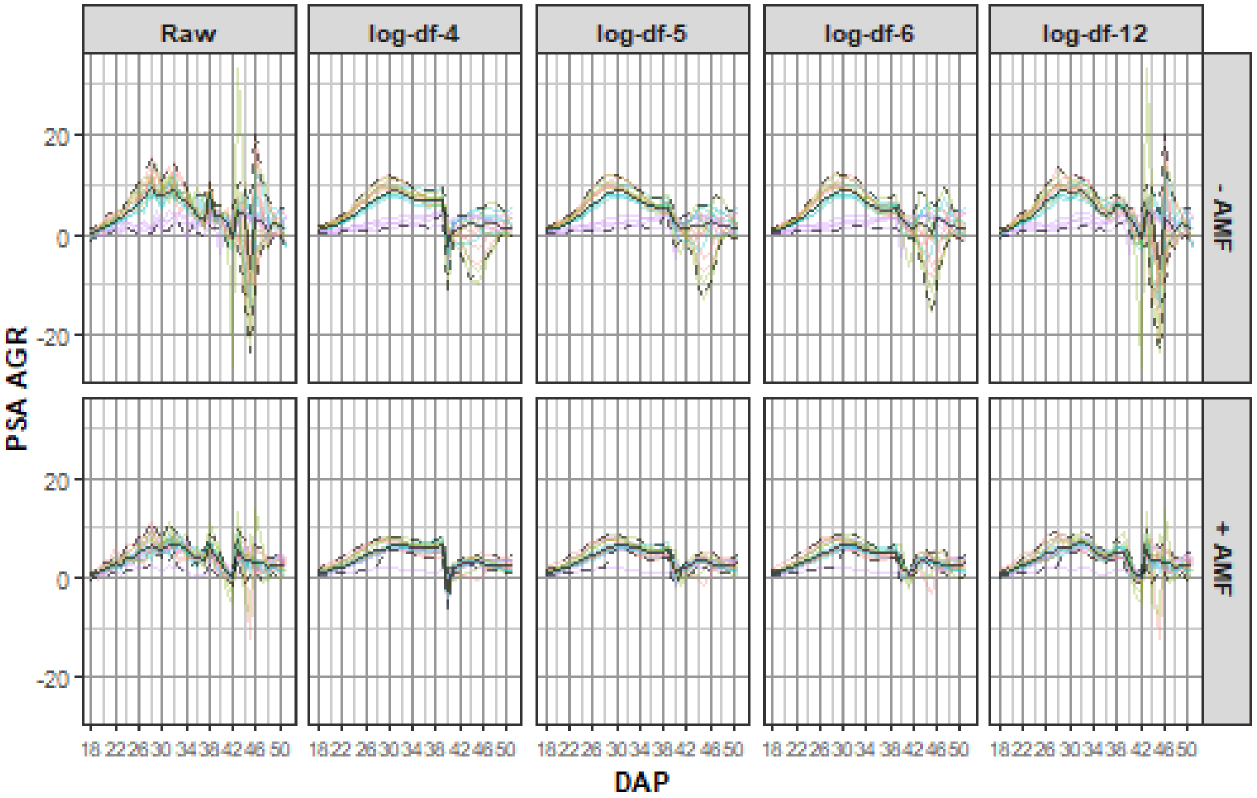


Plot for PS

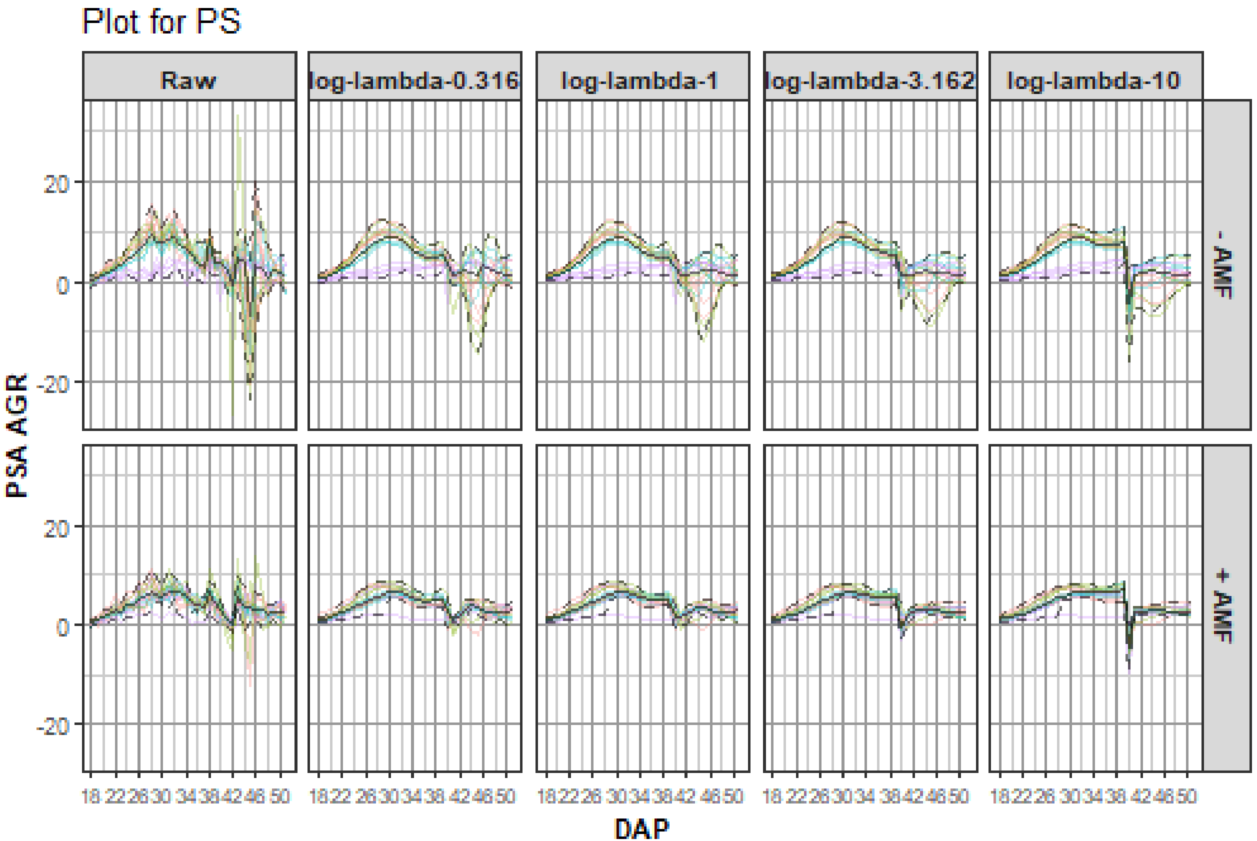


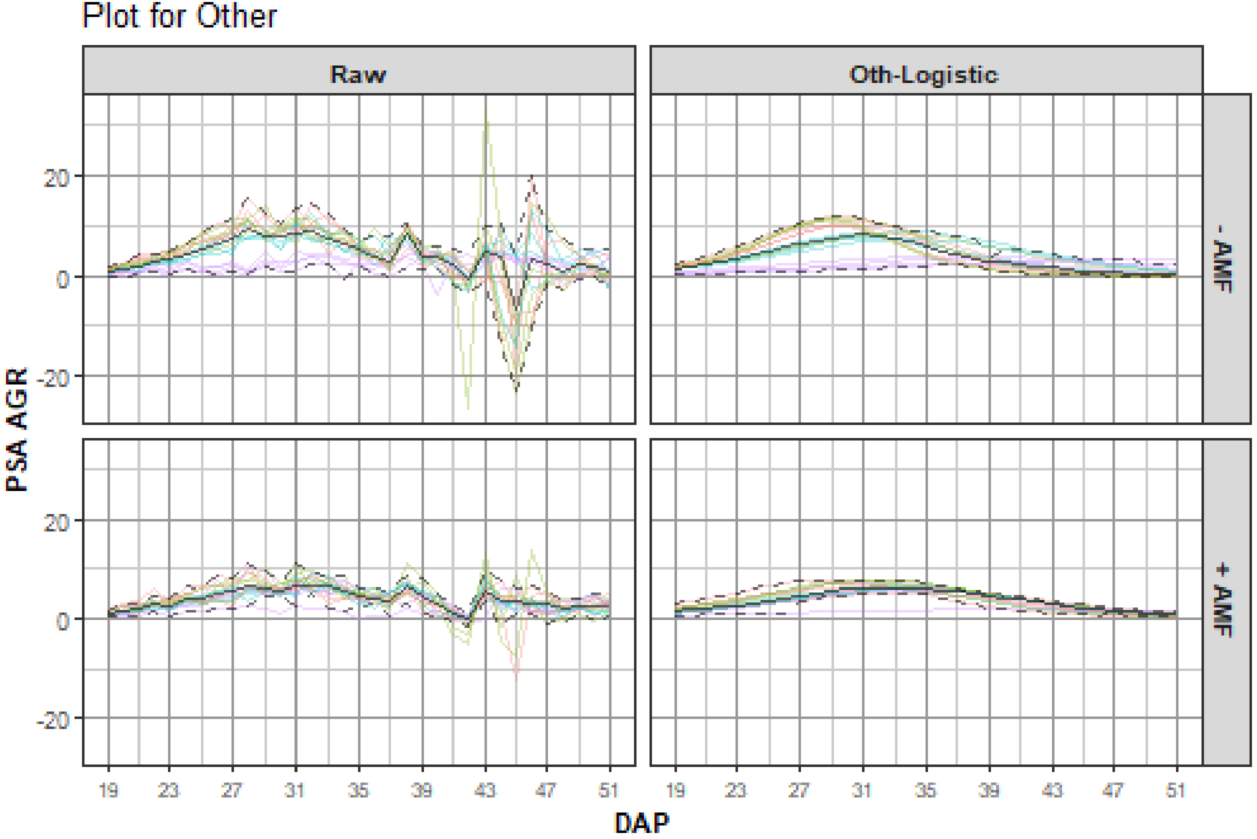


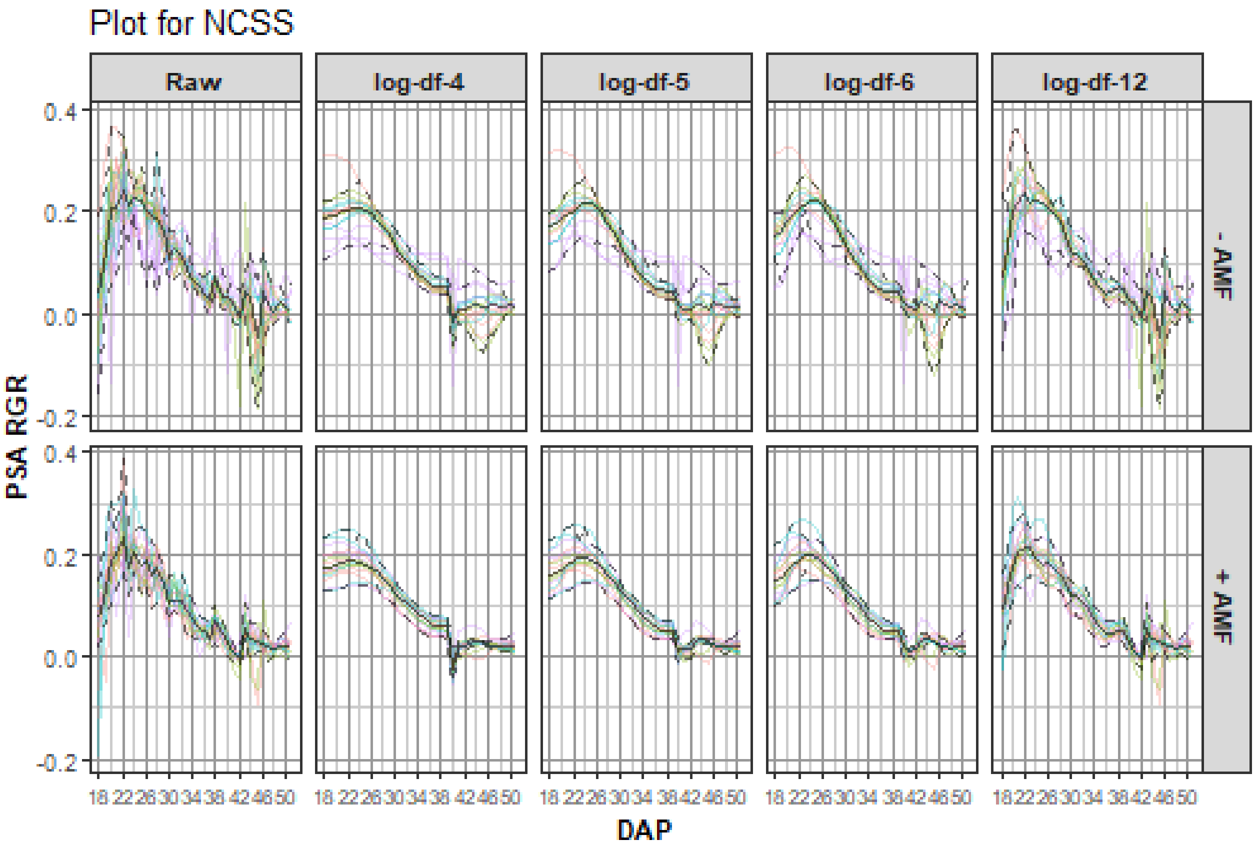
Plot for Other



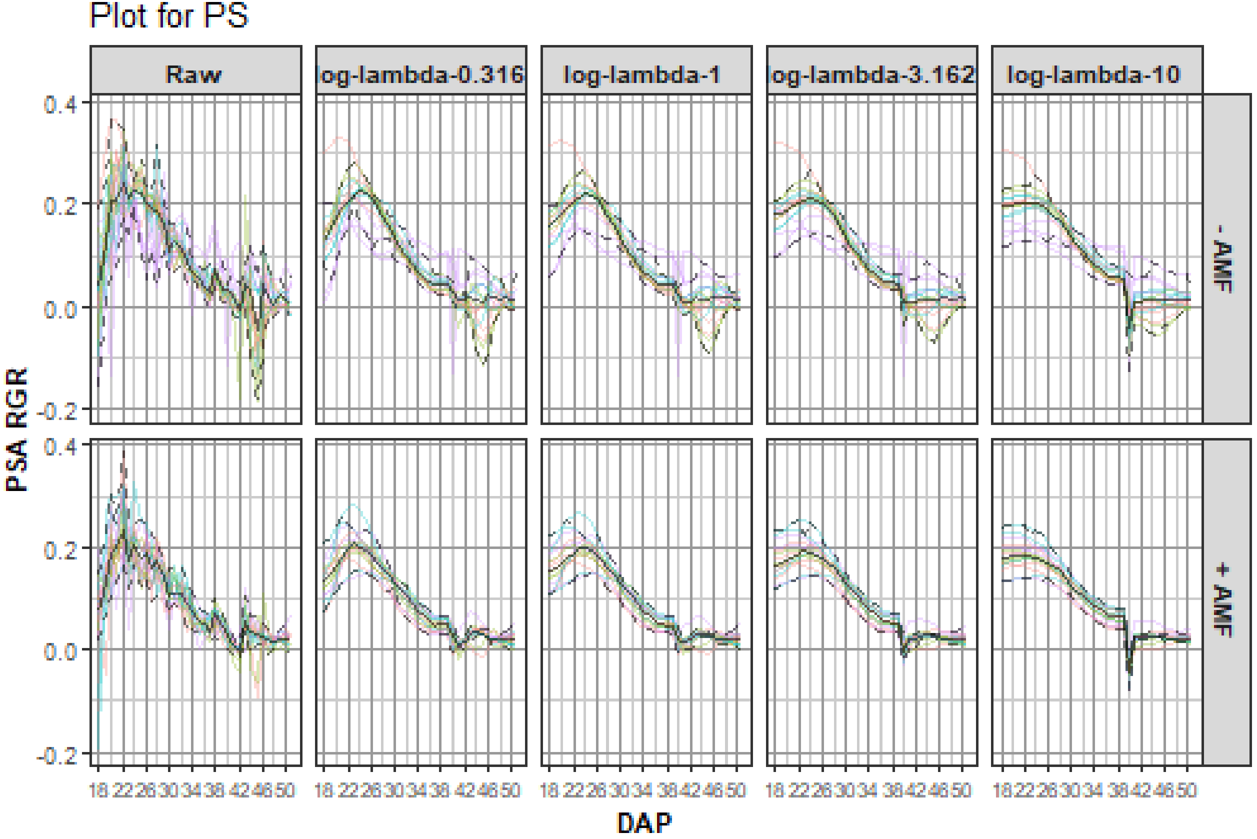
Plot for NCSS


Plot for PS
