

DBEN_testing_all_vars

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Summary:

Some models already have biomass at disturbance year, while others have 0 values. We consider this a feature of the models and accept that some models therefore are on year ‘ahead’ in the dynamics.

For some models, some variables which have a value of 0 at disturbance year, but then have non-zero values for other variables. Please double-check. i.e. WBgrowth shows 0, but height is already at >0 values? That’s of course plausible if height is initialised, but please clarify.

BiomeEP and BiomeES sometimes contain grasses in output that should be explicitly for wood. I can post-process the grasses ‘away’, but am wondering whether we in this case received output we asked for (i.e. WBgrowth). Please double-check.

Some of the jitteryness comes from the climate forcing. We may create a 30-year running mean to smoothen this in the paper. Other jitteryness I would like to discuss for individual outputs below (see my comments below).

From Amsterdam: -still not really resolved for me: How dependent is the disturbance recovery on how “disturbance/bare ground” was set up ?

NA = no output provided. I mention in the individual model TODOs sent via mail, whether I an output is needed. For ther rest, if you find you can easily add it, please go ahead for the next submission.

[TODOs for ANNEMARIE] JULES-RED sizeclass <1 currently set to 0, but is actually “NA”. Right now seems like there are 0 trees, instead of no output. `if(model_name == “JULES-RED”){ df[,4] <- NULL`

```
#knitr::opts_chunk$set(echo = TRUE)
library(ncdf4)
library(DGVMTools)
library(dplyr)
library(maps)
library(maptools)
library(gridExtra)
#source the format metadata for DBEN project to integrate with DGVMTools:
#source('Format-DBEN_paper1.R')
source("/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_intercomparison/P

## Layer: BINE (Boreal/Temperate Shade-Intolerant Needleleaved Evergreen Tree), plot colour = dodgerblue
##   With properties: =, growth.form=Tree, leaf.form=Needleleaved, phenology=Evergreen, shade.tolerance=
## Layer: NE (Boreal/Temperate Needleleaved Evergreen Tree), plot colour = darkblue
##   With properties: =, growth.form=Tree, leaf.form=Needleleaved, phenology=Evergreen, shade.tolerance=
## Layer: IBS (Shade-intolerant Broadleaved Summergreen Tree), plot colour = chartreuse
##   With properties: =, growth.form=Tree, leaf.form=Broadleaved, phenology=Summergreen, shade.tolerance=
## Layer: TeBS ((intermediate) shade tolerant broadleaf deciduous), plot colour = purple
```

```

## With properties: =, growth.form=Tree, leaf.form=Broadleaved, phenology=Summergreen, climate.zone=T
## Layer: TrIBE (Tropical Shade-intolerant Broadleaved Evergreen Tree), plot colour = orchid
## With properties: =, growth.form=Tree, leaf.form=Broadleaved, phenology=Evergreen, climate.zone=Trop
## Layer: TrBE (Tropical Broadleaved Evergreen Tree), plot colour = orchid4
## With properties: =, growth.form=Tree, leaf.form=Broadleaved, phenology=Evergreen, climate.zone=Trop
## Layer: TrBR (Tropical Broadleaved Raingreen Tree), plot colour = palevioletred
## With properties: =, growth.form=Tree, leaf.form=Broadleaved, phenology=Raingreen, climate.zone=Trop
## Layer: Grasses (C3 and/or C4 grasses), plot colour = dark grey
## With properties: =, growth.form=Grass, shade.tolerance=None, land.cover=Natural,
## Layer: Total (Total), plot colour = black
## With properties: type=Sum, land.cover=All,
## Layer: <1 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #00FF00
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <5 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #0AF102
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <10 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #14E405
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <15 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #1ED707
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <20 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #29C90A
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <30 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #33BC0D
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <40 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #3DAF0F
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <50 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #48A112
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <60 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #529415
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <70 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #5C8717
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <80 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #67791A
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <90 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #716C1C
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <100 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #7B5F1F
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <150 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #865122
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <200 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #904424
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <250 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #9A3727
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: 300+ (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #A52A2A
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: 1 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = light green
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: 2 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = dark green
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: 3 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = brown
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <1 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #00FF00
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <5 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #0AF102

```



```

## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <100 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #845421
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <150 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #8F4624
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: <200 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #9A3827
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Layer: >=200 (sizeclass_by_diameter_at_breastheight (cm)), plot colour = #A52A2A
## With properties: =, growth.form=Tree, leaf.form=Any, phenology=Any, climate.zone=Any, shade.toleran
## Quantity:      cveg (Vegetation Carbon Mass by PFT): Units=kgC m-2, Defined for format: DBEN, CF s
## Quantity:      albedo (surface reflectiveness of PFTs): Units=-, Defined for format: DBEN, CF stan
## Quantity:      z0 (roughness length (momentum)): Units=m, Defined for format: DBEN, CF standard_nam
## Quantity:      cwood (Wood Carbon Mass by PFT): Units=kgC m-2, Defined for format: DBEN, CF standa
## Quantity:      AGcwood (Aboveground woody biomass): Units=kgC m-2, Defined for format: DBEN, CF sta
## Quantity:      AGB (Aboveground total biomass): Units=kgC m-2, Defined for format: DBEN, CF standa
## Quantity:      cwood_size (Wood Carbon Mass by size class): Units=kgC m-2, Defined for format: DBE
## Quantity:      nstem_size (Stem number by size class): Units=count ha-1, Defined for format: DBEN,
## Quantity:      stemmort_rate (Stem mortality rate by size class): Units=% yr-1, Defined for format
## Quantity:      lai (Leaf area index): Units=m2 m-2, Defined for format: DBEN, CF standard_name=lea
## Quantity:      CA (Crown area): Units=m2 ha-1, Defined for format: DBEN, CF standard_name=crown_ar
## Quantity:      BA (Basal area): Units=m2 ha-1, Defined for format: DBEN, CF standard_name=basal_ar
## Quantity:      height (Mean PFT height in the 95% height percentile): Units=m, Defined for format:
## Quantity:      WBgrowth (Woody biomass growth): Units=kgC m-2 yr-1, Defined for format: DBEN, CF s
## Quantity:      BAgrowth (Basal area growth): Units=m2 ha-1 yr-1, Defined for format: DBEN, CF stan
## Quantity:      cmort (Wood Carbon Mass flux lost by size class): Units=kgC m-2 s-1, Defined for fo
## Quantity:      cmort_size (Wood Carbon Mass flux lost by size class): Units=kgC m-2 s-1, Defined f
## Quantity:      cmort_rate (% Wood Carbon Mass lost due to mortality, by size class): Units=% yr -1
## Quantity:      stemmort (Stem number flux lost by size class): Units=Count ha-1 yr-1, Defined for
## Quantity:      stemmort_size (Stem number flux lost by size class): Units=Count ha-1 yr-1, Defined
## Quantity:      gpp (gpp): Units=kgC m-2 yr-1, Defined for format: DBEN, CF standard_name=Gross_prin
## Quantity:      npp (npp): Units=kgC m-2 yr-1, Defined for format: DBEN, CF standard_name=Net_primar
## Quantity:      nbp (Net Biospheric Production): Units=kgC m-2 yr-1, Defined for format: DBEN, CF s
## Quantity:      cveg_dyn (Total Carbon mass Flux by Pft): Units=kgC m-2 yr-1, Defined for format: DI
## Quantity:      BA_size (BA by sizeclass): Units=m2 ha-1, Defined for format: DBEN, CF standard_nam
## Quantity:      stemmort_freezing (Stems lost due to freezing mortality): Units=count ha-1, Defined
## Quantity:      stemmort_freezing_rate (% stems lost due to freezing mortality): Units=% yr-1, Defi
## Quantity:      stemmort_cstarv (Stems lost due to carbon starvation mortality): Units=count ha-1,
## Quantity:      stemmort_cstarv_rate (% Stems lost due to carbon starvation mortality): Units=% yr-
## Quantity:      stemmort_background (Stems lost due to background mortality): Units=count ha-1, Def
## Quantity:      stemmort_background_rate ( %Stems lost due to background mortality): Units=% yr-1,
## Quantity:      stemmort_impact (Stems lost duee to impact mortality): Units=count ha-1, Defined fo
## Quantity:      stemmort_impact_rate (#Stems lost duee to impact mortality): Units=% yr-1, Defined
## Quantity:      stemmort_termination (Stems lost due to termination mortality): Units=count ha-1, D
## Quantity:      stemmort_termination_rate (% Stems lost due to termination mortality): Units=% yr-1
## Quantity:      stemmort_hydro (Stems lost due to hydraulic failure(?) mortality): Units=count ha-1
## Quantity:      stemmort_hydro_rate (% Stems lost due to hydraulic failure(?) mortality): Units=% y
## Quantity:      cmort_cstarv (Wood Carbon Mass flux lost through carbon starvation mortality): Unit
## carbon starvation mortality
## Quantity:      cmort_cstarv (%Wood Carbon Mass flux lost through carbon starvation mortality): Uni
## carbon starvation mortality
## Quantity:      cmort_cstarv_rate ( % Wood Carbon Mass lost through carbon starvation mortality): Un
## carbon starvation mortality
## Quantity:      cmort_hydro (Wood Carbon Mass flux lost through hydarulic failur mort.): Units=m2 ha
## hydraulic failure mortality

```

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## Quantity:      cmort_hydro_rate (% Wood Carbon Mass flux lost through hydarulic failur mort.): Units=
## hydraulic failure mortality
## Quantity:      cmort_res (Wood Carbon Mass flux lost due to Resource mortality): Units=kg C m-2 s-1
## Quantity:      cmort_res_rate (% Wood Carbon Mass lost, Resource mortality): Units=% yr-1, Defined for
## Quantity:      cmort_crowd (Wood Carbon Mass flux lost due to crowding mortality): Units=kg C m-2 s-1
## Quantity:      cmort_crowd_rate ( % Wood Carbon Mass lost due to crowding mortality): Units=% yr-1, Defined for
## Quantity:      cmort_dist (Wood Carbon Mass flux lost due to disturbance mortality): Units=kg C m-2 s-1
## Quantity:      cmort_dist_rate (% Wood Carbon Mass lost, disturbance mortality): Units=% yr-1, Defined for
## Quantity:      cmort_age (Wood Carbon Mass flux lost through old age mortality): Units=kg C m-2 s-1
## Quantity:      cmort_age_rate (% Wood Carbon Mass lost, old age mortality): Units=% s-1, Defined for
## Quantity:      cmort_dist (Wood Carbon Mass flux lost through disturbance mortality): Units=kg C m-2 s-1
## Quantity:      cmort_dist_rate (% Wood Carbon Mass lost through disturbance mortality): Units=% s-1, Defined for
## Quantity:      cmort_fire (Wood Carbon Mass flux lost through fire mortality): Units=kg C m-2 s-1
## Quantity:      cmort_fire_rate (% Wood Carbon Mass lost, fire mortality): Units=% s-1, Defined for
## Quantity:      cmort_greff (Wood Carbon Mass flux lost, low growth efficiency mortality): Units=kg C m-2 s-1
## Quantity:      cmort_greff_rate (% Wood Carbon Mass lost, growth efficiency mortality): Units=% s-1, Defined for
## Quantity:      cmort_other (Wood Carbon Mass flux lost, other mortality mechs.): Units=kg C m-2 s-1
## Quantity:      cmort_res (Wood Carbon Mass flux lost, other mortality mechs.): Units=kg C m-2 s-1
## Quantity:      cmort_other_rate ( % Wood Carbon Mass lost, other mortality mechs.): Units=kg C m-2 s-1, Defined for
## Quantity:      stemmort_fire (Number of stems lost through fire mortality): Units=count ha-1, Defined for format: DBEN, C
## Quantity:      stemmort_fire_rate (fire mortality rate): Units=% yr-1, Defined for format: DBEN, C
## Quantity:      stemmort_greff (Number of stems lost through low growth efficiency mortality): Units=count ha-1, Defined for
## Quantity:      stemmort_greff_rate (low growth efficiency mortality rate): Units=% yr-1, Defined for format: DBEN, C
## Quantity:      stemmort_other (Number of stems lost through other mortality mechs.): Units=count ha-1, Defined for
## Quantity:      stemmort_other_rate (mortality rate, other mechs.): Units=% yr-1, Defined for format: DBEN, C
## Quantity:      stemmort_age (Number of stems lost through age related mortality): Units=count ha-1, Defined for
## Quantity:      stemmort_age_rate (old age related mortality rate): Units=% yr-1, Defined for format: DBEN, C
## Quantity:      stemmort_dist (Number of stems lost through disturbance mortality): Units=count ha-1, Defined for
## Quantity:      stemmort_dist_rate ( disturbance mortality rate): Units=% yr-1, Defined for format: DBEN, C

```

```

#conversion helpers:

```

```

year_to_seconds = 60*60*24*365
seconds_to_year = 1/year_to_seconds

```

```

create_figs = TRUE

```

```

Figs_dir <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_intercompari

```

```

## set all file directories here:

```

```

file.dir.fates <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte
file.dir.lpjguess <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte

```

```

file.dir.orchidee <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte
file.dir.cablepop <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte
file.dir.julesred <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte
file.dir.biomeEP <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_inte
file.dir.biomeE_Standalone <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_r

```

```

#load observations

```

```

obs.path <- "/Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_intercompari

```

```

get_output_LPJGUESS <- function(site,run,var,file.dir,co2_levels = "PS_412ppm/"){
  model_name = "LPJGUESS"
  if(co2_levels == "PS_562ppm/"){
    file.dir. = paste0(file.dir,"PS_562ppm/")
  }
}

```

```

}else{
  file.dir = paste0(file.dir,"PS_412ppm/")
}

# set metadata
source.in <- defineSource(id = site,
                          dir = file.dir ,
                          format = DBEN,
                          name = paste(model_name, site,'-', run),
                          forcing.data = "cru_jra2.2")

var.to.plot <- getField_DBEN(source.in,
                             quant = get_quantity(var),
                             file.name = paste0(file.dir,
                                                  model_name,"_",var,"_",run,"_",site,".nc"),
                             model_name = model_name)

# change metadata
var.to.plot@first.year <- 1 # first year of simulation
var.to.plot@last.year <- dim(var.to.plot@data)[1]
# change real data:
var.to.plot@data$Year <- seq(1,dim(var.to.plot@data)[1])

# [TODO] probably change unit later in actual model output and for dben standard..
if(var == "cmort" | var == "cmort_age" |
   var == "cmort_other" | var == "cmort_greff" | var == "nbp") {
  #convert to -yr:
  end <- dim(var.to.plot@data)[2]
  var.to.plot@data[,4:end] <- var.to.plot@data[,4:end] * 1/year_to_seconds
  var.to.plot@quant@units <- "kgC m-2 yr-1"
}

if(var == "gpp" ){
  var.to.plot <- change_unit_stoy(var.to.plot)
}

return(var.to.plot)
}

get_output_BiomeEP <- function(site,run,var,file.dir,co2_levels){
  model_name = "BiomeEP"
  #site = c("Fi1")
  #run = c("p0")
  # set metadata
  source.in <- defineSource(id = site,
                            dir = file.dir ,
                            format = DBEN,
                            name = paste(model_name, site,'-', run),
                            forcing.data = "cru_jra2.2")

  #adress the fact that for filename with var = "cmort_size", the variable name within = "cmort"
  if(var== "cmort_size"){
    var.to.plot <- getField_DBEN(source.in,

```

```

        quant = get_quantity("cmort"),
        file.name = paste0(file.dir,co2_levels,"/",site,"/",
        model_name,"_",var,"_",run,"_",site,"_",co2_levels,".nc"),
        model_name = model_name)
}else if(var == "stemmort_size"){ # see above.
    var.to.plot <- getField_DBEN(source.in,
        quant = get_quantity("stemmort"),
        file.name = paste0(file.dir,co2_levels,"/",site,"/",
        model_name,"_",var,"_",run,"_",site,"_",co2_levels,".nc"),
        model_name = model_name)
}else{ # normal procedure:
    var.to.plot <- getField_DBEN(source.in,
        quant = get_quantity(var),
        file.name = paste0(file.dir,co2_levels,"/",site,"/",
        model_name,"_",var,"_",run,"_",site,"_",co2_levels,".nc"),
        model_name = model_name)
}

    #[TODO] probably change unit later..
if(var == "cmort" | var == "cmort_age" |
    var == "cmort_other" | var == "cmort_greff") {
    #convert to -yr:
    end <- dim(var.to.plot@data)[2]
    var.to.plot@data[,4:end] <- var.to.plot@data[,4:end] * 1/year_to_seconds
    var.to.plot@quant@units <- "kgC m-2 yr-1"
}
# if(var == "npp"){
#   var.to.plot <- change_npp_unit(var.to.plot)
#}
return(var.to.plot)
}

get_output_BiomeE_standalone <- function(site,run,var,file.dir,co2_levels){
    model_name = "BiomeE"
    if(co2_levels=="562ppm"){
        co2_levels = "eCO2"
    }
    if(co2_levels == "412ppm"){
        co2_levels = "aCO2"
    }
    #run = c("p0")
    # set metadata
    source.in <- defineSource(id = site,
        dir = file.dir.biomeE_Standalone ,
        format = DBEN,
        name = paste(model_name, site,'-', run),
        forcing.data = "cru_jra2.2")

    var.to.plot <- getField_DBEN(source.in,
        quant = get_quantity(var),
        file.name = paste0(file.dir,model_name,"_PS_",
        site,"_",co2_levels,

```

```

                                "_",run,"_",var,".nc") ,
                                model_name = model_name)

#paste0(file.dir,model_name,"_",run,"_",site,"_",co2_levels,"_00_",var,".nc")
# /Users/annemarie/Documents/1_TreeMort/2_Analysis/3_analysis_demographic_model_intercomparison/Pape
# [TODO] probably change unit later..
if(var == "cmort" | var == "cmort_age" |
    var == "cmort_other" | var == "cmort_greff") {
  #convert to -yr:
  end <- dim(var.to.plot@data)[2]
  var.to.plot@data[,4:end] <- var.to.plot@data[,4:end] * 1/year_to_seconds
  var.to.plot@quant@units <- "kgC m-2 yr-1"
}

return(var.to.plot)
}
get_output_CABLEPOP <- function(site,run,var,file.dir,co2_levels){
  model_name="CABLE-POP"
  # flexibly account for file naming:
  if(run == "0"){
    #benchmark run
    file.name = paste0(file.dir,co2_levels,"/",model_name,"_",var,"_P0_",site,".nc")
  }else{ # sensitivity runs:
    file.name = paste0(file.dir,co2_levels,"/",model_name,"_",var,"_PS_",site,"_",run,".nc")
  }

  # set metadata
  source.in <- defineSource(id = site,
                            dir = file.dir ,
                            format = DBEN,
                            name = paste(model_name, site,'-', run),
                            forcing.data = "cru_jra2.2")

  var.to.plot <- getField_DBEN(source.in,
                              quant = get_quantity(var),
                              file.name = file.name,
                              model_name="CABLE-POP")

  # CABLE-POP_AGcwood_PS_BCI_1.nc

  # split up size classes graph to make more readable.
  # create shared maximum y axis to make graphs more interpretable. maybe change back later
  ymax <- max(var.to.plot@data$Total)

  # print(plotTemporal(var.to.plot))#y.scale_log = TRUE))
  # p <- plotTemporal(var.to.plot)
  # [TODO] tidy..
  c("cmort_crowd", "cmort_dist", "cmort_res")
  # [TODO] probably change unit later..

```



```

    if(var == "cmort" | var == "cmort_crowd" | var == "cmort_dist" | var == "cmort_res"){
      var.to.plot <- change_unit_stoy(var.to.plot)
    }
    if(var == "npp" | var == "gpp" | var == "nbp"){
      var.to.plot <- change_unit_stoy(var.to.plot)
    }

    return(var.to.plot)
  }
}

get_output_JULESRED <- function(site,run,var,file.dir,co2_levels){
  model_name = "JULES-RED"
  # set metadata
  source.in <- defineSource(id = site,
                           dir = file.dir ,
                           format = DBEN,
                           name = paste(model_name, site,'-', run),
                           forcing.data = "cru_jra2.2")

  var.to.plot <- getField_DBEN(source.in,
                              quant = get_quantity(var),
                              file.name = paste0(file.dir,
                                                  model_name,"_",var,"_PS_",co2_levels,"_",site,"_",run,".nc"),
                              model_name = model_name)

  # split up size classes graph to make more readable.
  # create shared maximum y axis to make graphs more interpretable. maybe change back later
  ymax <- max(var.to.plot@data$Total)

  #print(plotTemporal(var.to.plot))#y.scale_log = TRUE))
  p <- plotTemporal(var.to.plot)

  # [TODO] probably change unit later..
  if(var == "cmort" | var == "cmort_age" |
     var == "cmort_other" | var == "cmort_greff") {
    #convert to -yr:
    end <- dim(var.to.plot@data)[2]
    # var.to.plot@data[,4:end] <- var.to.plot@data[,4:end] * 1/year_to_seconds
    var.to.plot@quant@units <- "kgC m-2 yr-1"
  }

  if(var == "npp" | var == "gpp" | var == "nbp"){
    var.to.plot <- change_unit_stoy(var.to.plot)
  }

  return(var.to.plot)
}

get_output_FATES <- function(site,run,var,file.dir,model_name){
  model_name = "FATES"
  if(site == "FIN"){siteFates="fi"}
  if(site == "BIA"){siteFates = "bia"}
  if(site == "BCI"){siteFates = "bci"}

```

```

if(run == "P0"){runFates = "p0"}
  # set metadata
  source.in <- defineSource(id = site,
                           dir = file.dir ,
                           format = DBEN,
                           name = paste(model_name, site, '-', run),
                           forcing.data = "cru_jra2.2")

# obtain total stemmort from under and overstory:
if(var == "stemmort"){ #
  var.to.plot_under <- getField_DBEN(source.in,
                                     quant = get_quantity(var),
                                     file.name = paste0(file.dir,site,"/",runFates,"/",
                                                         model_name,"_",var,"_",
                                                         runFates,"_",siteFates,"_understory.nc"),
                                     model_name = model_name)

  var.to.plot_over <- getField_DBEN(source.in,
                                    quant = get_quantity(var),
                                    file.name = paste0(file.dir,site,"/",runFates,"/",
                                                         model_name,"_",var,"_",
                                                         runFates,"_",siteFates,"_overstory.nc"),
                                    model_name = model_name)

  var.to.plot <- var.to.plot_under # "initilise" to keep metadata
  var.to.plot@data[,4:20] <- var.to.plot_under@data[,4:20] + var.to.plot_over@data[,4:20]

  #print(plotTemporal(var.to.plot))

  if(create_figs == TRUE){
    jpeg(filename = paste0(Figs_dir,paste(var, run, site, model_name,sep="_"),".jpeg") )
    print(plotTemporal(var.to.plot))
    dev.off()
  }

}else{
  var.to.plot <- getField_DBEN(source.in,
                              quant = get_quantity(var),
                              file.name = paste0(file.dir,site,"/",runFates,"/",
                                                    model_name,"_",var,"_",runFates,"_",siteFates,".nc"),
                              model_name = model_name)

  #[TODO] probably change unit later..
  if(var == "npp" | var == "gpp" | var == "nbp"){
    var.to.plot <- change_unit_stoy(var.to.plot)
  }

  } # done reading in variables
  return(var.to.plot)
}

#temporary function, to change units for some fluxes where needed
change_unit_stoy <- function(var_to_plot){
  year_to_seconds = 31536000

```

```

    #convert to -yr:
    end <- dim(var_to_plot@data)[2]
    var_to_plot@data[,4:end] <- var_to_plot@data[,4:end] * year_to_seconds
    var_to_plot@quant@units <- "kgC m-2 yr-1"
    return(var_to_plot)
}

#aesthetics for consistent plotting
#x allowed to be biome name or site name, for more convenient use
get_biome_colour <- function(x){

  #preparation:
  biomes <- c("Boreal","Temperate","Tropics")
  sites <- c("FIN", "BIA", "BCI")
  cols <- c(1,1,1)#c("dark green","light green","brown")

  #automatic colour coding for biome based on site name:
  if(x %in% sites){
    #retrieval:
    ret_col <- cols[sites==x]
  }

  if(x %in% c("Boreal","Temperate","Tropics")){
    #retrieval:
    ret_col <- cols[biomes==x]
  }

  return(ret_col)
}

#turn into object with function that returns colour when giving it model-name later..
get_model_colour <- function(model){
  # PREPARATION:
  models <- c("FATES","JULES-RED","ORCHIDEE","LPJ-GUESS","CABLE-POP","BiomeEP","BiomeE-Standalone")
  model_cols <- c("orange","red","blue","light blue","grey","purple","magenta")
  plot_mod_cols <- data.frame(models,model_cols)

  #RETRIEVAL:
  ret_col <- plot_mod_cols[which(plot_mod_cols$models == model), ]$model_cols
  return(ret_col)
}

#stand-structure related shared objects:
sc <- c( "<1" , "<5" , "<10" , "<15" , "<20" , "<30" , "<40" , "<50" , "<60" , "<70" , "<80" ,

#to deal with different file naming conventions:
runs = c("P1","P2","P3","P4","P5","P6","P7")

```

```

runs_biomeEP <- c("P0","PS1","PS2","PS3","PS4","PS5","PS6")

#Disturbance: stand-replacing (resetting to initial conditions) and stochastic with mean frequency
#of:0.01, 0.02, 0.04, 0.08, 0.20, 0.40 (corresponding to the file names: _01, _02, _04, _08, _20, _40)
runs_biomeES <- c("00","01", "02", "04", "08", "20", "40")
runs_julesred = c("1","2","3","4","5","6","7")
runs_cablepop = c("1","2","3","4","5","6","7")
#[TODO] re-naming of biomeEP scenarios once PS1 is run.

#biome-specific points on graphs:
Tropics_pch = 16
Temperate_pch = 16
Boreal_pch = 16

# function to plot a model's stand structure output alongside observations.
# nstem_size can be plotted on log yaxis (log = TRUE) or not
# ylim_ext can override automatically generated ylim values.
# model name must match the model name used for get_model_colour
# var the DBEN variable that should be plotted.
stand_structure_benchmarks <- function(model_name = "LPJ-GUESS",site_in = site,log =TRUE, var_in = var,

  if(model_name == "LPJ-GUESS"){

  }
  if(model_name == "BiomeEP"){
    model_out <- get_output_BiomeEP(site = site_in,run = "P0",var = var_in,file.dir = file.dir.biomeEP,
  }

#####
if(var_in == "nstem_size"){
  ##plot models - nstem_size
  dbh_classes_plot <- stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num
  #subset of dbh- classes for plotting, because in the observations there are no more than that.
  #[TODO]would ideally subset with this vector of column names, but it somehow doesnt, work. doing th
  dbh_classes_sel <- c( "<1" , " <5" , " <10", "<15", " <20" , " <30", " <40" , "<50" , " <60" ,

  #make ylims flexible, or prescribe from external:
  max_model_output <- max(model_out@data[,
    c( "<1" , " <5" , " <10", "<15", " <20" , " <30", " <40"
      "<90" , " <100", " <150" , "<200", ">=200")])
  min_model_output <- max(model_out@data[,
    c( "<1" , " <5" , " <10", "<15", " <20" , " <30", " <40"
      "<90" , " <100", " <150" , "<200", ">=200")])
  max_obs <- max( na.omit(stand_structure_obs[,c("AGB_size_kgCm.2","AGB_size_upper_kgCm.2","AGB_size_
  min_obs <- min( na.omit(stand_structure_obs[,c("AGB_size_kgCm.2","AGB_size_upper_kgCm.2","AGB_size_

  #check if external ylims are present or not:
  if(is.null(ylim_ext)){ # not present, obtain ylim_set from within
    ylim_set = c(min(min_obs,min_model_output),max(max_obs,max_model_output))

```

```

}else{
  ylim_set = ylim_ext # present. pass external ylims to ylim_set
}

  #if nstem should be logged:
  if(log ==TRUE){

    if(is.null(ylim_ext)){ # not present, obtain ylim_set from within
      ylim_set = log(ylim_set)
      ylim_set[ylim_set ==-Inf] <- -2
    }

    plot(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
          log(model_out@data[model_out@data$Year == max(model_out@data$Year),
            c( "<1" ,    "<5" ,    "<10", "<15", "<20" , "<30",    "<40" , "<50" , "<60" ,
              "<90" , "<100", "<150" , "<200", ">=200")]],
          ylim = ylim_set ,col= get_model_colour(model_name),pch=16,cex=1.5,ylab="")

    points(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
            log(stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_ha.1),
            col= get_biome_colour(site))
    arrows(stand_structure_obs$dbh_classes_num,
            log(stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_lower_ha.1),
            stand_structure_obs$dbh_classes_num,
            log(stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_upper_ha.1),
            length = 0.00, angle = 90, code = 3,
            col= get_biome_colour(site) )
    mtext(site,adj=0.95,side=3,line=-1.3)
    mtext(side=2,"log(nstem_size) (nstem)",line=2,outer=FALSE)