Raw
log-lambda-0.316
log-lambda-1
log-lambda-3.162
log-lambda-10
- AMF
+ AMF
PSA AGR
20
0
-20
DAP
18
22
26
30
34
38
42
46
50

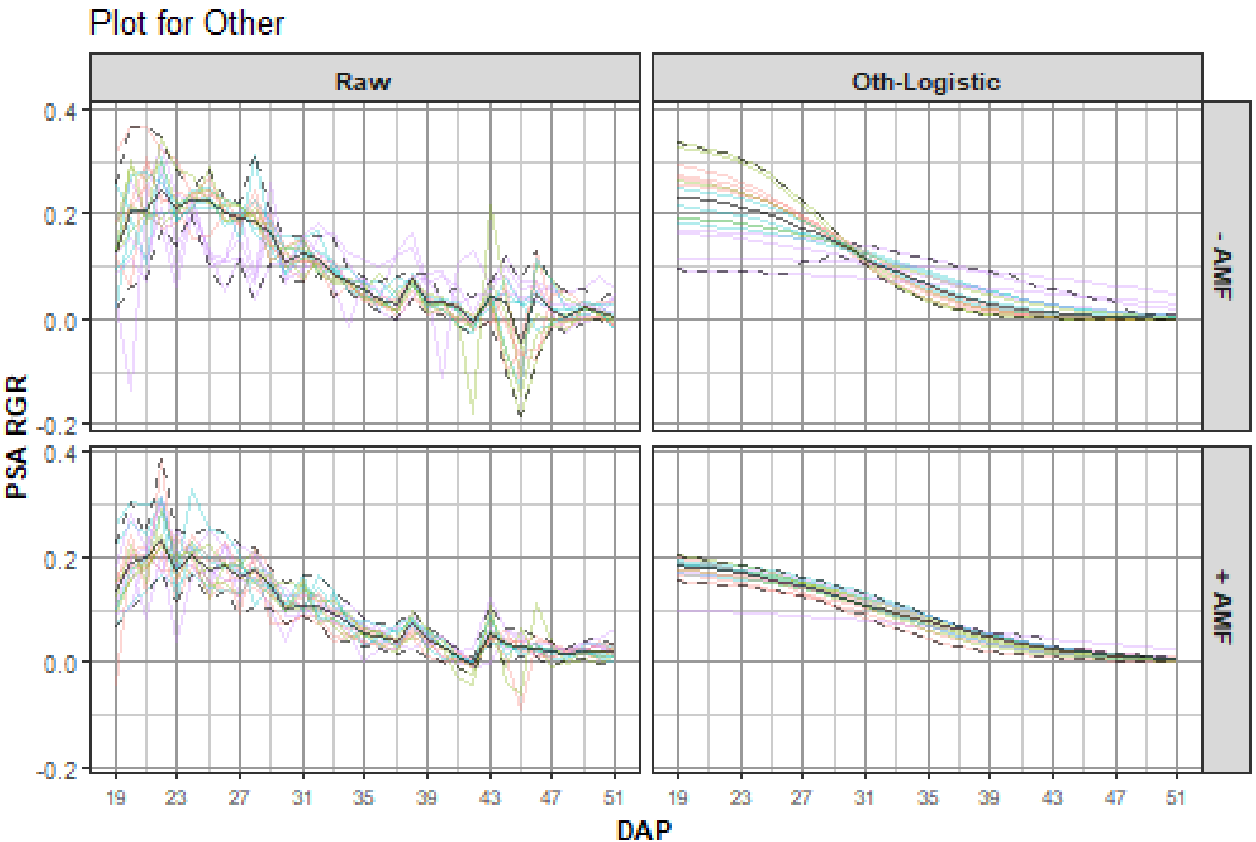

Plot for Other
Raw
Oth-Logistic
- AMF
+ AMF
PSA AGR
20
0
-20
DAP
19
23
27
31
35
39
43
47
51

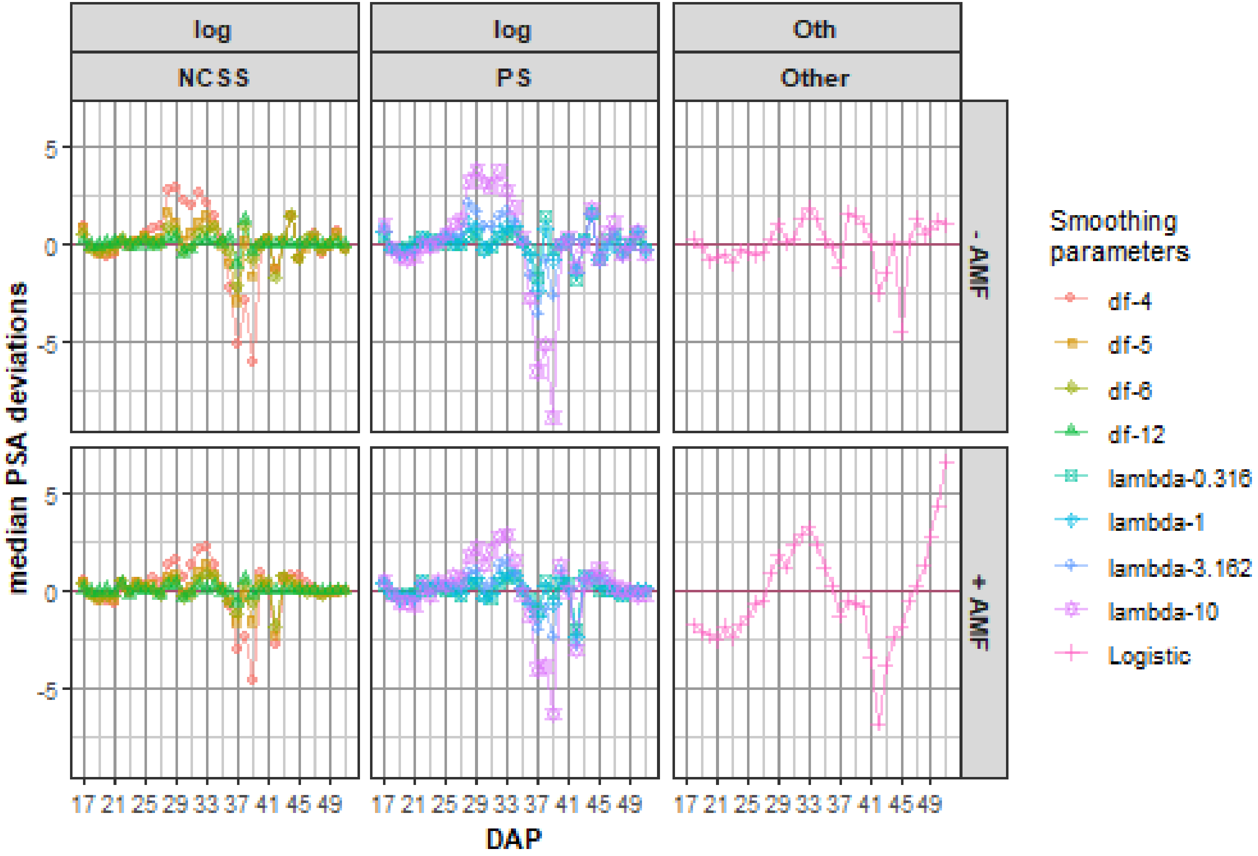


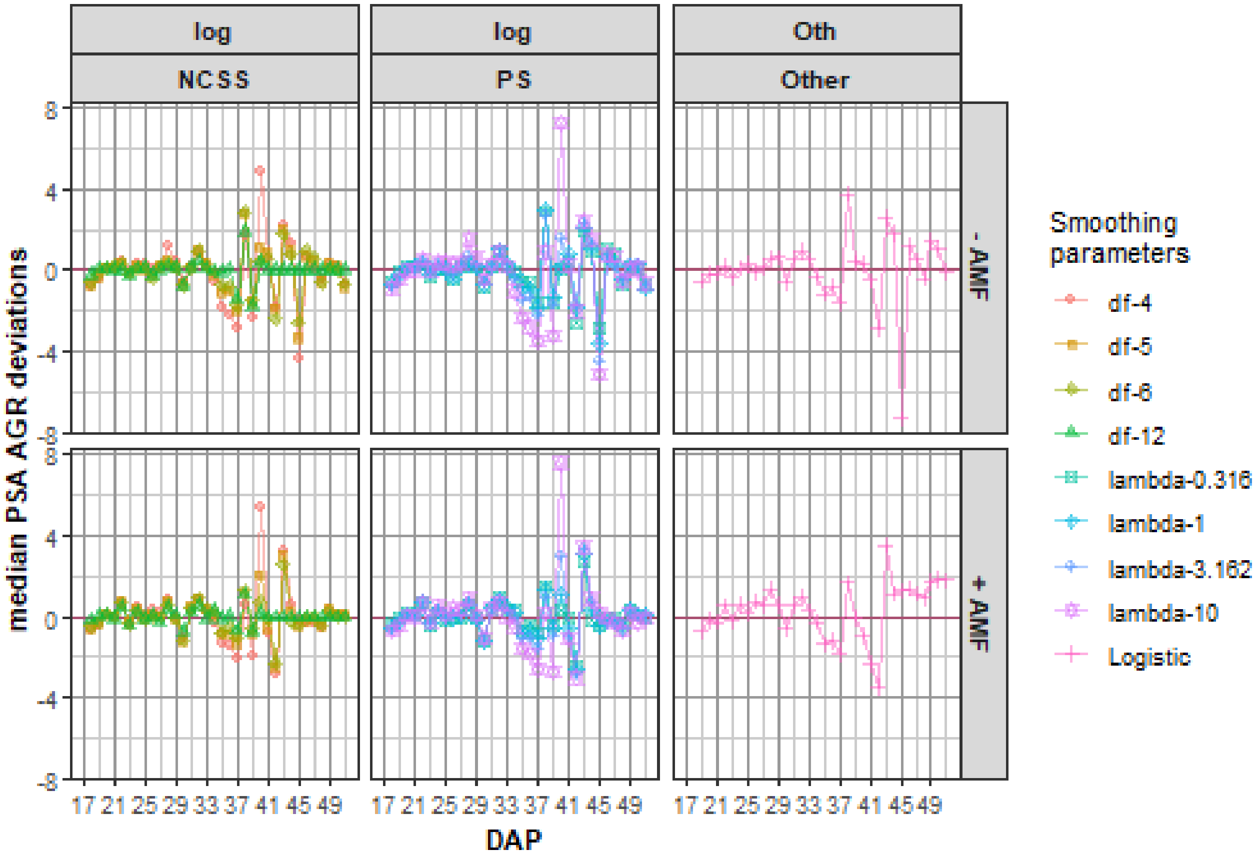
Plot for NCSS

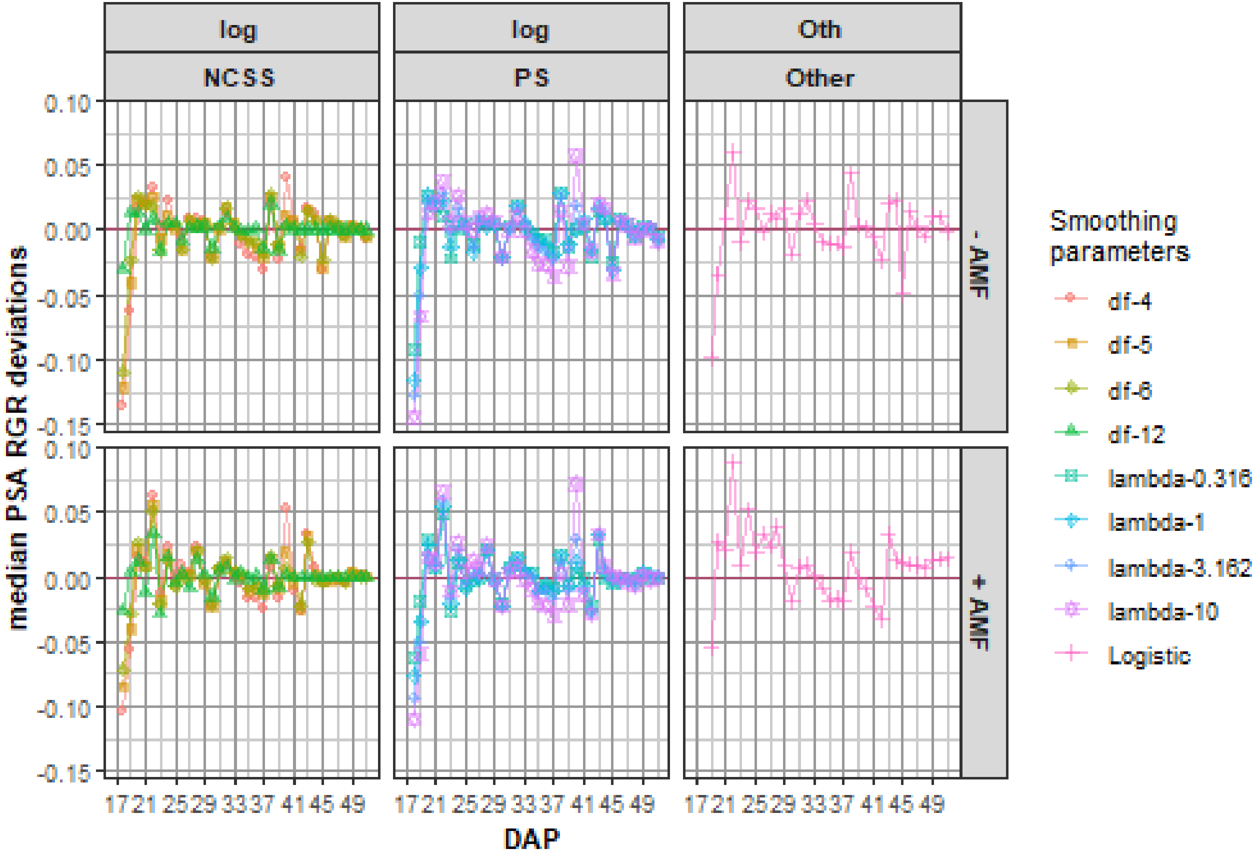


Plot for PS

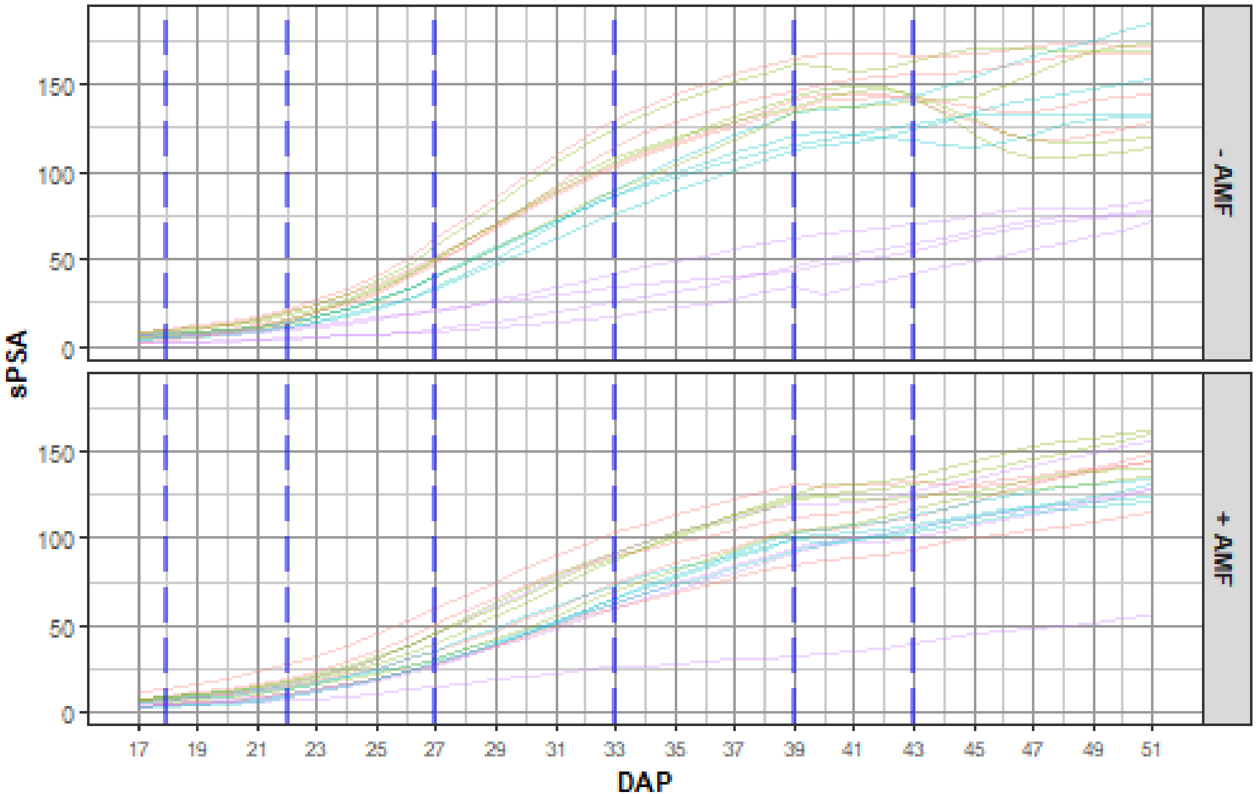

Plot for Other
Raw
Oth-Logistic
- AMF
+ AMF
PSA RGR
0.4
0.2
0.0
-0.2
19
23
27
31
35
39
43
47
51
DAP


log
NCSS
log
PS
Oth
Other
- AMF
+ AMF
median PSA deviations
5
0
-5
17 21 25 29 33 37 41 45 49
DAP
Smoothing parameters
df-4
df-5
df-6
df-12
lambda-0.316
lambda-1
lambda-3.162
lambda-10
Logistic

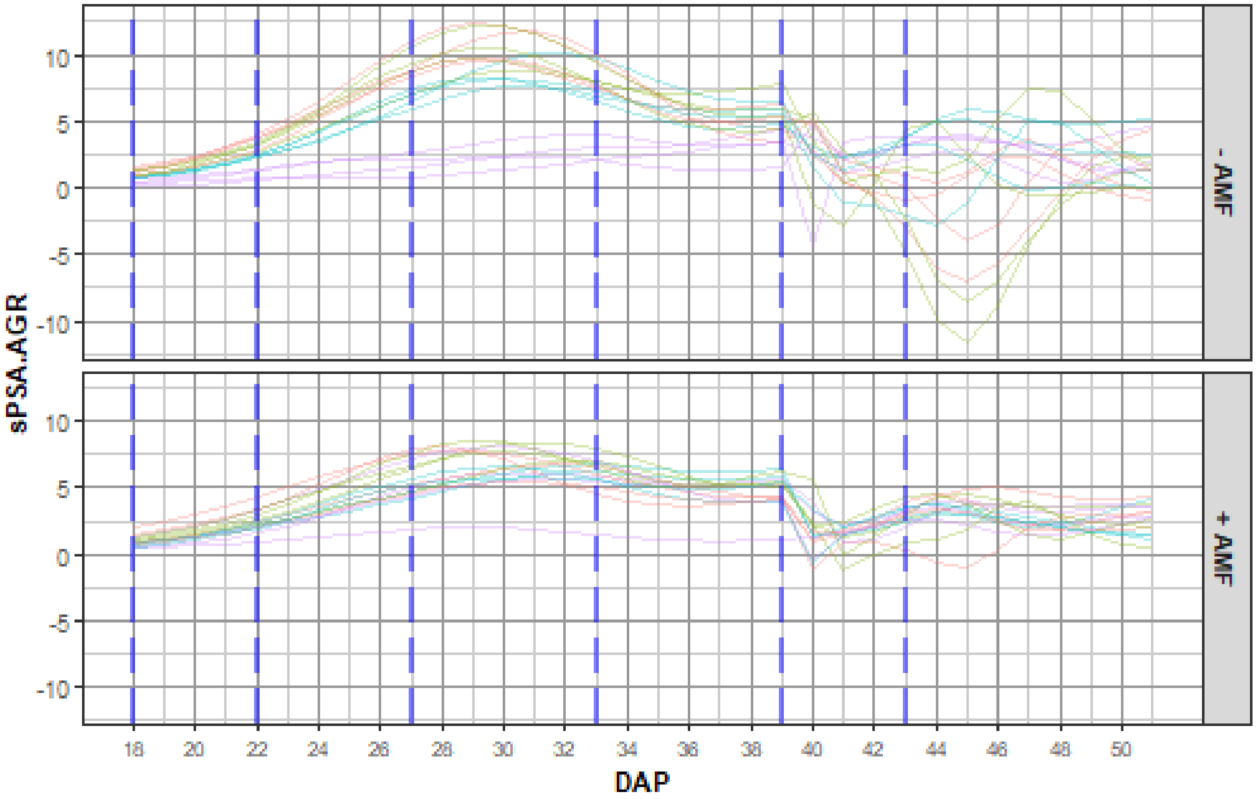

log
NCSS
log
PS
Oth
Other
- AMF
+ AMF
median PSA AGR deviations
8
4
0
-4
-8
17 21 25 29 33 37 41 45 49
DAP
Smoothing parameters
df-4
df-5
df-6
df-12
lambda-0.316
lambda-1
lambda-3.162
lambda-10
Logistic