  }else { # nstem not logged

    plot(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
          model_out@data[model_out@data$Year == max(model_out@data$Year), c( "<1" ,    "<5" ,    "<10", "<15", "<20" , "<30",
            "<40" , "<50" , "<60" , "<90" , "<100", "<150" , "<200", ">=200")]],
          ylim = ylim_set ,col= get_model_colour(model_name),pch=16,cex=1.5)

    points(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
            stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_ha.1,
            col= get_biome_colour(site))
    arrows(stand_structure_obs$dbh_classes_num,
            stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_lower_ha.1,
            stand_structure_obs$dbh_classes_num,
            stand_structure_obs[which(stand_structure_obs$site == site),]$nstem_size_upper_ha.1,
            length = 0.00, angle = 90, code = 3,
            col= get_biome_colour(site) )
    mtext(site,adj=0.95,side=3,line=-1.3)
    mtext(side=2,"nstem_size (nstem)",line=2,outer=FALSE)
  }
}

```

```

}

#####
if(var_in == "cwood_size"){
  # cwood plots
  max_model_output <- max(model_out@data[,c( "<1" ,   "<5" ,   "<10", "<15", "<20" ,
                                             "<30",   "<40" , "<50" , "<60" , "<70" , "<80" , "<90" ,
max_obs <- max( na.omit(stand_structure_obs[,c("AGB_size_kgCm.2","AGB_size_upper_kgCm.2","AGB_size_

  #check if external ylims are present or not:
if(is.null(ylim_ext)){ # not present, obtain ylim_set from within
  ylim_set = c(0,max(max_obs,max_model_output) + max(max_obs,max_model_output)*0.1)
}else{
  ylim_set = ylim_ext # present. pass external ylims to ylim_set
}

plot(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
     model_out@data[model_out@data$Year == max(model_out@data$Year), c( "<1" ,   "<5" , "<10", "<15",
                                                                           "<30",   "<40" , "<50" ,
     ylim = ylim_set ,col= get_model_colour(model_name),pch=16,cex=1.5,ylab="")

points(stand_structure_obs[which(stand_structure_obs$site == site),]$dbh_classes_num,
       stand_structure_obs[which(stand_structure_obs$site == site),]$AGB_size_kgCm.2, col= get_bior
arrows(stand_structure_obs$dbh_classes_num,
       stand_structure_obs[which(stand_structure_obs$site == site),]$AGB_size_lower_kgCm.2,
       stand_structure_obs$dbh_classes_num,
       stand_structure_obs[which(stand_structure_obs$site == site),]$AGB_size_upper_kgCm.2,
       length = 0.00, angle = 90, code = 3,
       col= get_biome_colour(site) )
mtext(site,adj=0.95,side=3,line=-1.3)

mtext(side=2,"AGcwood (kgC m-2)",line=2,outer=FALSE)
}

}

#convenience function for grid.arrange
#passes back ggplot object for each model_output (input)
create_gobj <-function(model_out, y.lim = NULL){
  p_out <- plotTemporal(model_out, legend.position = "none", title = model_out@source@name, y.lim )

return(p_out)
}

```

Individual variables

Plotted for all model variables, in order of occurrence in the protocol table. Sometimes I have questions to the model outputs. Please, everyone if you come across something fishy, point it out, and the people who know the models, please feel responsible in answering the questions.

cwood_size and nstem_size are not plotted here.

cveg

Model	Comments
BiomeEP	
LPJ-GUESS	
FATES	AHES: Why is cveg not 0 at disturbance year?
BiomeES	AHES: Why is cveg not 0 at disturbance year? AHES: -> Grasses ?
JULES-RED	AHES: Why is cveg not 0 at disturbance year?

```

var = "cveg"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim

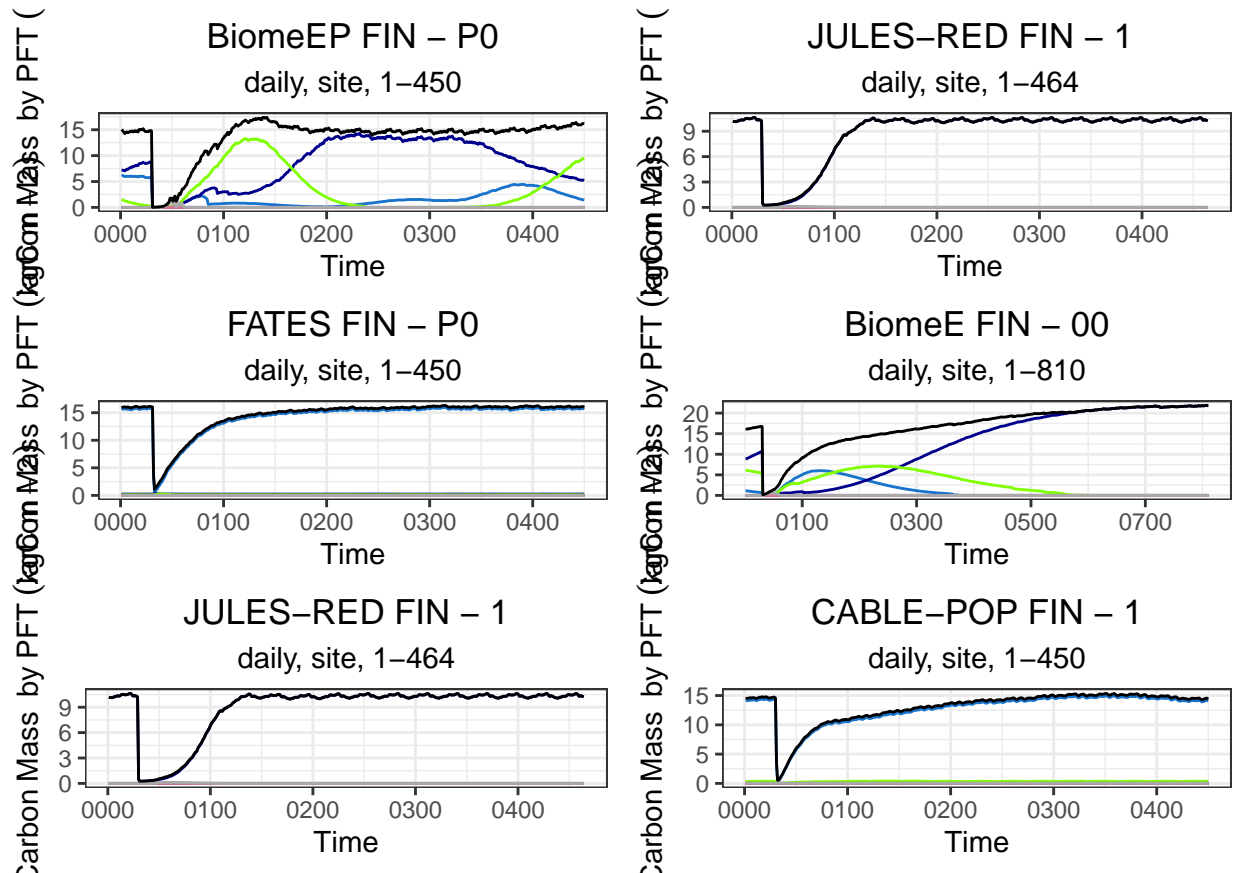
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pJULESRED,pFATES,pBiomeES,pJULESRED,pCABLEPOP)

```



AGcwood

Model	Comments
BiomeEP	AHES: no AGcwood variable. Right now we are not comparing like-for-like here. What do we do for the paper: argue with low leaf carbon content ("The biomass of leaves is low, 0.2~0.4 kg C m ⁻² .) or remove leaf fraction?
LPJ-GUESS	
FATES	
BiomeES	
JULES-RED	AHES: Why does this not go to 0 at distyear?

```

var = "AGcwood"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")

```



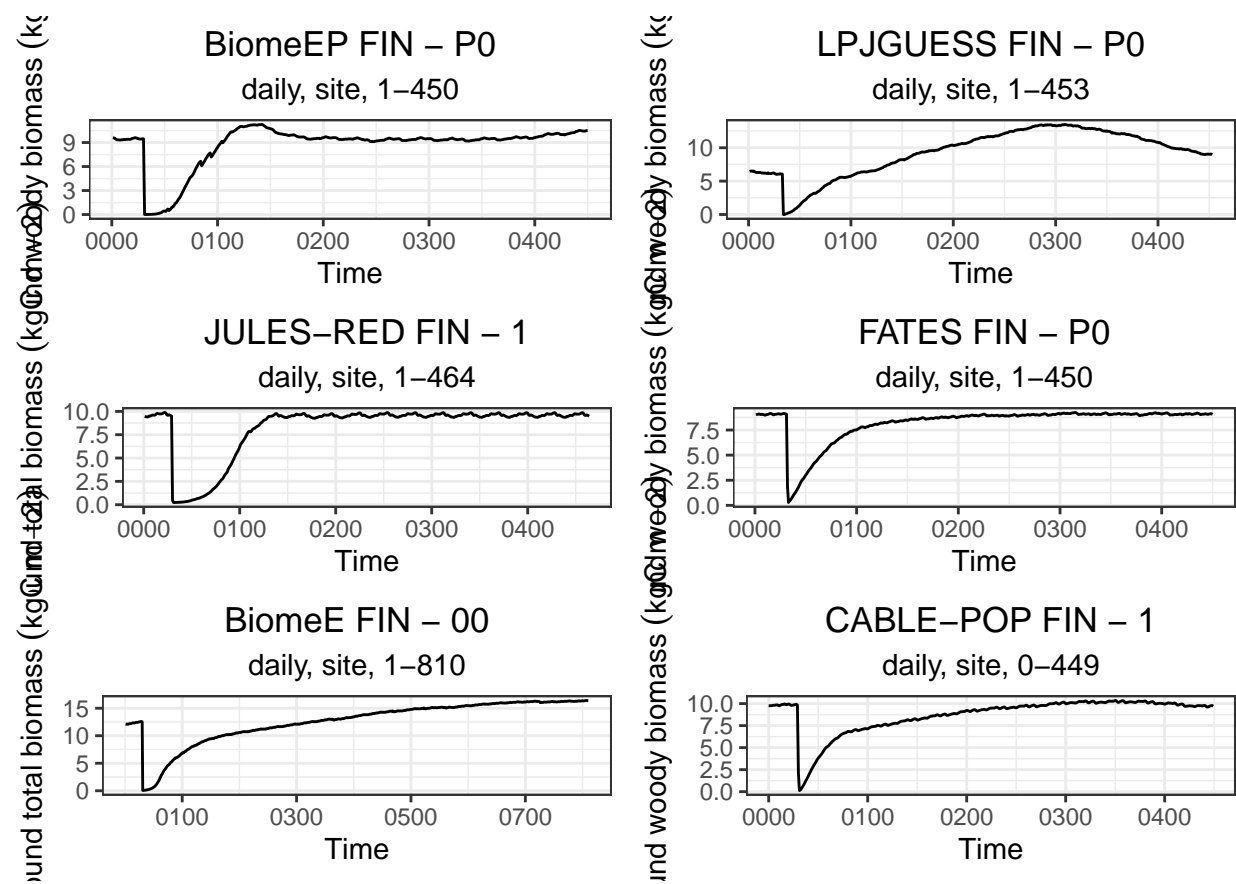
```
pFATES <- create_gobj(FATES)

#AHES: AGB not AGcwood
BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = "AGB", file.dir.biomeE_Standalone,co2_level = "PS_412ppm")
pBiomeES <- create_gobj(BiomeES)

#AHES: AGB here AGcwood - note that the automated plotting will provide the wrong metadata for this plot
JULESRED <- get_output_JULESRED(site,run = "1",var = "AGB",file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)
```



cwood

Model	Comments
BiomeEP	
LPJ-GUESS	
FATES	AHES: Why does this not go to 0 at distyear?

Model	Comments
BiomeES	AHES: cwood goes to 0, so in other plots i.e. cveg the non-0 amount is indeed cause by the grass fraction (makes sense to me)
JULES-RED	AHES: Why does this not go to 0 at distyear?

```

var = "cwood"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name ="FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level

```

```
## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim
```

```

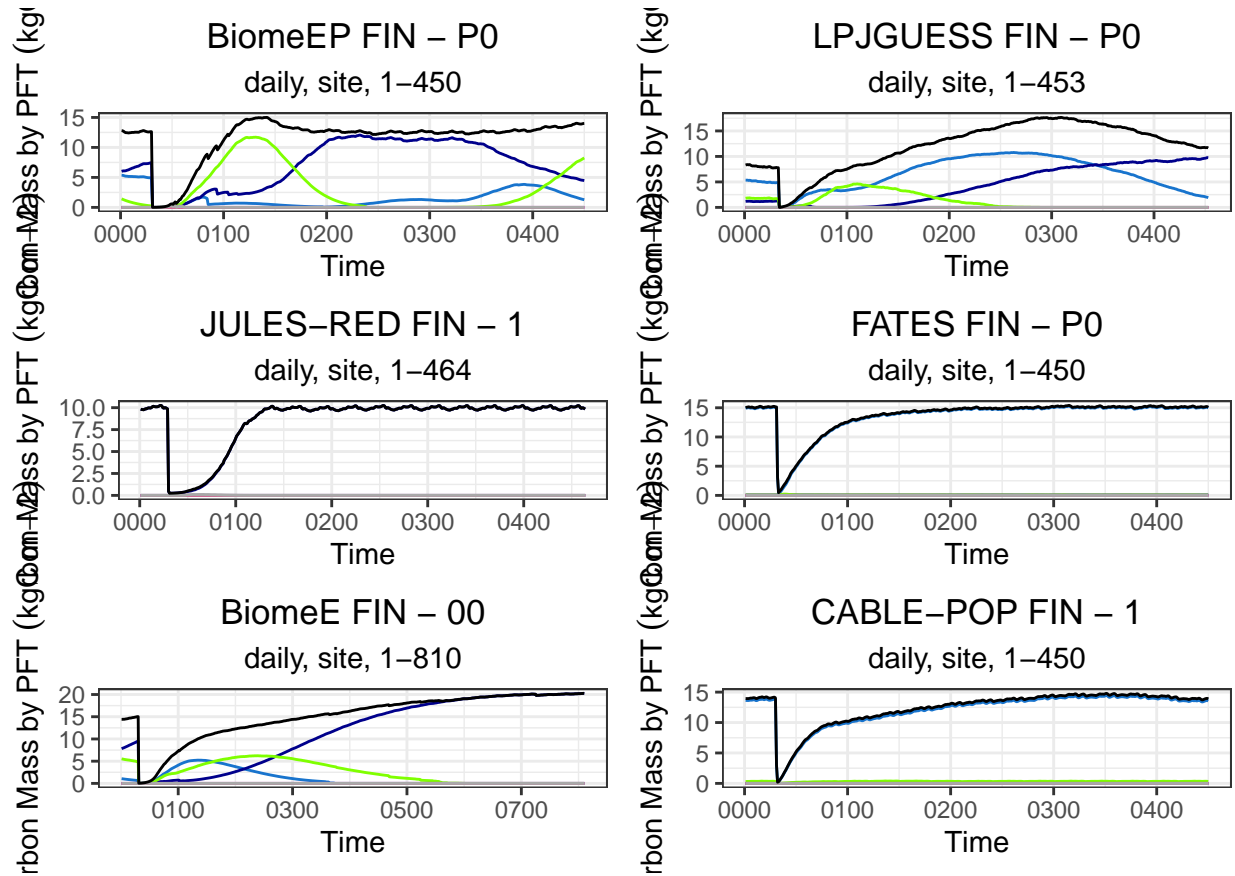
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run ="1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```



lai

Model	Comments
BiomeEP	
LPJ-GUESS	
FATES	Why is LAI never 0?
BiomeES	Why is LAI never 0? -> Grass fraction?
JULES-RED	Why is LAI never 0?
CABLE-POP	Why is LAI never 0?

```

var = "lai"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