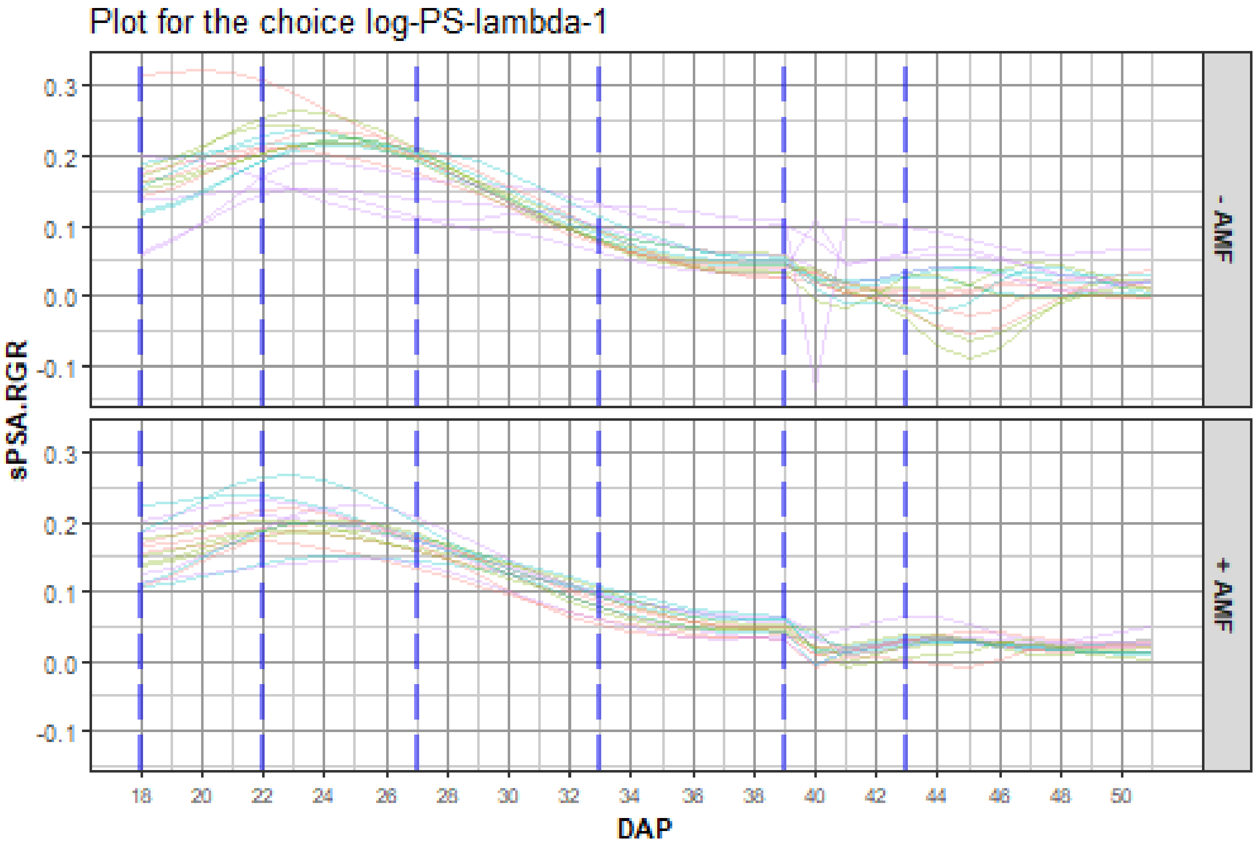

log
NCSS
log
PS
Oth
Other
- AMF
+ AMF
median PSA RGR deviations
0.10
0.05
0.00
-0.05
-0.10
-0.15
17 21 25 29 33 37 41 45 49
DAP
Smoothing parameters
df-4
df-5
df-6
df-12
lambda-0.316
lambda-1
lambda-3.162
lambda-10
Logistic

Plot for the choice log-PS-lambda-1



Plot for the choice log-PS-lambda-1





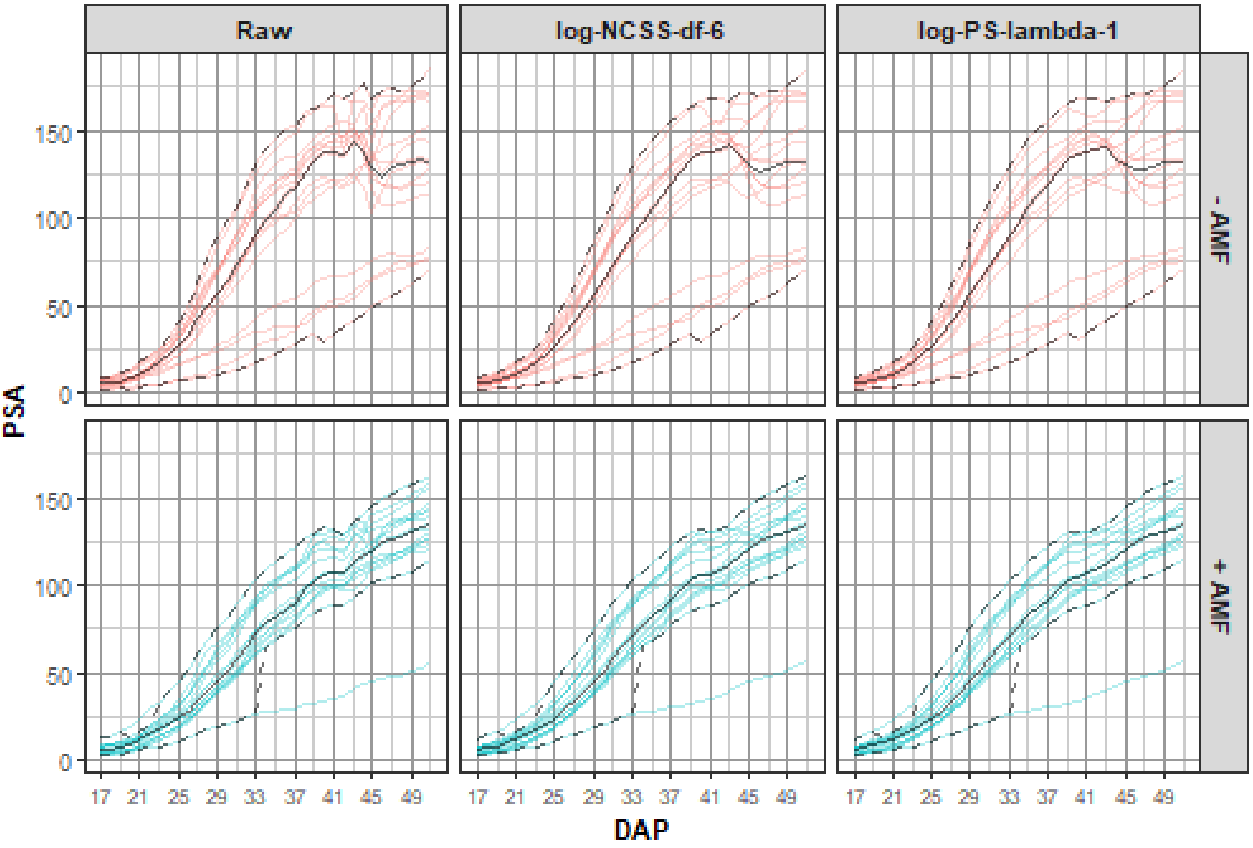
Compare log smoothing of PSA for NCSS with DF = 6 and PS with lambda = 1

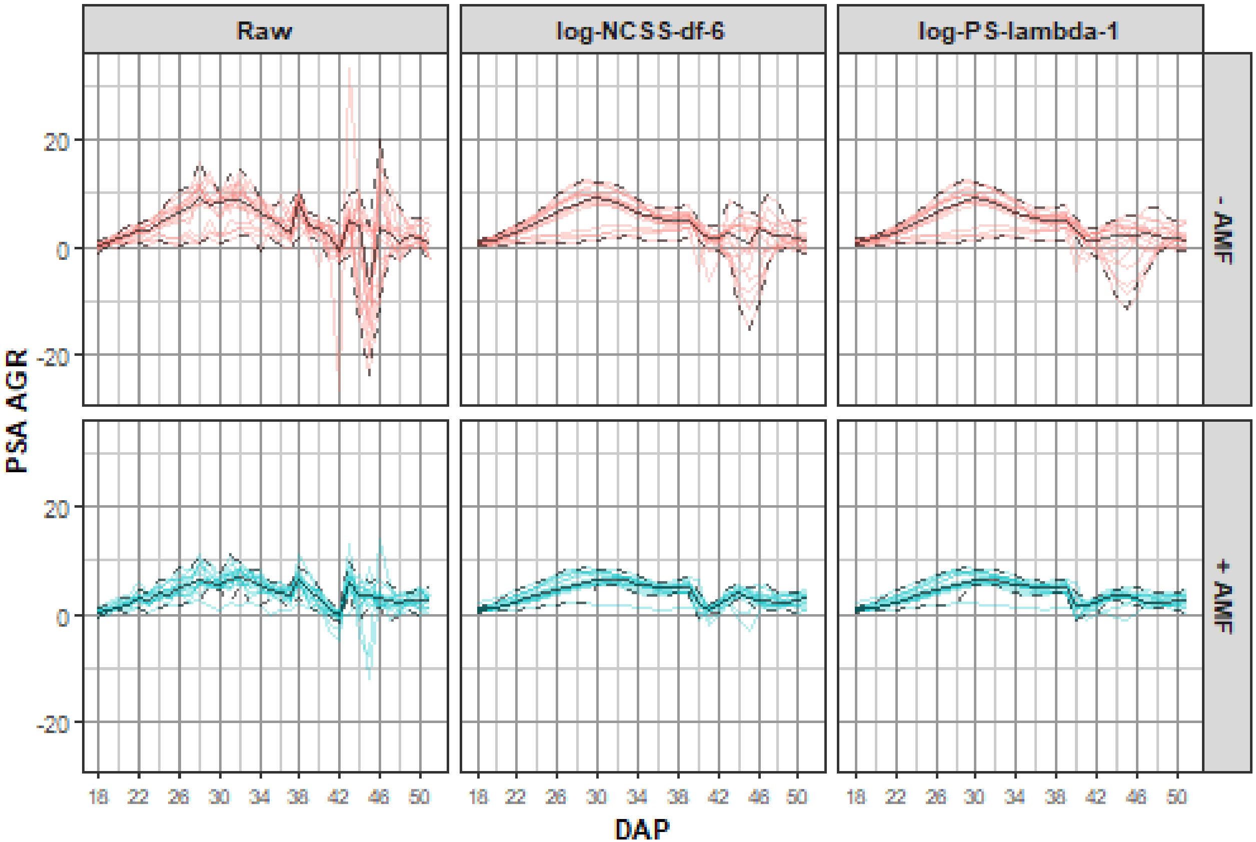
Now compare what appear to be the best smooths for natural cubic smoothing splines (NCSS-df-6) and P-splines (PS-lambda-1) using `traitSmooth`. This is done by supplying `smoothing.args` with a `list` of `parallel` vectors, each vector being of length two. The argument `chosen.smooth.args` is set to `NULL` so that one of the smooths is not chosen for output. Again, arguments are included to control the smoothing and the layout of the profile and median-deviations plots.

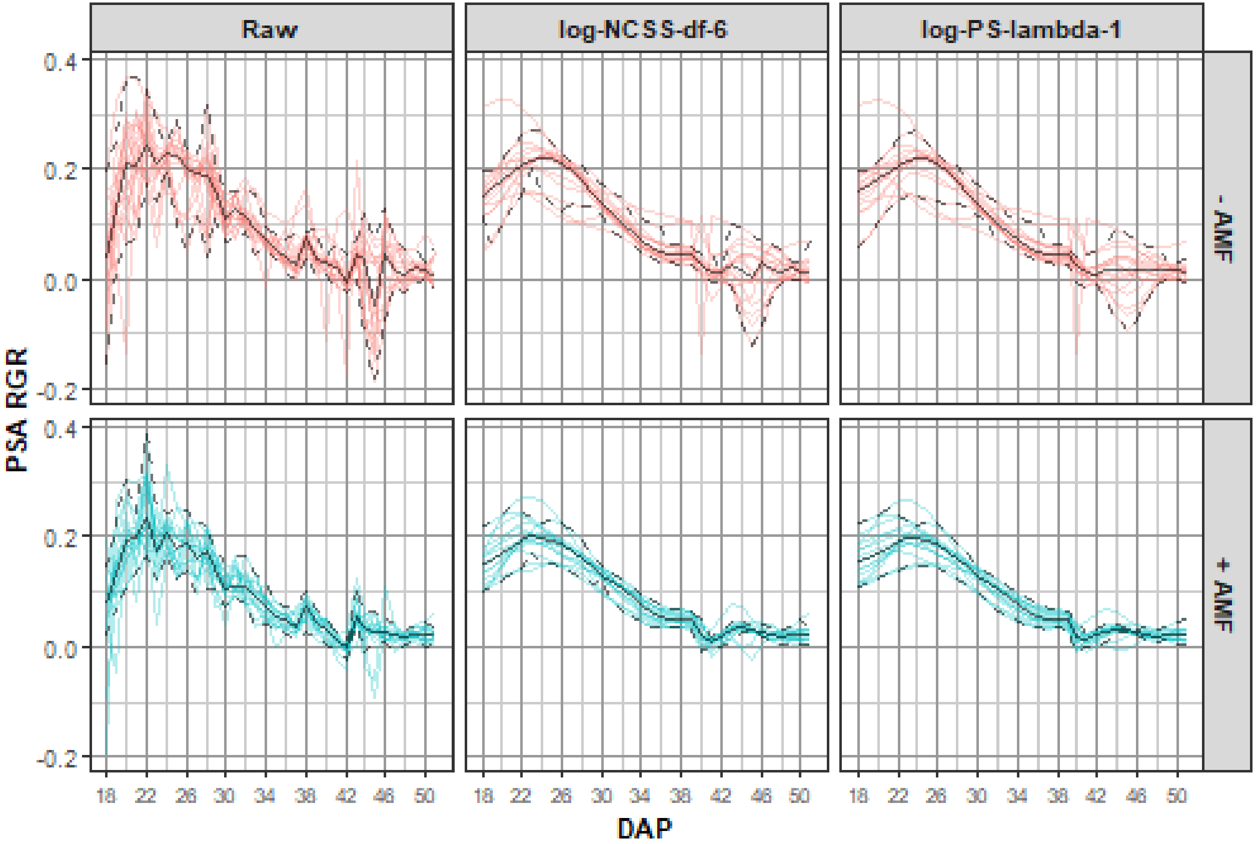
Smoothing based on P-splines is chosen because it tends to smooth somewhat more than that based on NCSS splines, especially after DAP 45. Consequently, there is no need to change the values of the `chosen.splines` argument from the default values.