```

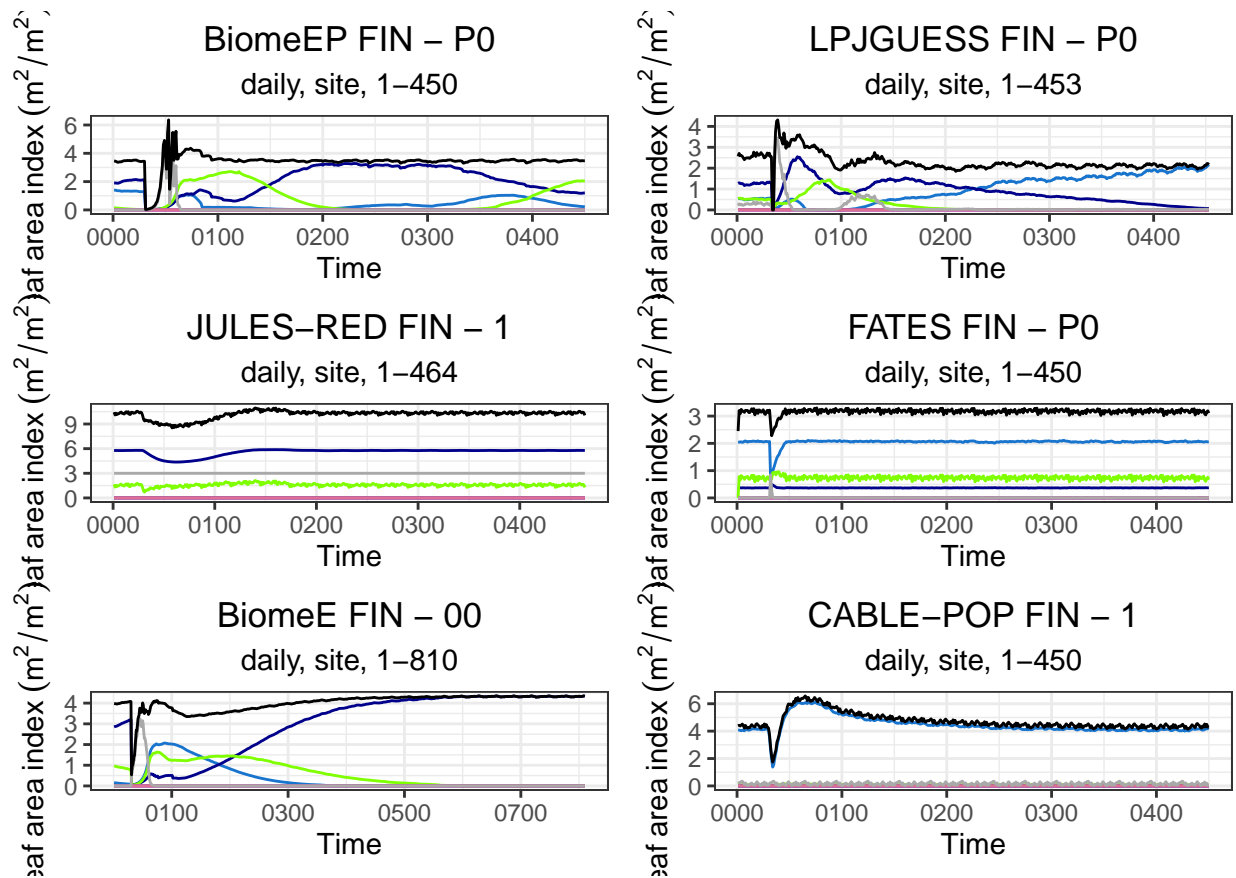
```
## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim
```

```
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)
```



##Crown Area — Projected crown area or PFT /multi canopy crown area ?

Issue with Crown area variable definition

How to standardise amongst models? What do we want to compare against? I would say satellite observations? Is Crownarea otherwise comparable against any other observations? Maybe some LIDAR observations?

Model	Comments
JULES-RED	projected crown area?
LPJ-GUESS	projected crown area?

Model	Comments
BiomeEP	multi-canopy structure /multi LAI based?
BiomeES	multi-canopy structure /multi LAI based?
FATES	multi-canopy structure /multi LAI based?
CABLE-POP	projected crown area?

```

var = "CA"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim

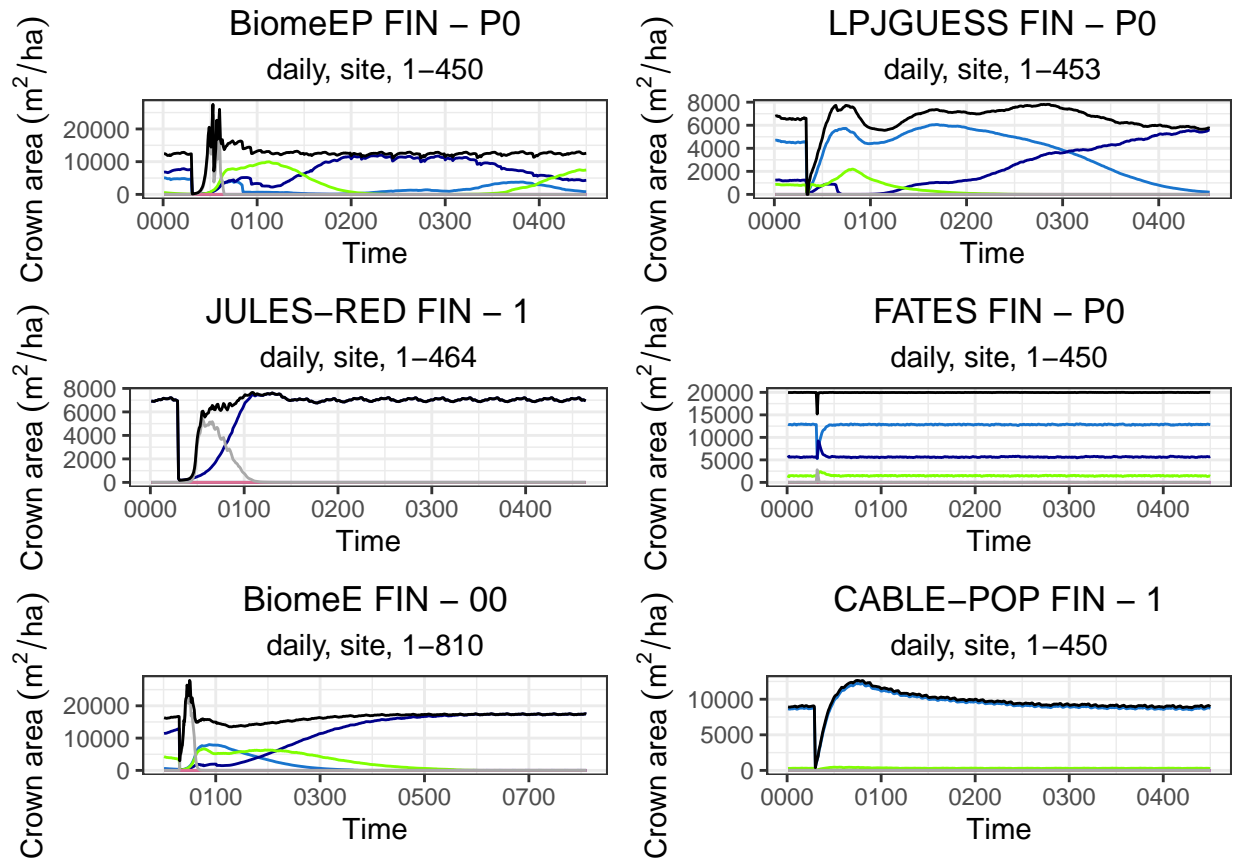
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```



BA

Model	Comments
BiomeEP	AHES: Grasses shouldn't have basal area output.
LPJ-GUESS	
FATES	AHES: BA output missing
BiomeES	
JULES-RED	
CABLE-POP	

```

var = "BA"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

#FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
#plotTemporal(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

```

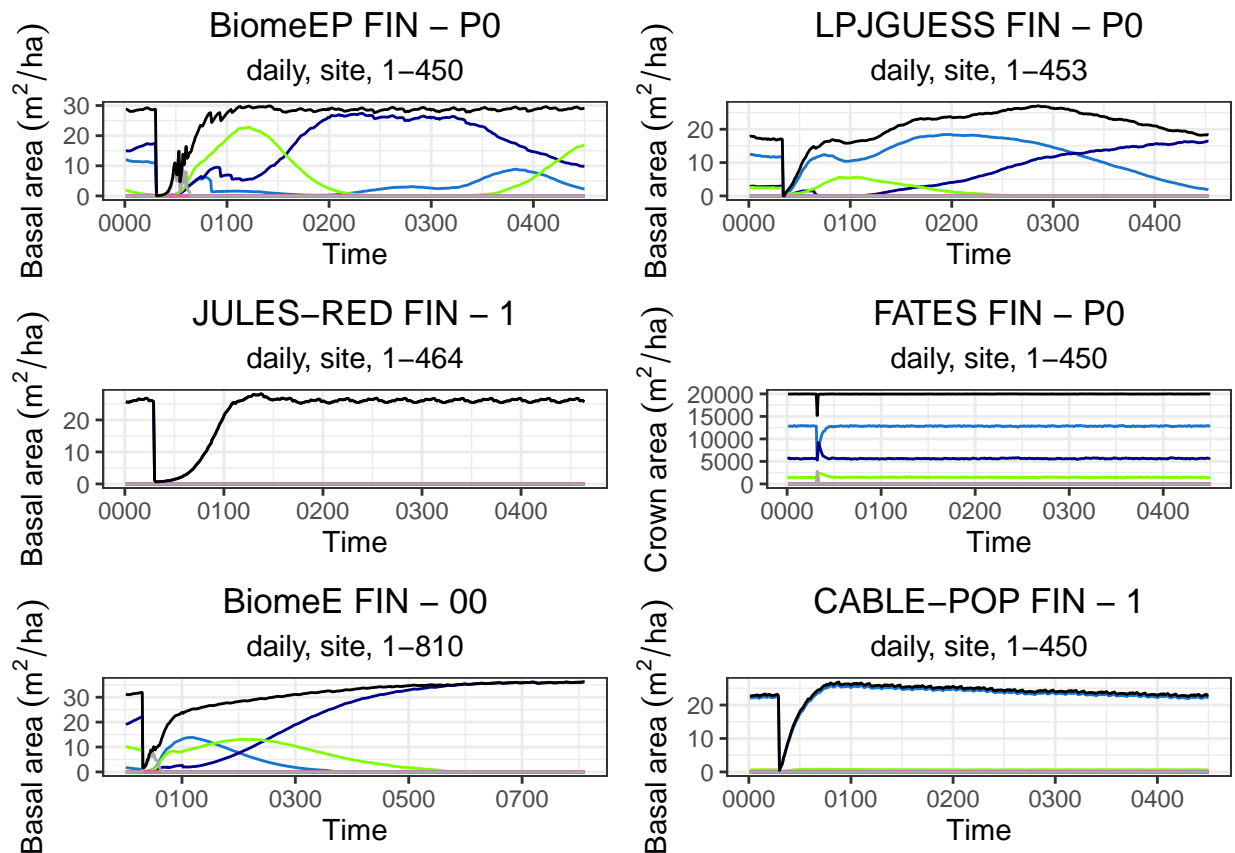
```
## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim
```

```
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)
```



height

[TODO] for height - remove “Total” column, instead plot max, but dotted Height output ambiguous between models. So the y-axis here is misleading and I cannot fully interpret it. Reported in Protocol: “95 th percentile of tree height”

Model	Comments
BiomeEP	AHES: height never goes to 0.
LPJ-GUESS	

Model	Comments
FATES	AHES: no height output. Jessica “We don’t have 95th percentile of height in FATES. I can do crown area weighted height if useful?”
BiomeES	AHES: v. jittery. Why? AHES: height never goes to 0.
JULES-RED	AHES: height never goes to 0.
CABLE-POP	AHES: height never goes to 0.

```

var = "height"
site = "FIN"
run = "P0"
BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)
min(BiomeEP@data$Total)

## [1] 20.28285

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)
# height output confirmed: mean PFT height in 95th percentile.

#FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name ="FATES")
#plotTemporal(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dimension does not exist"

pBiomeES <- create_gobj(BiomeES)
min(BiomeES@data$Total)

## [1] 7.416

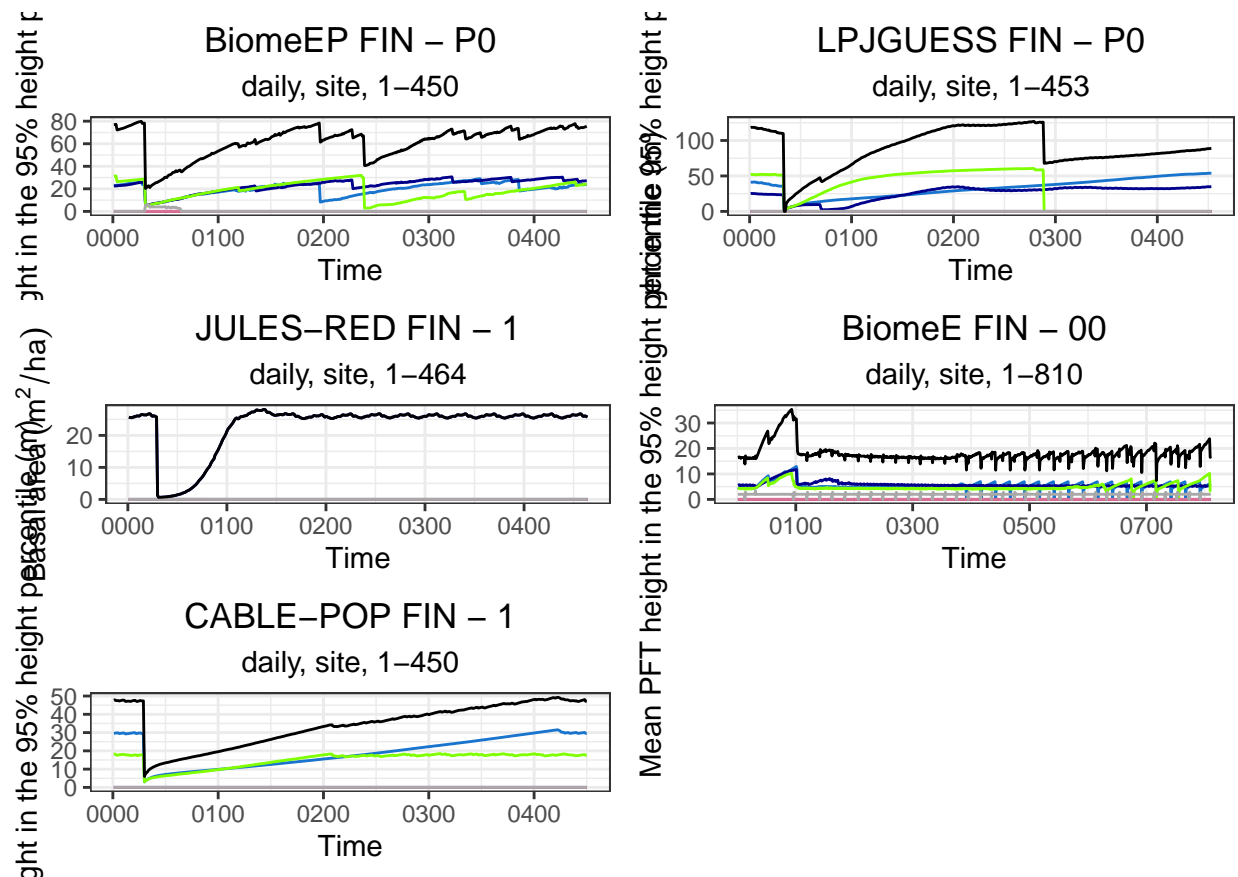
# height confirmed: "95 th percentile of tree height"

JULESRED <- get_output_JULESRED(site,run ="1",var = var,file.dir.julesred,co2_levels = "412ppm")
pCABLEPOP <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pBiomeES,pCABLEPOP)

```

roughness - optional output

The two models which provide this output currently have two orders of magnitude difference in their values.

Model	Comments
BiomeEP	NA
LPJ-GUESS	NA
FATES	AHES: Does show any dynamics in keeping with regrowth dynamics. why?
BiomeES	NA
JULES-RED	NA
CABLE-POP	NA

```

var = "z0"
site = "FIN"
run = "P0"
#BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
#plotTemporal(BiomeEP)

#LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
#plotTemporal(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")

```

```

pFATES <- create_gobj(FATES)

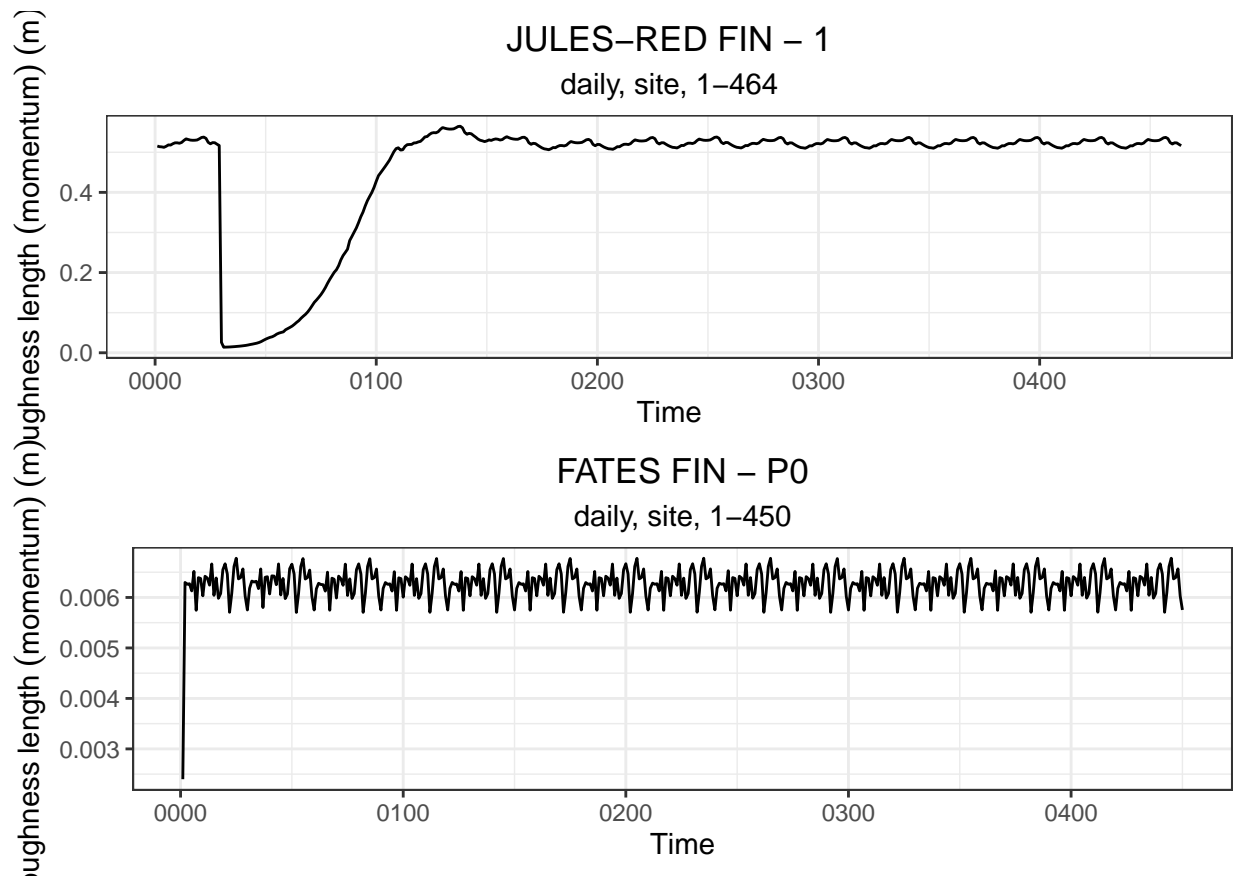
#BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level = "412ppm")
#plotTemporal(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

#CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
#pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pJULESRED,pFATES)

```



albedo - optional output

Model	Comments
BiomeEP	NA
LPJ-GUESS	AHES: NA[TODO] get this from post processing still..
FATES	AHES: Does show any dynamics in keeping with regrowth dynamics. why?
BiomeES	NA

Model	Comments
JULES-RED CABLE-POP	AHES: no trace of regrowth, but in the same bulpark as JULES-RED when in equilibrium. Juergen Knauer in email: drop this variable. AHES: but maybe easy to fix?

```

var = "albedo"
site = "FIN"
run = "P0"

#BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
#plotTemporal(BiomeEP)

#LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
#plotTemporal(LPJGUESS)

#FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
#plotTemporal(FATES)

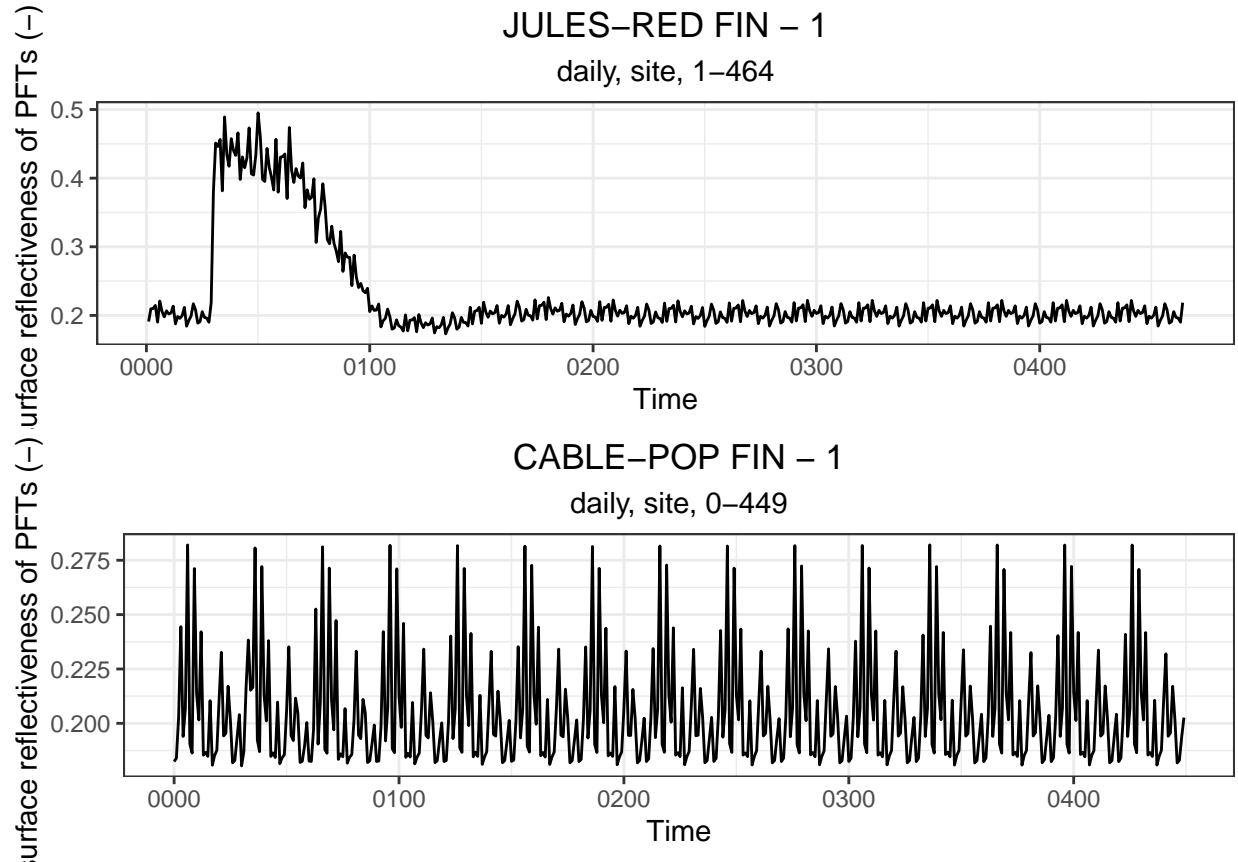
#BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "PS_412ppm")
#plotTemporal(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pJULESRED,pCABLEPOP)

```



WBgrowth

Model	Comments
BiomeEP	AHES: remove grasses. double-check the output is indeed woody biomass only, not something like cveg or another carbon pool.
LPJ-GUESS	AHES: not gross growth?!
FATES	AHES: never goes to 0.
BiomeES	AHES: remove grasses. double-check the output is indeed woody biomass only, not something like cveg or another carbon pool.
JULES-RED	AHES: remove grasses. double-check the output is indeed woody biomass only, not something like cveg or another carbon pool.
AHES: why no BINE PFT in FIN? CABLE-POP	AHES: WBgrowth rate not much influenced by regrowth-dynamics. AHES: add PFT dimension easily possible? (not to worry for this analysis?)

```
var = "WBgrowth"
site = "FIN"
run = "P0"
```

```

BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level

```

```
## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim"

```

```

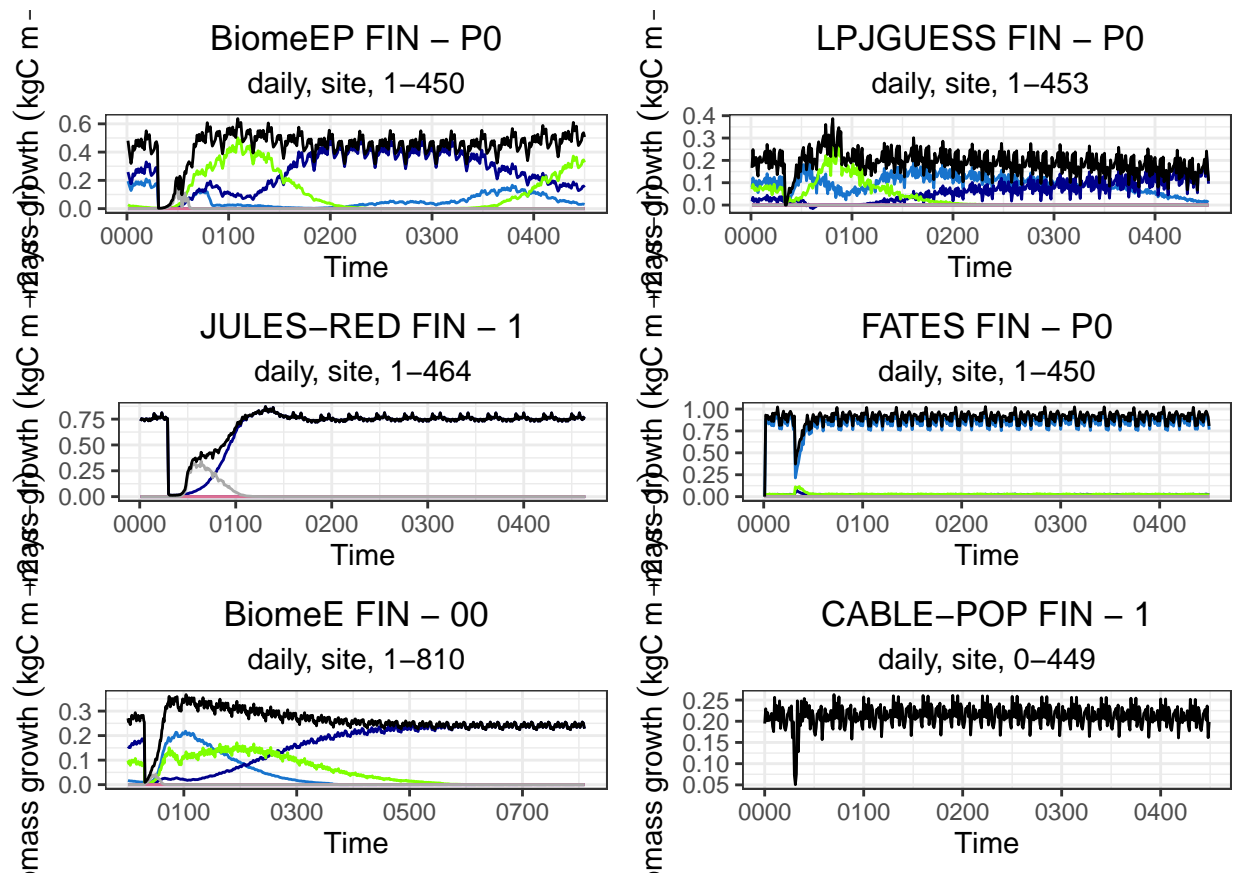
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```