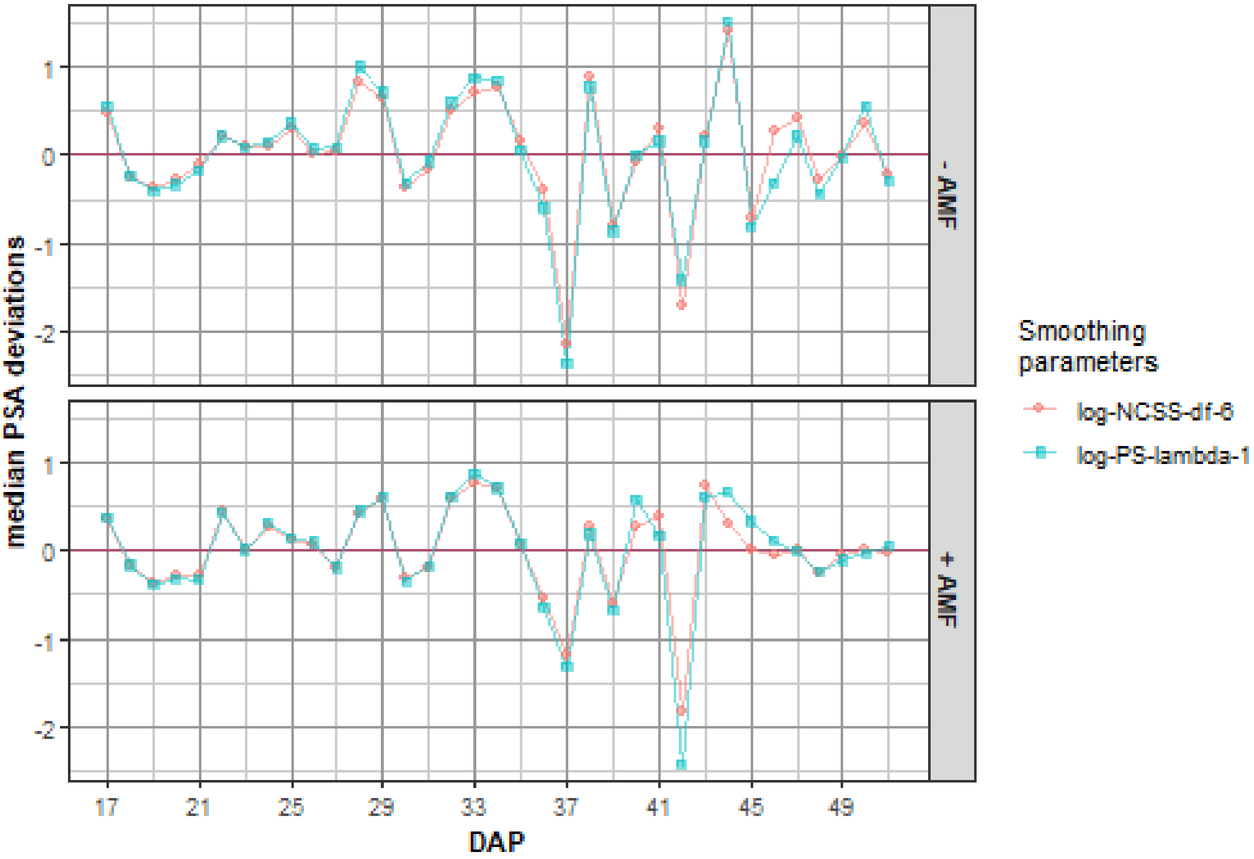
```
smth.dat <- traitSmooth(data = longi.dat,
                        response = "PSA", response.smoothed = "sPSA",
                        individuals = "Snapshot.ID.Tag", times = "DAP",
                        keep.columns = c("AMF","Zn"),
                        smoothing.args =
                          args4smoothing(smoothing.methods = c("log", "log"),
                                         spline.types = c("N", "P"),
                                         df = c(6, NA), lambdas = c(NA, 1),
                                         combinations = "parallel",
                                         smoothing.segments = DAP.segs),
                        chosen.smooth.args = NULL,
                        profile.plot.args =
                          args4profile_plot(plots.by = NULL,
```

```
                                        facet.x = tune.fac, facet.y = "AMF",
                                        facet.labeller = labeller(AMF = labelAMF),
                                        colour.column = "AMF"),
                      meddevn.plot.args =
                        args4meddevn_plot(plots.by = NULL, plots.group = tune.fac,
                                          facet.x = ".", facet.y = "AMF",
                                          facet.labeller = labeller(AMF = labelAMF)))
```



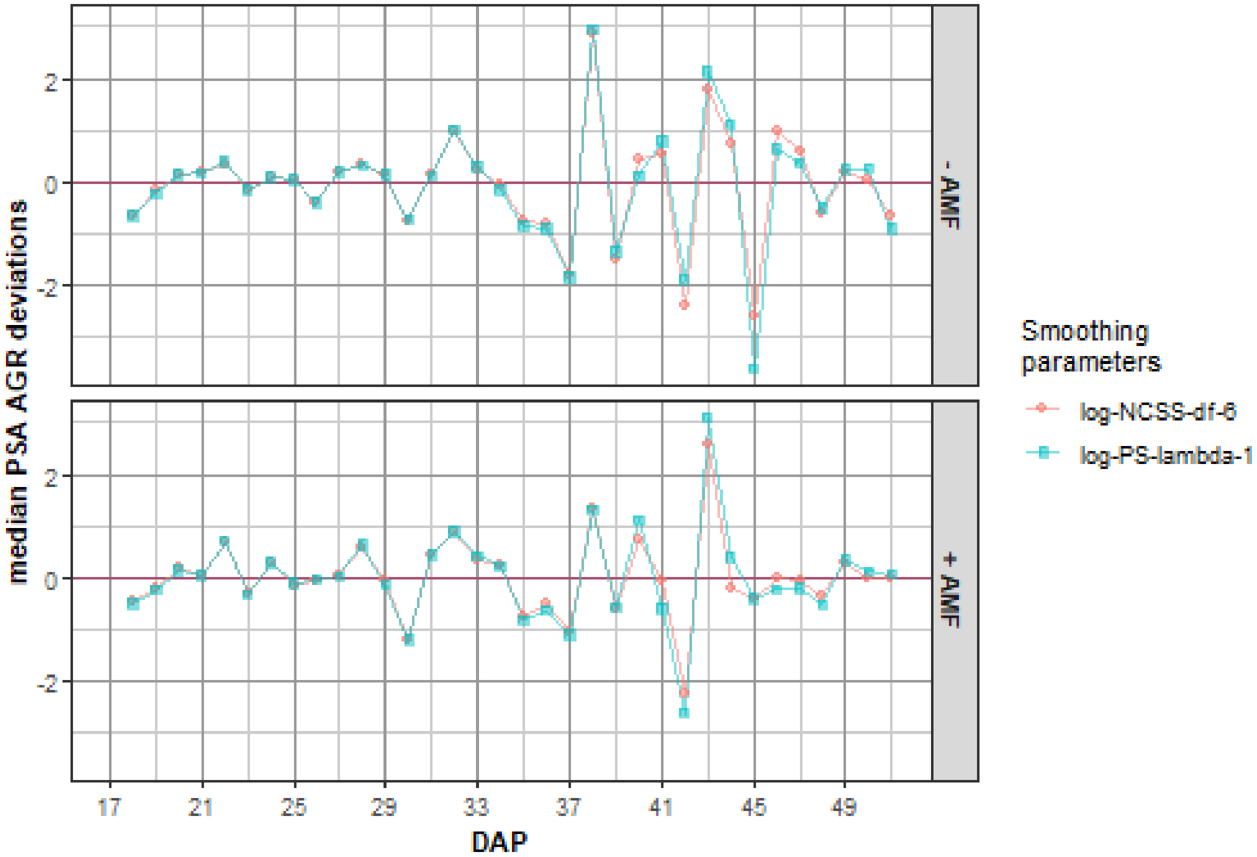

Raw
log-NCSS-df-6
log-PS-lambda-1
- AMF
+ AMF
PSA AGR
20
0
-20
18 22 26 30 34 38 42 46 50
DAP


Raw
log-NCSS-df-6
log-PS-lambda-1
- AMF
+ AMF
PSA RGR
0.4
0.2
0.0
-0.2
18 22 26 30 34 38 42 46 50
DAP

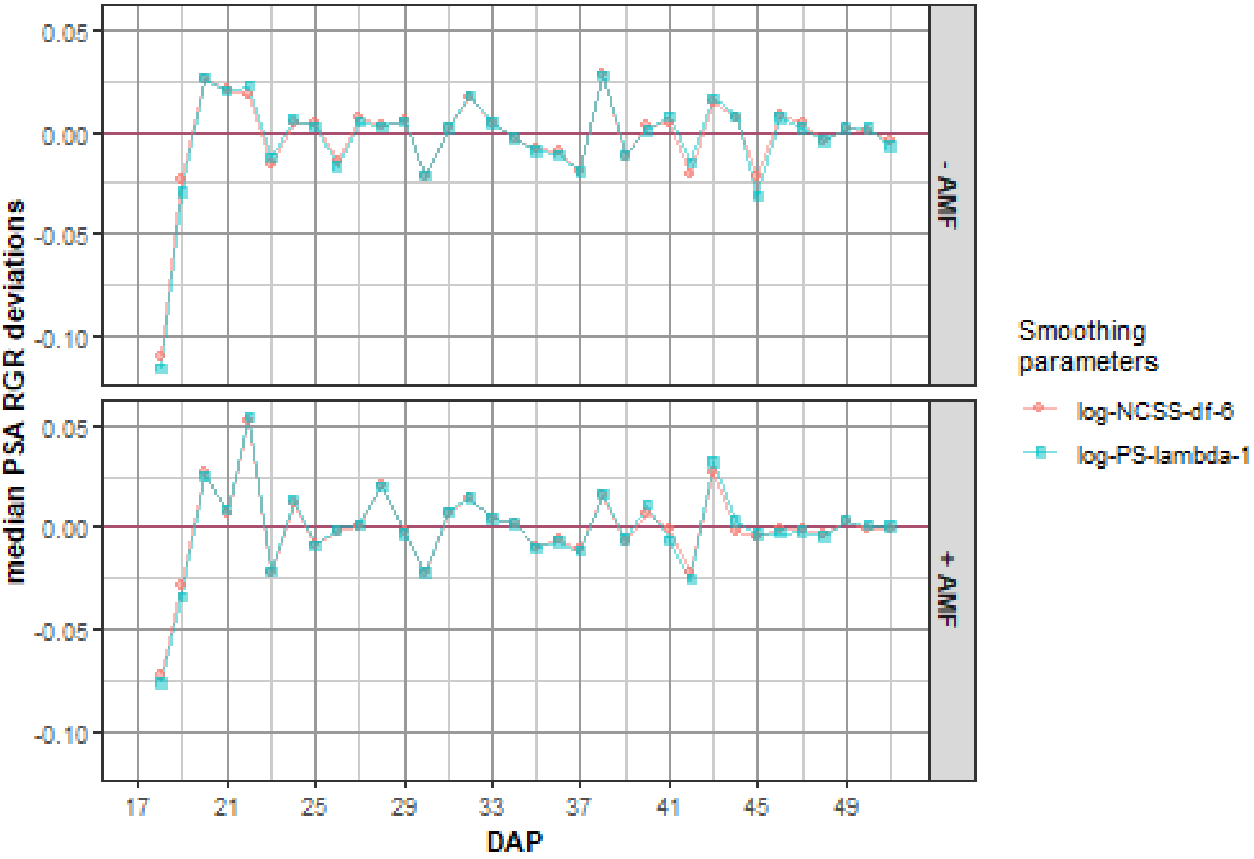


```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (‘geom_line()‘).
```

```
## Warning: Removed 4 rows containing missing values or values outside the scale range
## (‘geom_point()‘).
```



```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_line()`).
## Removed 4 rows containing missing values or values outside the scale range
## (`geom_point()`).
```



Extract the chosen smooth, adding it to longi.dat

```
longi.dat <- traitSmooth(data = smth.dat,
                         response = "PSA", response.smoothed = "sPSA",
                         individuals = "Snapshot.ID.Tag", times = "DAP",
                         keep.columns = c("AMF","Zn"),
                         smoothing.args = NULL, which.plots = "none",
                         chosen.smooth.args =
                           args4chosen_smooth(smoothing.methods = "log",
                                              spline.types = "PS", lambdas = 1),
                         chosen.plot.args =
                           args4chosen_plot(facet.y = "AMF",
                                            facet.labeller = labeller(AMF = labelAMF),
                                            colour.column = "Zn",
                                            ggplotFuncs = vline.DAP.endpts),
                         mergedata = tomato.dat)
```