BAGrowth

Model	Comments
BiomeEP	AHES: remove grasses. double-check the output is BAGrowth, not something like cveg or another carbon pool. Units are also v.high.
LPJ-GUESS	AHES: maybe not gross growth?
FATES	NA
BiomeES	AHES: remove grasses. double-check the output is indeed woody biomass only, not something like cveg or another carbon pool.
JULES-RED	AHES: negative basal area growth.
CABLE-POP	AHES: add PFT dimension easily possible? (not to worry for this analysis?)

```

var = "BAGrowth"
site = "FIN"
run = "P0"

BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

#FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
#plotTemporal(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim

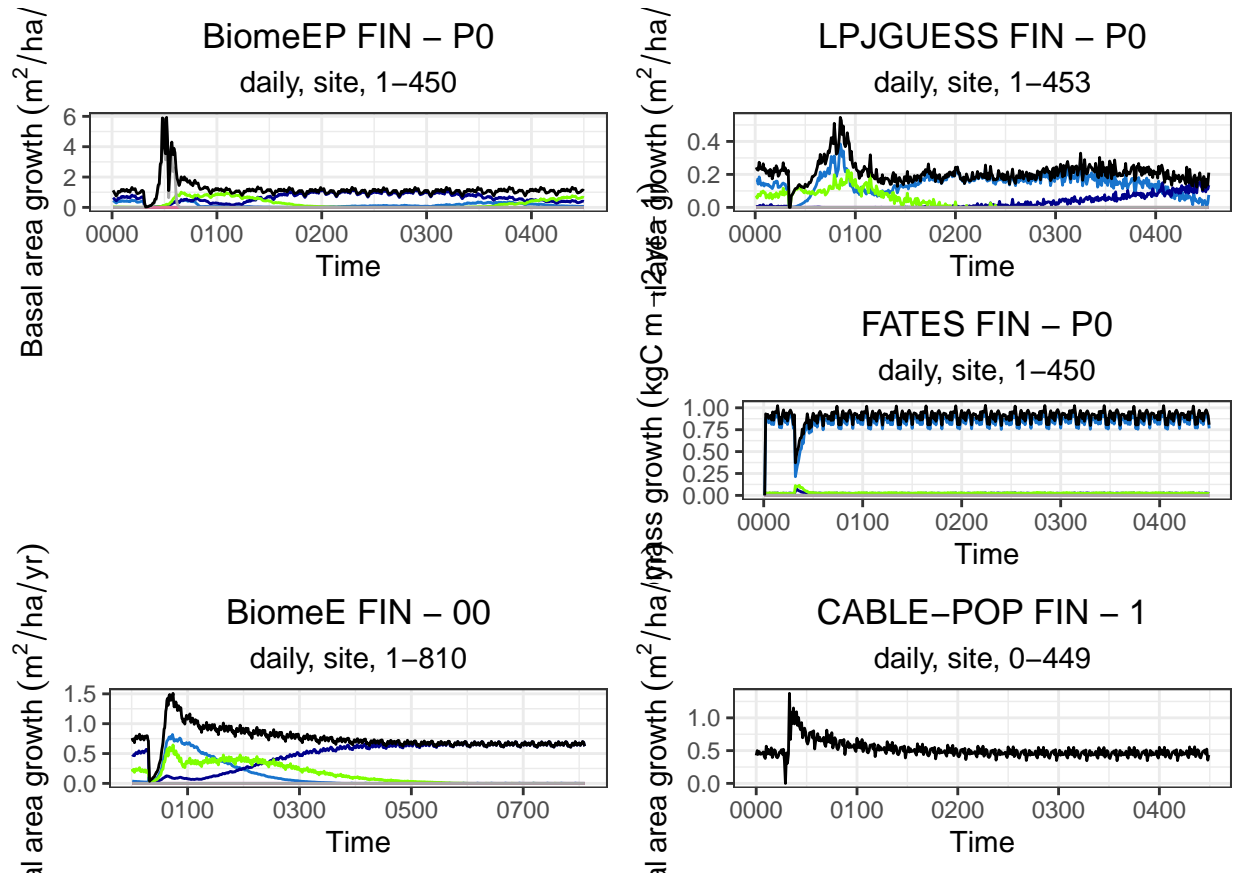
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED,y.lim = c(-6,2))

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```



cmort

BiomeEP, BiomeE and Jules-RED seem to reset to bare ground as a mechanism to introduce disturbance. The rest of the models kills all trees. That way, the mortality flux at the disturbance event is recorded in the output.

Model	Comments
BiomeEP	
LPJ-GUESS	
FATES	
BiomeES	
JULES-RED	
CABLE-POP	Added all mortalities together. according to JK, have to potentially remove cmort_res. This should be done once I have patch-scale data.

```
var = "cmort"
site = "FIN"
run = "P0"
```

```
BiomeEP <- get_output_BiomeEP(site,run,var = "cmort_size",file.dir = file.dir.biomeEP,co2_levels = "412")
pBiomeEP <- create_gobj(BiomeEP)
```

```

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = "cmort_size", file.dir.biomeE_Standalone,
pBiomeES <- create_gobj(BiomeES)

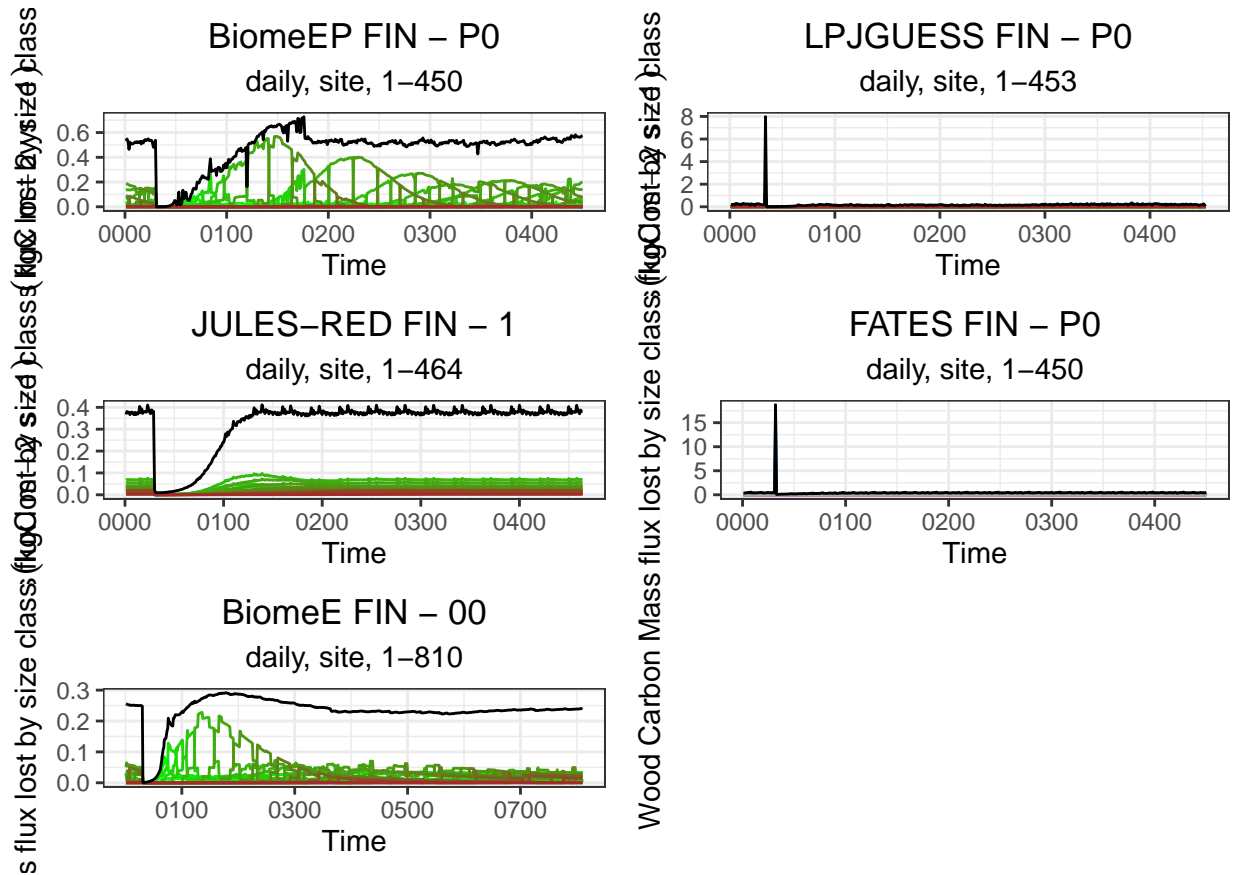
JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

#sum up all cmort mechanisms:
CABLEPOP_ccrowd <- get_output_CABLEPOP(site,run = "0",var = "cmort_crowd",file.dir.cablepop,co2_levels = "PS_412ppm/")
CABLEPOP_cdust <- get_output_CABLEPOP(site,run = "0",var = "cmort_dust",file.dir.cablepop,co2_levels = "PS_412ppm/")
CABLEPOP_cres <- get_output_CABLEPOP(site,run = "0",var = "cmort_res",file.dir.cablepop,co2_levels = "PS_412ppm/")

CABLEPOP <-CABLEPOP_ccrowd@data$Total +CABLEPOP_cdust@data$Total +CABLEPOP_cres@data$Total

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES)

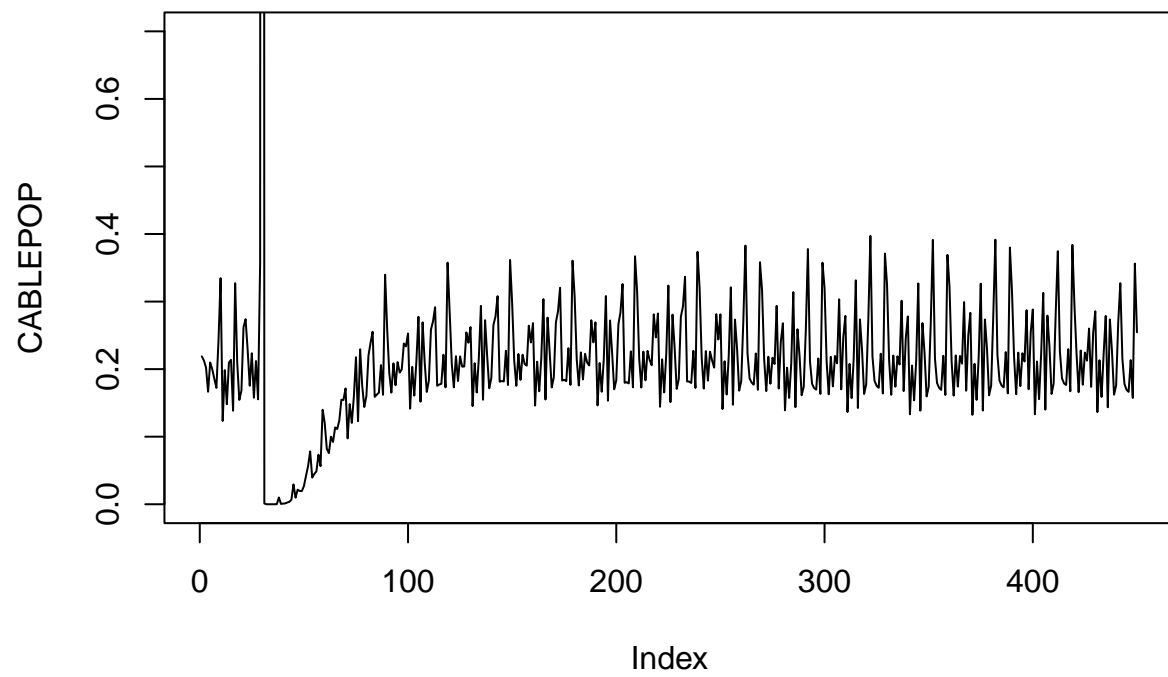
```



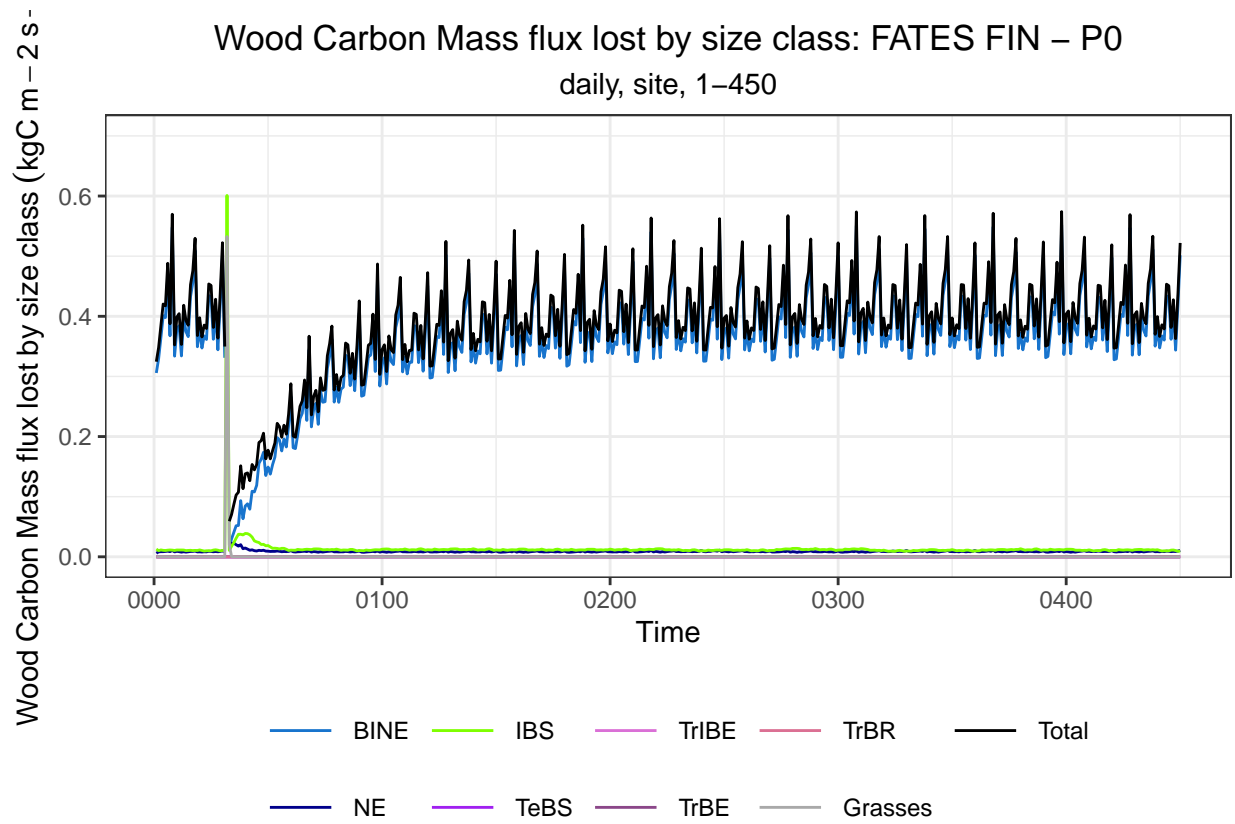
```

plot(CABLEPOP,type="l",ylim=c(0,0.7))

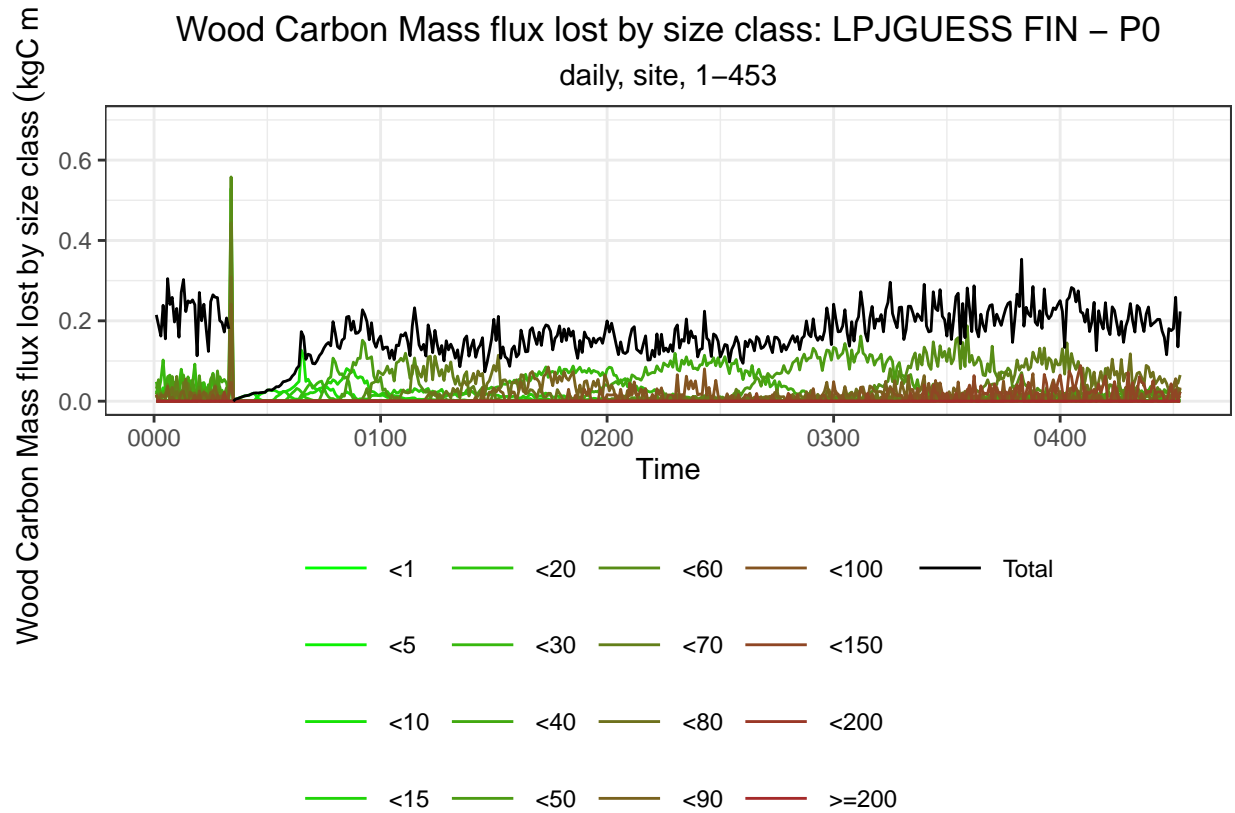
```

```
plotTemporal(FATES,y.lim=c(0,0.7))
```



```
plotTemporal(LPJGUESS,y.lim=c(0,0.7))
```



is the budget closed?

woody growth_rate - mort_rate = 0 (in equilibrium)

Model	Comments
BiomeEP	AHES: too low. One possibility - are the grasses included in the cmort output ?
LPJ-GUESS	AHES: show age mortality (=decline to negative), "Equilibrium" probably maybe more dynamic than other models. OK confirmed with TOM .
FATES	AHES: too high
BiomeES	
JULES-RED	TOO high in equilibrium
CABLE-POP	AHES: With cmort_res included, too low, when cmort_res excluded too high.

Or is this "OK" for CABLE-POP? To me there seems to be a bias, that needs to be adressed.

```
par(mfrow = c(2,3), oma=c(1,2,1,1), mar=c(1,1,1,1))

var = "cmort"
site = "BCI"
```

```

run = "P0"

BiomeEP_cmort <- get_output_BiomeEP(site,run,var = "cmort_size",file.dir = file.dir.biomeEP,co2_levels = "412ppm")
LPJGUESS_cmort <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm")
FATES_cmort <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
BiomeES_cmort <- get_output_BiomeE_standalone(site,run = "00",var = "cmort_size", file.dir.biomeE_Standalone,co2_levels = "412ppm")
JULESRED_cmort <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")

#sum up all cmort mechanisms:
c("cmort_crowd", "cmort_dist", "cmort_res")

## [1] "cmort_crowd" "cmort_dist" "cmort_res"

CABLEPOP_ccrowd <- get_output_CABLEPOP(site,run = "0",var = "cmort_crowd",file.dir.cablepop,co2_levels = "412ppm")
CABLEPOP_cdist <- get_output_CABLEPOP(site,run = "0",var = "cmort_dist",file.dir.cablepop,co2_levels = "412ppm")
CABLEPOP_cres <- get_output_CABLEPOP(site,run = "0",var = "cmort_res",file.dir.cablepop,co2_levels = "412ppm")

CABLEPOP <-CABLEPOP_ccrowd@data$Total +CABLEPOP_cdist@data$Total +CABLEPOP_cres@data$Total
CABLEPOP <-CABLEPOP_ccrowd@data$Total +CABLEPOP_cdist@data$Total

#####
##wbgrowth
var = "WBgrowth"
BiomeEP_WBgrowth <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
#plotTemporal(BiomeEP_WBgrowth)

LPJGUESS_WBgrowth <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm")
FATES_WBgrowth <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
BiomeES_WBgrowth <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dimension does not exist"

JULESRED_WBgrowth <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
CABLEPOP_WBgrowth <- get_output_CABLEPOP(site,run = "0",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")

#####
##AGcwood
var = "AGcwood"
BiomeEP_AGcwood <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
LPJGUESS_AGcwood <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm")
#plotTemporal(LPJGUESS_AGcwood)

FATES_AGcwood <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")

```

```

BiomeES_AGcwood <- get_output_BiomeE_standalone(site,run = "00",var = "AGB", file.dir.biomeE_Standalone

JULESRED_AGcwood <- get_output_JULESRED(site,run = "1",var = "AGB",file.dir.julesred,co2_levels = "412p

CABLEPOP_AGcwood <- get_output_CABLEPOP(site,run = "0",var = var,file.dir.cablepop,co2_levels = "PS_412p

#####

plot(LPJGUESS_WBgrowth@data$Total - LPJGUESS_cmort@data$Total, type="l",main = "LPJGUESS",ylim=c(-2,1))
#woody growth - woody biomass*mort_rate = 0

plot(JULESRED_WBgrowth@data$Total - JULESRED_cmort@data$Total, type="l",main ="JULESRED")
#solved

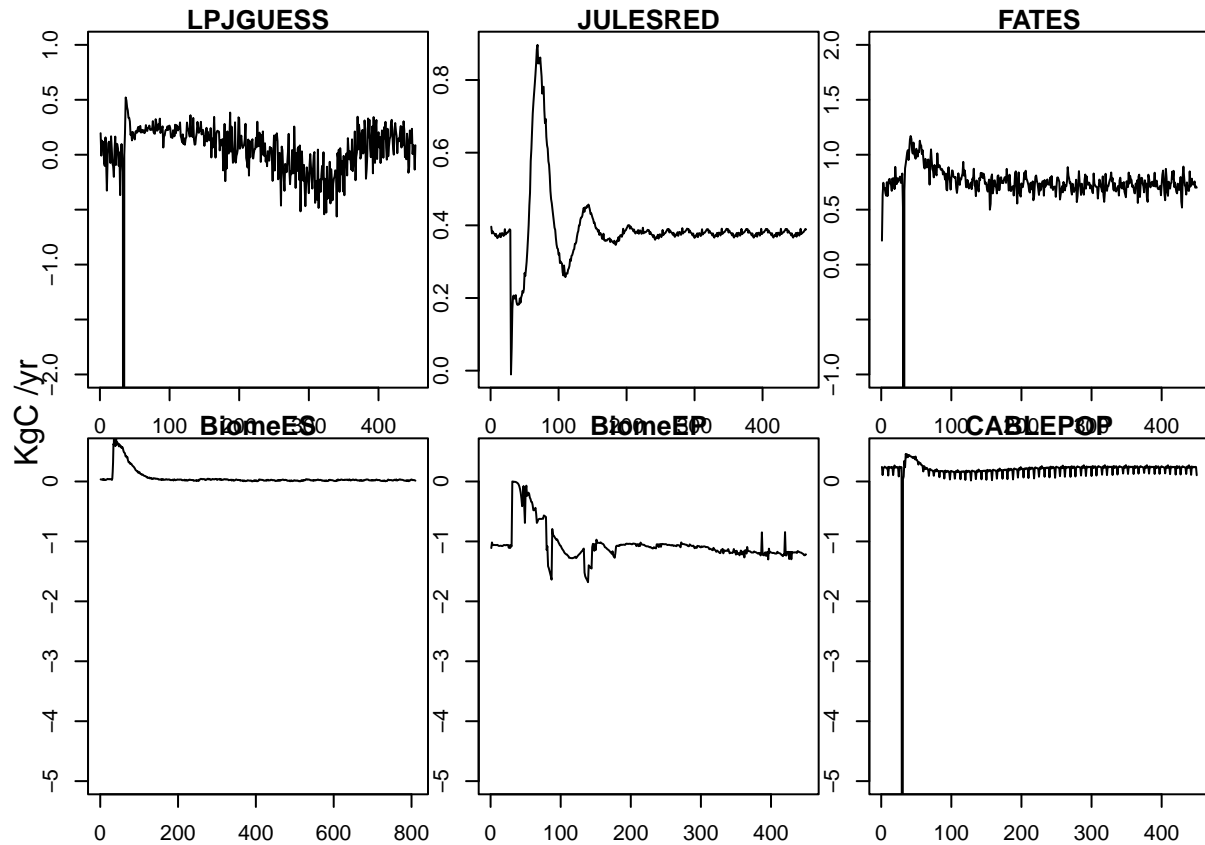
plot(FATES_WBgrowth@data$Total - FATES_cmort@data$Total, type="l",ylim= c(-1,2),main ="FATES")

plot(BiomeES_WBgrowth@data$Total - BiomeES_cmort@data$Total, type="l",ylim= c(-5,0.5),main ="BiomeES")

plot(BiomeEP_WBgrowth@data$Total - BiomeEP_cmort@data$Total, type="l",ylim= c(-5,0.5),main = "BiomeEP")
#Grasses?

plot(CABLEPOP_WBgrowth@data$Total - CABLEPOP, type="l",ylim= c(-5,0.5),main = "CABLEPOP")
mtext(outer=TRUE , "KgC /yr",side =2,line = 0.8)

```



nb:grasses included for BiomeES and BiomeEP in some outputs.

stemmort

Model	Comments
BiomeEP	AHES: Unit low: should be numer of stems /year. *nstems[y-1] ?
LPJ-GUESS	
BiomeES	AHES: Unit low: should be numer of stems /year. *nstems[y-1] ?Why so jittery? Biology model structure or post-processing?
JULES-RED	AHES: what causes the small oscillations on top of the general number flux dynamics?
CABLE-POP	NA

FATES- AHES: output year 1: stem number flux almost 0 AHES: strange oscillations in __overstory.nc, due to PFT2 (e.g. simyear 32)

Year	Lat	Lon	<1	<5	<10	<15	<20
32	62.25	23.25	0	1678.8756	572.7487876	164.84464856	88.34444358

these numbers are also present in the .netcdf file, so not a read-in error. or is this just a quick transition of trees from under- to over-story after the disturbance? But I what is this oscillation exactly?