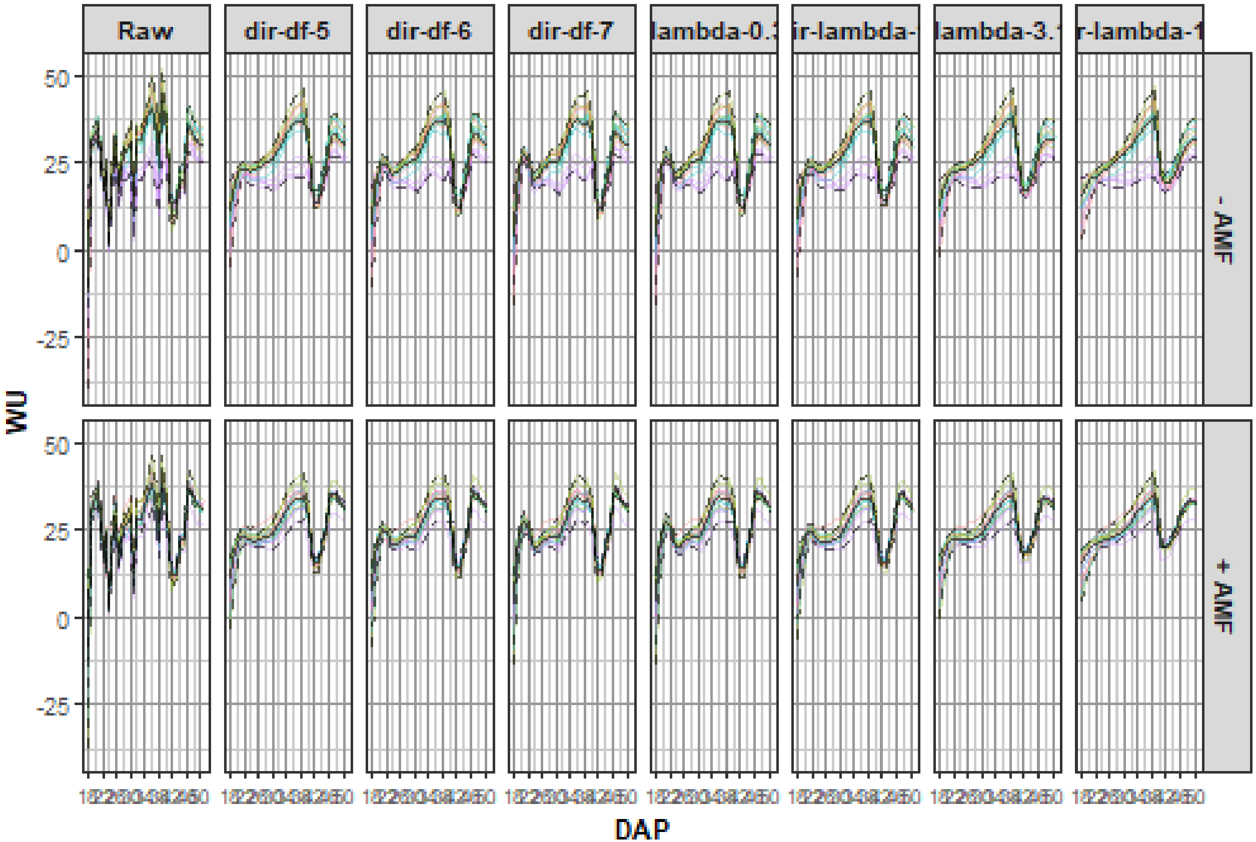
Step III: Investigate the smoothing of the WU

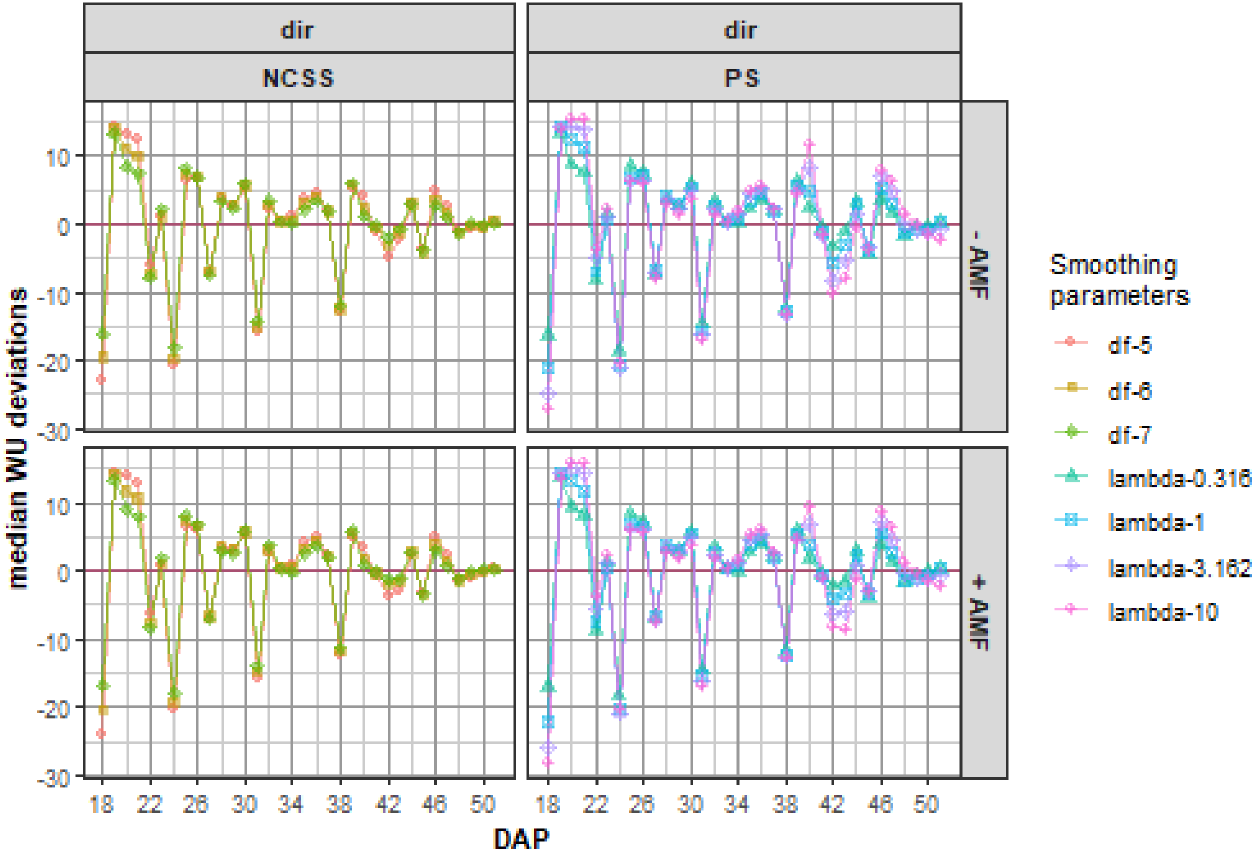
Explore the smooths of WU for a range of smoothing parameters

For WU, we take a slightly different approach to that taken with PSA. We first examine the fits for a range of smoothing parameters, setting the `traitSmooth` argument `chosen.smooth.args` to `NULL` so that a single smooth is not chosen for output. We then examine the two smooths that are the main contenders and finally do plots for the smooth chosen from these two. Again, a segmented smooth involving two segments has also been specified with the breakpoint for the segments being DAP 39.

The function `traitSmooth` is used to produce the smooths. However, because no `chosen.smooth.args` is being specified, the function `probeSmooths` could be called directly instead. In this case, the `get.rates` and `trait.types` arguments from `probeSmooths` are set to `FALSE` and to `"response"` so that only the response is smoothed, without the calculation of growth rates from the smoothed response.

```
suppressWarnings(
  smth.dat <- traitSmooth(data = longi.dat,
                          response = "WU", response.smoothed = "sWU",
                          individuals = "Snapshot.ID.Tag", times = "DAP",
                          keep.columns = c("AMF","Zn"),
                          trait.types = "response",
                          smoothing.args =
                            args4smoothing(smoothing.methods = "direct",
                                           smoothing.segments = DAP.segs),
                          chosen.smooth.args = NULL,
                          profile.plot.args =
                            args4profile_plot(plots.by = NULL,
                                              facet.y = "AMF",
                                              colour.column = "Zn",
                                              facet.labeller = labeller(AMF = labelAMF)),
                          meddevn.plot.args =
                            args4meddevn_plot(plots.by = NULL,
                                              facet.y = "AMF",
                                              facet.labeller = labeller(AMF = labelAMF))))
```

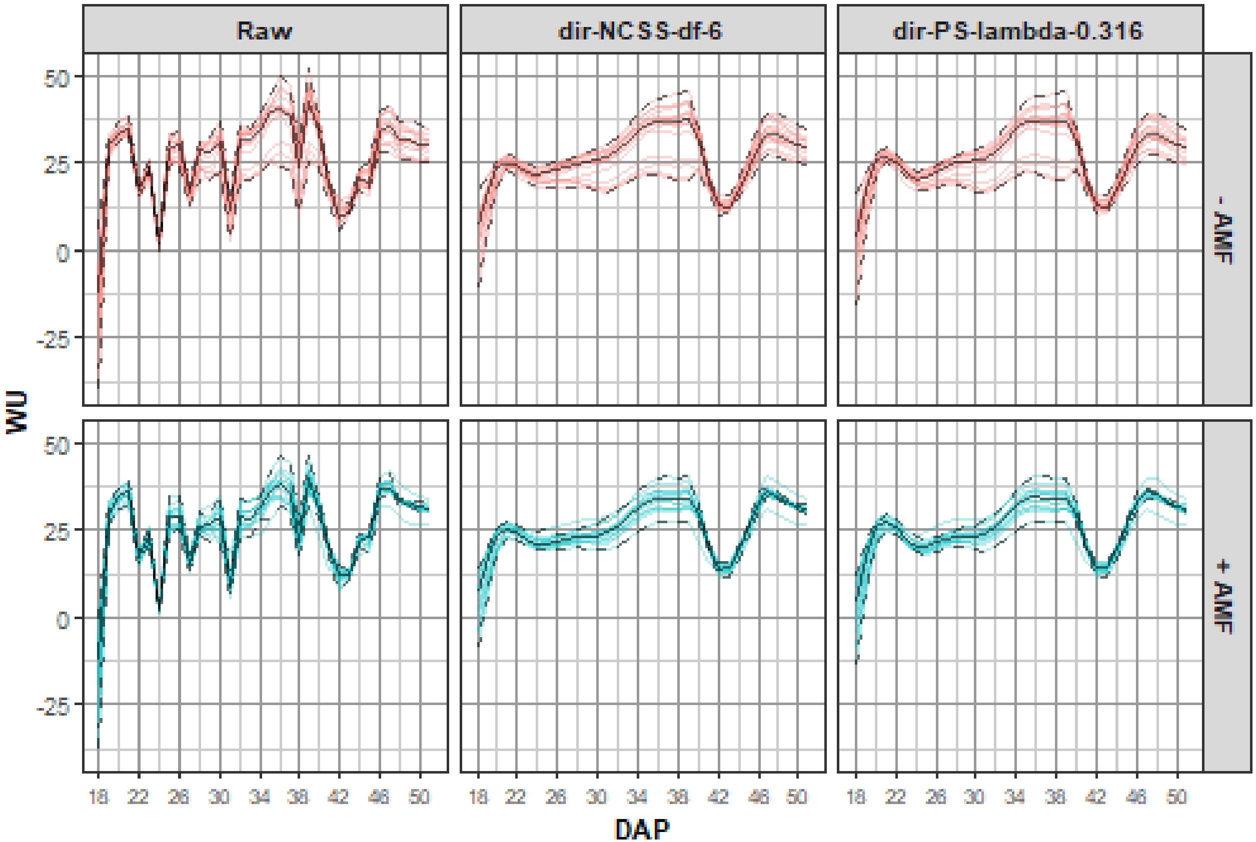

Raw
dir-df-5
dir-df-6
dir-df-7
lambda-0.3
ir-lambda-
lambda-3.1
r-lambda-1
- AMF
+ AMF
WU
50
25
0
-25
DAP

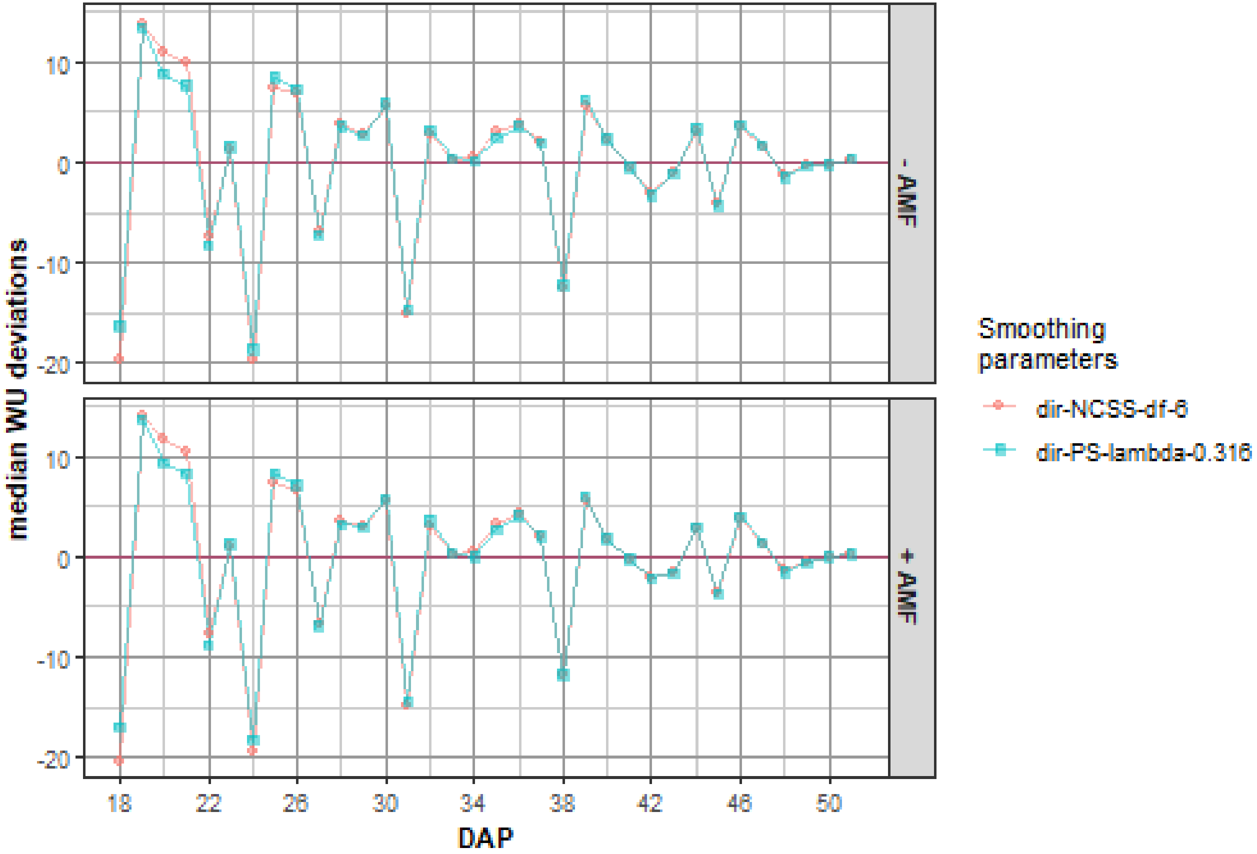

dir
NCSS
dir
PS
- AMF
+ AMF
median WU deviations
10
0
-10
-20
-30
18
22
26
30
34
38
42
46
50
DAP
Smoothing parameters
df-5
df-6
df-7
lambda-0.316
lambda-1
lambda-3.162
lambda-10

Produce plots comparing direct smoothing of WU for NCSS with DF = 6 and PS with lambda = 0.316

Now compare what appear to be the best smooths for natural cubic smoothing splines (`NCSS-df-6`) and for P-splines (`PS-lambda-0.316`). The function `traitSmooth` is used for the comparison, `probeSmooths` could be called directly instead. The PS splines with $\lambda = 0.316$ are chosen because they tend to smooth a little less than the NCSS splines, especially before DAP 26.

```r
suppressWarnings(
  traitSmooth(data = smth.dat,
              response = "WU", response.smoothed = "sWU",
              individuals = "Snapshot.ID.Tag", times = "DAP",
              trait.types = "response",
              smoothing.args = args4smoothing(smoothing.methods = c("dir", "dir"),
                                              spline.types = c("N", "P"),
                                              df = c(6, NA), lambdas = c(NA, 0.316),
                                              smoothing.segments = DAP.segs,
                                              combinations = "parallel"),
              chosen.smooth.args = NULL,
              profile.plot.args =
                args4profile_plot(plots.by = NULL,
                                  facet.x = tune.fac, facet.y = "AMF",
                                  colour.column = "AMF",
                                  facet.labeller = labeller(AMF = labelAMF)),
              meddevn.plot.args =
                args4meddevn_plot(plots.by = NULL, plots.group = tune.fac,
                                  facet.x = ".", facet.y = "AMF",
                                  facet.labeller = labeller(AMF = labelAMF))))
```

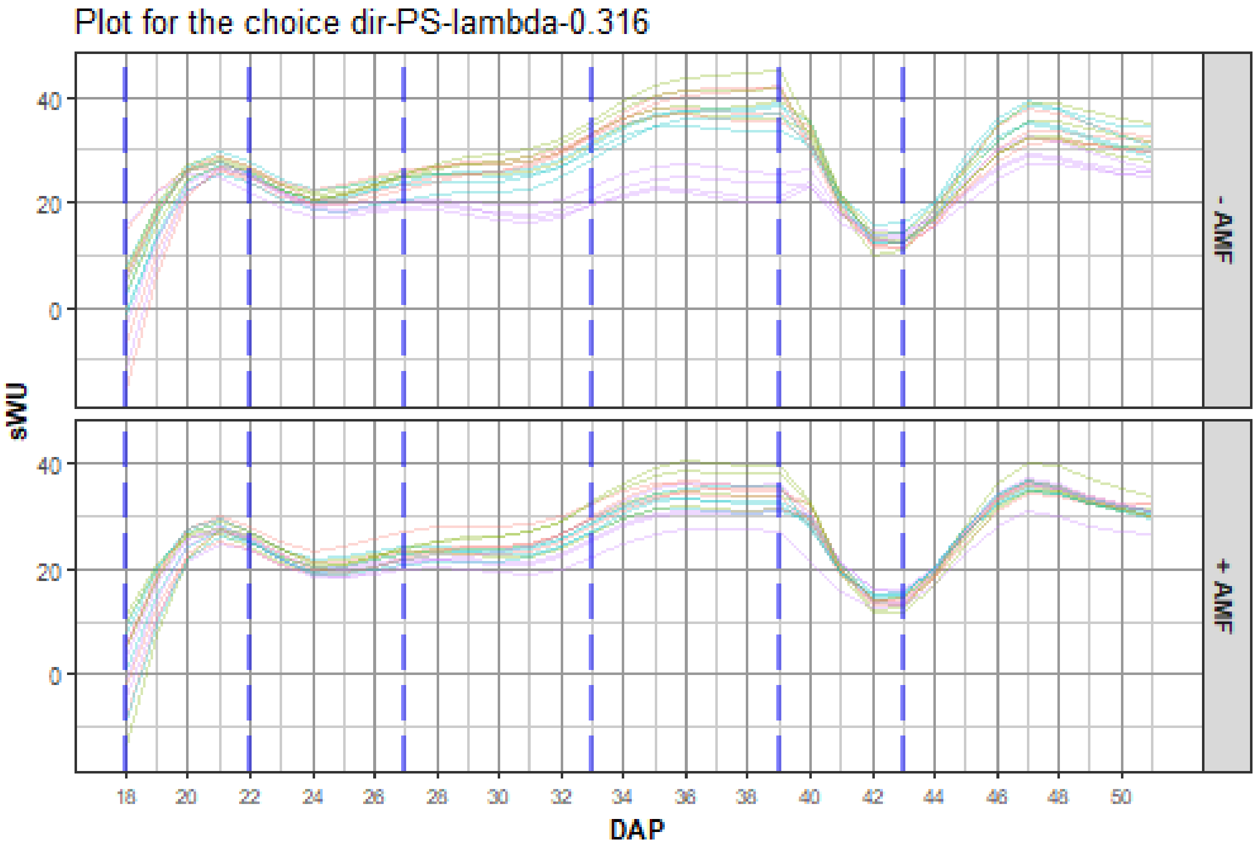

Raw
dir-NCSS-df-6
dir-PS-lambda-0.316
- AMF
+ AMF
WU
50
25
0
-25
18
22
26
30
34
38
42
46
50
DAP


- AMF
+ AMF
median WU deviations
10
0
-10
-20
18
22
26
30
34
38
42
46
50
DAP
Smoothing parameters
dir-NCSS-df-6
dir-PS-lambda-0.316

Produce the plots for the chosen smooth and add it to longi.dat

Here `traitSmooth` is used to fit the two smooths specified in `spar.schemes` in the previous step and the `chosen.splines` argument is set for the fit using `PS` splines with $\lambda = 0.316$.

```
longi.dat <- traitSmooth(data = smth.dat,
                         response = "WU", response.smoothed = "sWU",
                         individuals = "Snapshot.ID.Tag", times = "DAP",
                         trait.types = "response",
                         smoothing.args = NULL, which.plots = NULL,
                         chosen.smooth.args =
                           args4chosen_smooth(smoothing.method = "direct",
                                              spline.type = "PS",
                                              lambdas = 0.316),  #tried 1 first
                         chosen.plot.args =
                           args4chosen_plot(facet.y = "AMF",
                                            facet.labeller = labeller(AMF = labelAMF),
                                            colour.column = "Zn",
                                            ggplotFuncs = vline.DAP.endpts),
                         mergedata = longi.dat)
```



Step IV: Identify potential outliers and remove if justified

A plant was identified as slow growing. Even though its pot had been inoculated with AMF, it had low AMF root colonization and a random mutated shoot phenotype, which could explain why its behaviour was consistent with a plant that was not inoculated with AMF. We omit the it from further analysis.

Omit responses for the outlier plant

The outlier plant is omitted by setting all of its responses to `NA`, i.e. the metadata for the plant is retained in `longi.dat`.

```
#Identify the plant
omit <- with(longi.dat, Zn==90 & AMF=="+" & Block ==4)
#Identify the responses columns
NA.cols <- match("Weight.After", names(longi.dat)):length(longi.dat)
responses.all <- names(longi.dat)[NA.cols]
#Set the responses for the plant to NA
longi.dat[responses.all] <- lapply(longi.dat[responses.all],
                                   function(kcol, omit)
                                   {
                                     kcol[omit] <- NA
                                     return(kcol)
                                   }, omit = omit)
```

Step V: Extract single-valued traits for each individual

In this step, traits that have a single-value for each plant (cart) are created from the smoothed PSA (sPSA) and the smoothed WU (sWU), along with the derived traits sPSA AGR, sPSA RGR, sWUR (smoothed Water Use Rate) and sPSA.sWUI (smoothed Water Use Index with sPSA as the numerator). The single-valued traits are based on a set of endpoints for DAP intervals. The DAP endpoints that were chosen, as described by Brien et al. (2020), are 18, 22, 27, 33, 39, 43 and 51. Corresponding to these endpoints are the time intervals DAP 18–22, DAP 22–27, DAP 27–33, DAP 33–39, DAP 39–43 and DAP 43–51. Based on these endpoints and intervals, the following single-valued traits are to be computed:

1. **single-times traits:** sPSA for each DAP
2. **growth rates for a time interval:** sPSA AGR and sPSA RGR for the six intervals.
3. **water use traits for a time interval:** sWU, sWUR and sPSA.sWUI for the six intervals.
4. **total for the overall imaging period:** sWU for DAP 18–51.
5. **maximum for the overall imaging period:** maximum of the sPSA AGR during DAP 18–51 and the DAP on which it occurred.

```
indv.cols <- c("Snapshot.ID.Tag", "Lane", "Position", "Block", "Cart", "AMF", "Zn")
indv.dat <- subset(longi.dat, subset = DAP == DAP.endpts[1],
                   select = indv.cols)
indv.dat <- traitExtractFeatures(data = longi.dat,
                                 starts.intvl = DAP.starts, stops.intvl = DAP.stops,
                                 responses4singletimes = "sPSA",
                                 responses4intvl.rates = "sPSA", growth.rates = c("AGR", "RGR"),
                                 water.use4intvl.traits = "sWU", responses4water = "sPSA",
                                 responses4overall.total = "sWU",
                                 responses4overall.max = "sPSA.AGR",
                                 mergedata = indv.dat)
```

Finalise

```r
indv.dat <- with(indv.dat, indv.dat[order(Snapshot.ID.Tag), ])
summary(indv.dat)
```

```
##  Snapshot.ID.Tag    Lane      Position  Block      Cart     AMF        Zn
##  Length:32          6:16   5      : 2   1:8   1      :4    -   :16   0   :8
##  Class :character   7:16   6      : 2   2:8   2      :4    +   :15   10  :8
##  Mode  :character          7      : 2   3:8   3      :4   NA's: 1   40  :8
##                            8      : 2   4:8   4      :4             90  :7
##                            9      : 2         5      :4             NA's:1
##                            10     : 2         6      :4
##                            (Other):20         (Other):8
##    sPSA.18          sPSA.22          sPSA.27         sPSA.33
##  Min.   : 2.128   Min.   : 4.032   Min.   : 8.37   Min.   : 17.01
##  1st Qu.: 4.789   1st Qu.:10.501   1st Qu.:28.65   1st Qu.: 63.87
##  Median : 6.742   Median :14.077   Median :39.35   Median : 86.92
##  Mean   : 6.710   Mean   :13.978   Mean   :37.76   Mean   : 79.95
##  3rd Qu.: 8.398   3rd Qu.:16.807   3rd Qu.:47.84   3rd Qu.: 97.53
##  Max.   :14.100   Max.   :27.612   Max.   :61.20   Max.   :129.59
##  NA's   :1        NA's   :1        NA's   :1       NA's   :1
##    sPSA.39          sPSA.43          sPSA.51       sPSA.AGR.18to22
##  Min.   : 34.33   Min.   : 41.16   Min.   : 71.27   Min.   :0.3905
##  1st Qu.: 96.46   1st Qu.:105.27   1st Qu.:122.76   1st Qu.:1.4727
##  Median :115.53   Median :123.55   Median :133.45   Median :1.6730
##  Mean   :110.98   Mean   :118.08   Mean   :134.50   Mean   :1.8170
##  3rd Qu.:133.76   3rd Qu.:140.45   3rd Qu.:154.31   3rd Qu.:2.3631
##  Max.   :164.69   Max.   :166.76   Max.   :185.36   Max.   :3.3781
##  NA's   :1        NA's   :1        NA's   :1        NA's   :1
##  sPSA.RGR.18to22  sPSA.AGR.22to27  sPSA.RGR.22to27  sPSA.AGR.27to33
##  Min.   :0.1131   Min.   :0.7833   Min.   :0.1262   Min.   : 1.441
##  1st Qu.:0.1613   1st Qu.:3.6237   1st Qu.:0.1824   1st Qu.: 5.793
##  Median :0.1827   Median :4.8037   Median :0.2005   Median : 7.266
##  Mean   :0.1854   Mean   :4.7572   Mean   :0.1961   Mean   : 7.032
##  3rd Qu.:0.2026   3rd Qu.:6.2821   3rd Qu.:0.2165   3rd Qu.: 8.582
##  Max.   :0.3192   Max.   :8.0144   Max.   :0.2461   Max.   :11.397
##  NA's   :1        NA's   :1        NA's   :1        NA's   :1
##  sPSA.RGR.27to33   sPSA.AGR.33to39 sPSA.RGR.33to39   sPSA.AGR.39to43
##  Min.   :0.08414   Min.   :1.434   Min.   :0.03775   Min.   :-0.7949
##  1st Qu.:0.11848   1st Qu.:4.700   1st Qu.:0.04582   1st Qu.: 1.4347
##  Median :0.12585   Median :5.391   Median :0.05582   Median : 1.9842
##  Mean   :0.12554   Mean   :5.171   Mean   :0.05843   Mean   : 1.7757
##  3rd Qu.:0.13267   3rd Qu.:5.862   3rd Qu.:0.06661   3rd Qu.: 2.4714
##  Max.   :0.16237   Max.   :7.349   Max.   :0.11699   Max.   : 3.1744
##  NA's   :1         NA's   :1       NA's   :1         NA's   :1
##  sPSA.RGR.39to43    sPSA.AGR.43to51  sPSA.RGR.43to51      sWU.18to22
##  Min.   :-0.00663   Min.   :-3.694   Min.   :-0.02885   Min.   : 79.80
##  1st Qu.: 0.01199   1st Qu.: 1.539   1st Qu.: 0.01038   1st Qu.: 85.77
##  Median : 0.01797   Median : 2.510   Median : 0.02115   Median : 96.43
##  Mean   : 0.01900   Mean   : 2.052   Mean   : 0.01831   Mean   : 93.61
##  3rd Qu.: 0.02424   3rd Qu.: 3.384   3rd Qu.: 0.02619   3rd Qu.:100.05
##  Max.   : 0.06542   Max.   : 5.224   Max.   : 0.06864   Max.   :104.25
##  NA's   :1          NA's   :1        NA's   :1          NA's   :1
##   sWUR.18to22    sPSA.sWUI.18to22    sWU.22to27      sWUR.22to27
##  Min.   :19.95   Min.   :0.01654   Min.   : 90.13   Min.   :18.03
```

```
##  1st Qu.:21.44   1st Qu.:0.06260   1st Qu.:102.34   1st Qu.:20.47  
##  Median :24.11   Median :0.07068   Median :109.55   Median :21.91  
##  Mean   :23.40   Mean   :0.07817   Mean   :107.81   Mean   :21.56  
##  3rd Qu.:25.01   3rd Qu.:0.10147   3rd Qu.:112.68   3rd Qu.:22.54  
##  Max.   :26.06   Max.   :0.13012   Max.   :125.61   Max.   :25.12  
##  NA's   :1       NA's   :1         NA's   :1        NA's   :1      
##  sPSA.sWUI.22to27    sWU.27to33     sWUR.27to33    sPSA.sWUI.27to33
##  Min.   :0.03858   Min.   :106.0   Min.   :17.67   Min.   :0.07756  
##  1st Qu.:0.16720   1st Qu.:140.8   1st Qu.:23.46   1st Qu.:0.24544  
##  Median :0.22553   Median :152.7   Median :25.45   Median :0.27223  
##  Mean   :0.21811   Mean   :150.9   Mean   :25.15   Mean   :0.27200  
##  3rd Qu.:0.27152   3rd Qu.:165.4   3rd Qu.:27.56   3rd Qu.:0.31508  
##  Max.   :0.35963   Max.   :182.4   Max.   :30.41   Max.   :0.40126  
##  NA's   :1         NA's   :1       NA's   :1       NA's   :1        
##    sWU.33to39     sWUR.33to39    sPSA.sWUI.33to39    sWU.39to43   
##  Min.   :126.7   Min.   :21.12   Min.   :0.05969   Min.   :65.15  
##  1st Qu.:190.5   1st Qu.:31.75   1st Qu.:0.13273   1st Qu.:74.32  
##  Median :211.3   Median :35.21   Median :0.15037   Median :77.46  
##  Mean   :204.2   Mean   :34.04   Mean   :0.15159   Mean   :77.00  
##  3rd Qu.:223.1   3rd Qu.:37.19   3rd Qu.:0.17207   3rd Qu.:80.52  
##  Max.   :259.4   Max.   :43.24   Max.   :0.20415   Max.   :83.88  
##  NA's   :1       NA's   :1       NA's   :1         NA's   :1      
##   sWUR.39to43    sPSA.sWUI.39to43     sWU.43to51     sWUR.43to51  
##  Min.   :16.29   Min.   :-0.04207   Min.   :190.6   Min.   :23.83  
##  1st Qu.:18.58   1st Qu.: 0.07150   1st Qu.:230.5   1st Qu.:28.81  
##  Median :19.37   Median : 0.10263   Median :242.5   Median :30.32  
##  Mean   :19.25   Mean   : 0.09285   Mean   :238.7   Mean   :29.84  
##  3rd Qu.:20.13   3rd Qu.: 0.13108   3rd Qu.:249.8   3rd Qu.:31.23  
##  Max.   :20.97   Max.   : 0.19489   Max.   :268.5   Max.   :33.56  
##  NA's   :1       NA's   :1          NA's   :1       NA's   :1      
##  sPSA.sWUI.43to51        sWU         sPSA.AGR.max    sPSA.AGR.max.DAP
##  Min.   :-0.13026   Min.   :701.0   Min.   : 3.963   Min.   :12.00   
##  1st Qu.: 0.04992   1st Qu.:858.5   1st Qu.: 6.150   1st Qu.:13.00   
##  Median : 0.08270   Median :884.0   Median : 7.744   Median :14.00   
##  Mean   : 0.06762   Mean   :874.0   Mean   : 7.791   Mean   :15.77   
##  3rd Qu.: 0.10781   3rd Qu.:922.0   3rd Qu.: 9.148   3rd Qu.:16.00   
##  Max.   : 0.15907   Max.   :988.0   Max.   :12.423   Max.   :35.00   
##  NA's   :1          NA's   :1       NA's   :1        NA's   :1
```

```r
head(indv.dat)
```

```
##   Snapshot.ID.Tag Lane Position Block Cart AMF Zn  sPSA.18   sPSA.22  sPSA.27
## 1          061472    6        5     1    1   -  0 9.856841 21.132127 61.20433
## 2          061473    6        6     1    2   + 10 8.219937 15.732854 39.75138
## 3          061474    6        7     1    3   - 90 2.469923  4.032111 10.07049
## 4          061475    6        8     1    4   + 40 8.971075 14.864706 31.21562
## 5          061476    6        9     1    5   + 90 4.823554  9.198190 27.09603
## 6          061477    6       10     1    6   - 40 4.998369 11.434154 33.88250
##     sPSA.33   sPSA.39   sPSA.43   sPSA.51 sPSA.AGR.18to22 sPSA.RGR.18to22
## 1 129.58879 164.69352 166.75700 171.47291       2.8188215       0.1906572
## 2  87.87222 123.11477 131.05159 159.65092       1.8782293       0.1622972
## 3  24.91082  46.28202  58.39061  77.96569       0.3905471       0.1225258
## 4  65.05030  99.72473 107.67442 131.06986       1.4734077       0.1262460
## 5  62.69652  94.52888 105.67301 127.43397       1.0936589       0.1613739
```

```
## 6  89.76055 133.80166 143.57346 185.36485       1.6089464       0.2068733
##   sPSA.AGR.22to27 sPSA.RGR.22to27 sPSA.AGR.27to33 sPSA.RGR.27to33
## 1        8.014441       0.2126847       11.397410       0.1250247
## 2        4.803705       0.1853787        8.020140       0.1322065
## 3        1.207676       0.1830638        2.473389       0.1509488
## 4        3.270184       0.1483858        5.639112       0.1223737
## 5        3.579568       0.2160761        5.933415       0.1398198
## 6        4.489670       0.2172588        9.313008       0.1623745
##   sPSA.AGR.33to39 sPSA.RGR.33to39 sPSA.AGR.39to43 sPSA.RGR.39to43
## 1        5.850789      0.03995334       0.5158698     0.003112841
## 2        5.873758      0.05620555       1.9842058     0.015618520
## 3        3.561867      0.10324189       3.0271466     0.058100365
## 4        5.779072      0.07120882       1.9874220     0.019174584
## 5        5.305394      0.06843325       2.7860332     0.027861036
## 6        7.340184      0.06653549       2.4429507     0.017622072
##   sPSA.AGR.43to51 sPSA.RGR.43to51 sWU.18to22 sWUR.18to22 sPSA.sWUI.18to22
## 1       0.5894883     0.003485951   97.91084    24.47771       0.11515871
## 2       3.5749165     0.024674829   97.85921    24.46480       0.07677272
## 3       2.4468849     0.036139220   94.46701    23.61675       0.01653687
## 4       2.9244298     0.024577301  101.82429    25.45607       0.05788041
## 5       2.7201203     0.023406106   96.41753    24.10438       0.04537179
## 6       5.2239236     0.031934903   98.41988    24.60497       0.06539112
##   sWU.22to27 sWUR.22to27 sPSA.sWUI.22to27 sWU.27to33 sWUR.27to33
## 1   111.4264    22.28527       0.35962943   174.3139    29.05232
## 2   105.6890    21.13780       0.22725657   151.6969    25.28282
## 3    90.1329    18.02658       0.06699416   106.0449    17.67415
## 4   107.0495    21.40991       0.15274160   142.7822    23.79703
## 5   103.1972    20.63943       0.17343342   134.7183    22.45304
## 6   109.6825    21.93651       0.20466657   154.0212    25.67021
##   sPSA.sWUI.27to33 sWU.33to39 sWUR.33to39 sPSA.sWUI.33to39 sWU.39to43
## 1        0.3923063   222.8187    37.13645        0.1575484   80.88604
## 2        0.3172169   203.3876    33.89793        0.1732778   79.70746
## 3        0.1399438   126.7266    21.12110        0.1686403   69.79265
## 4        0.2369671   185.1663    30.86106        0.1872610   77.46181
## 5        0.2642588   183.3993    30.56655        0.1735686   82.71278
## 6        0.3627944   220.4028    36.73380        0.1998210   80.27464
##   sWUR.39to43 sPSA.sWUI.39to43 sWU.43to51 sWUR.43to51 sPSA.sWUI.43to51 sWU
## 1    20.22151       0.02551094   234.1140    29.26424       0.02014364 936
## 2    19.92687       0.09957441   240.2925    30.03657       0.11901881 890
## 3    17.44816       0.17349372   203.2074    25.40092       0.09633057 706
## 4    19.36545       0.10262720   242.5382    30.31727       0.09646084 866
## 5    20.67819       0.13473290   249.2872    31.16090       0.08729273 855
## 6    20.06866       0.12172963   262.7254    32.84067       0.15906873 933
##   sPSA.AGR.max sPSA.AGR.max.DAP
## 1    12.422797               13
## 2     8.415909               15
## 3     4.444479               23
## 4     6.198353               17
## 5     6.100730               14
## 6    10.090972               16
```

Step VI: Save to files

Save data files as csv, Excel and rda files

```
save(longi.dat, file="longi.dat.rda")
write.csv(longi.dat, "longi.dat.csv", row.names = F)
WriteXLS("longi.dat", ExcelFileName = "longi.dat.xlsx", SheetNames = "longi.dat",
         row.names = FALSE, BoldHeaderRow = TRUE, AdjWidth = TRUE, FreezeRow = 1)
save(indv.dat, file="indv.dat.rda")
write.csv(indv.dat, "indv.dat.csv", row.names = F)
WriteXLS("indv.dat", ExcelFileName = "indv.dat.xlsx", SheetNames = "indv.dat",
         row.names = FALSE, BoldHeaderRow = TRUE, AdjWidth = TRUE, FreezeRow = 1)
```

Save the workspace image

```
save.image("Tomato.RData")
```

Reference

Brien, C. J. (2025) *growthPheno: Functional Analysis of Phenotypic Growth Data to Smooth and Extract Traits*. R package Version 3.1.10. http://cran.at.r-project.org/package=growthPheno.

Brien, C., Jewell, N., Garnett, T., Watts-Williams, S. J., & Berger, B. (2020). Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. *Plant Methods*, **16**, 36. http://dx.doi.org/10.1186/s13007-020-00577-6.

Pinheiro J., Bates D., and R Core Team (2023). *nlme: Linear and Nonlinear Mixed Effects Models*. R package version 3.1-164, https://CRAN.R-project.org/package=nlme.