```
var = "stemmort"
site = "FIN"
run = "P0"

BiomeEP <- get_output_BiomeEP(site,run,var = "stemmort_size",file.dir = file.dir.biomeEP,co2_levels = "PS_412ppm/")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

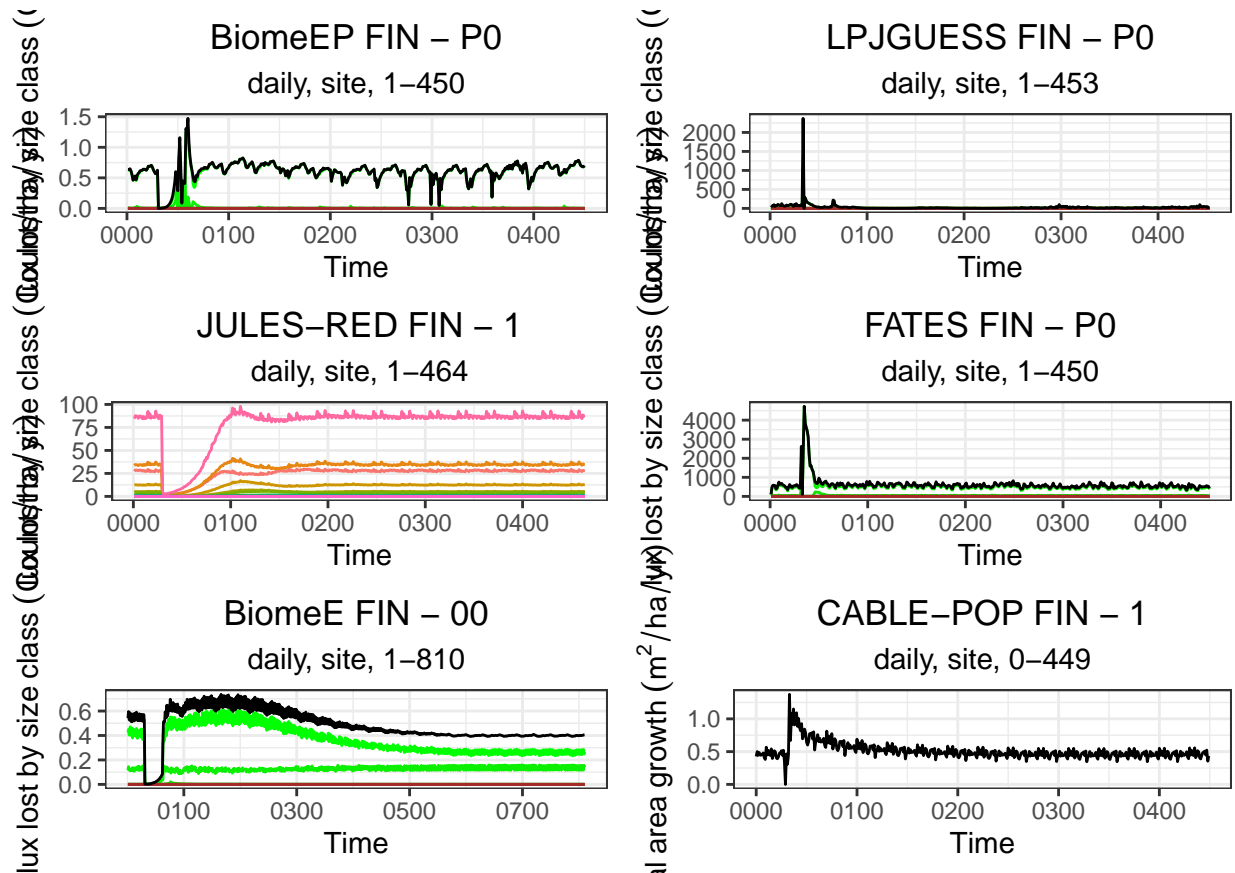
FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = "stemmort_size", file.dir.biomeE_Standalone = file.dir.biomeE_Standalone)
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

#CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
#plotTemporal(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)
```



gpp

Model	Comments
BiomeEP	AHES: netcdf only 0 values for gpp for BCI -double check output
LPJ-GUESS	
FATES	
BiomeES	
JULES-RED	AHES:FIN: only PFT2 really active. PFT1 never present?
CABLE-POP	

```

var = "gpp"
site = "FIN"
run = "P0"

BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")

## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim

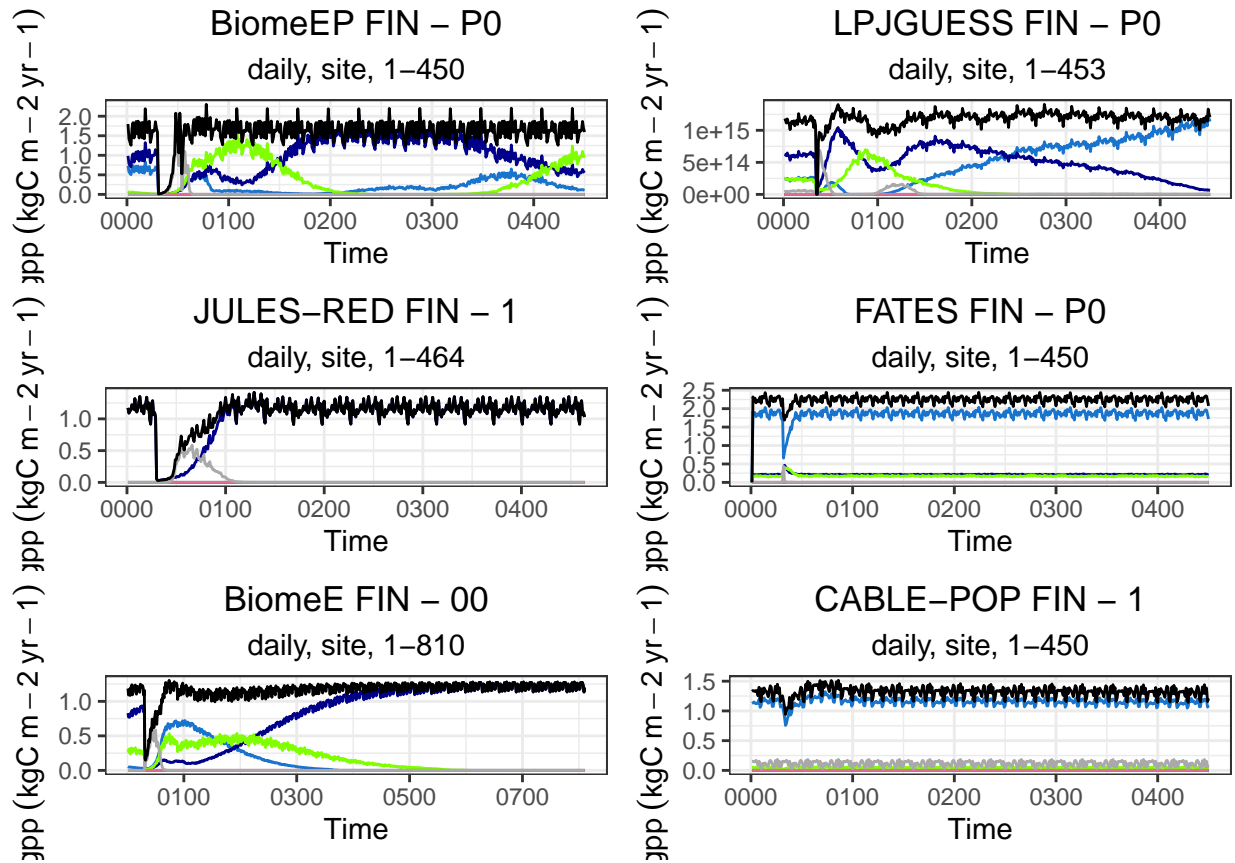
pBiomeES <- create_gobj(BiomeES)

JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
pJULESRED <- create_gobj(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```

npp

Model	Comments
BiomeEP	
LPJ-GUESS	
FATES	AHES: simulation output year 1 negative
BiomeES	
JULES-RED	AHES:FIN: only PFT2 really active. PFT1 never present?

CABLE-POP

```
var = "npp"
site = "FIN"
run = "P0"

BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
```

```
pFATES <- create_gobj(FATES)
```

```
BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_level,
```

```
## [1] "vobjtovarid4: **** WARNING **** I was asked to get a varid for dimension named PFT BUT this dim
```

```
pBiomeES <- create_gobj(BiomeES)
```

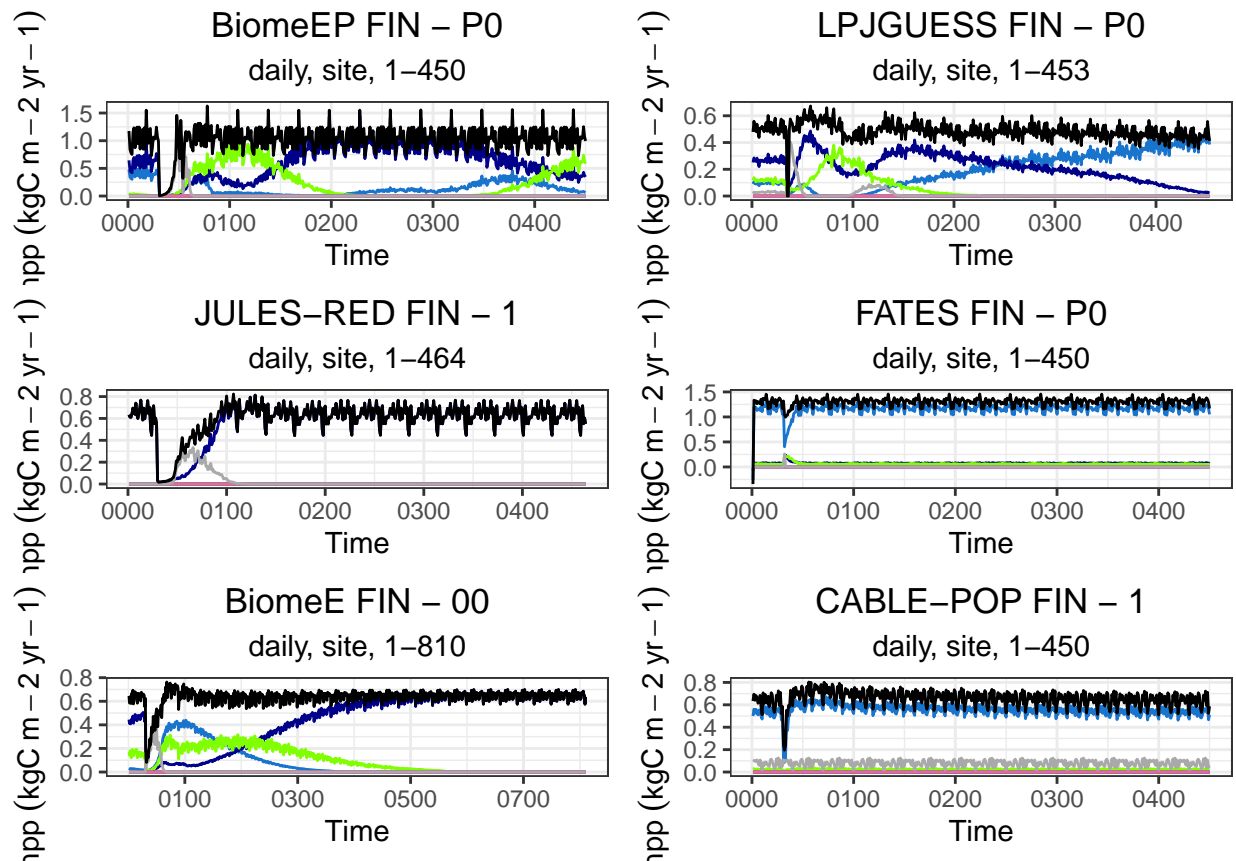
```
JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
```

```
pJULESRED <- create_gobj(JULESRED)
```

```
CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
```

```
pCABLEPOP <- create_gobj(CABLEPOP)
```

```
grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)
```



nbp

From the protocol: “Positive flux is into the land.”

post-disturbance, there is a less positive flux into the land for FATES

Model	Comments
BiomeEP	
LPJ-GUESS	AHES: dynamics post disturbance look a bit odd.. double-check output; does soil C increase?
FATES	AHES: Seems to me in terms of NBP, FATES is not yet(?) in equilibrium. Seems to always take up more than it releases. different to other models or overaccounting of output? First output value needs double-checking.
BiomeES	
JULES-RED	NA
CABLE-POP	

```

var = "nbp"
site = "FIN"
run = "P0"

BiomeEP <- get_output_BiomeEP(site,run,var = var,file.dir = file.dir.biomeEP,co2_levels = "412ppm")
pBiomeEP <- create_gobj(BiomeEP)

LPJGUESS <- get_output_LPJGUESS(site,run,var,file.dir = file.dir.lpjguess,co2_levels = "PS_412ppm/")
pLPJGUESS <- create_gobj(LPJGUESS)

FATES <- get_output_FATES(site,run,var,file.dir=file.dir.fates,model_name = "FATES")
pFATES <- create_gobj(FATES)

BiomeES <- get_output_BiomeE_standalone(site,run = "00",var = var, file.dir.biomeE_Standalone,co2_levels = "412ppm")
pBiomeES <- create_gobj(BiomeES)

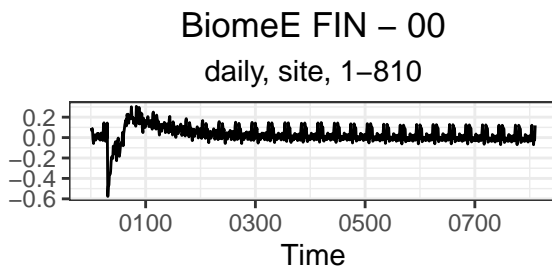
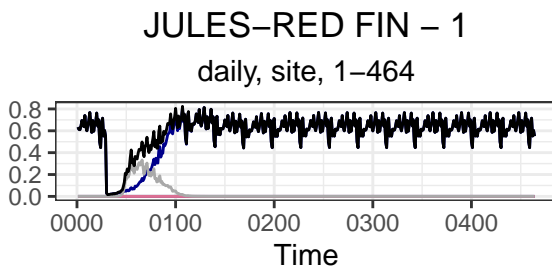
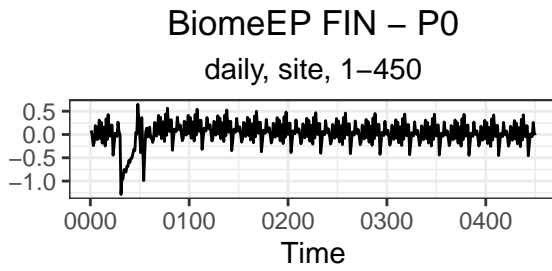
#JULESRED <- get_output_JULESRED(site,run = "1",var = var,file.dir.julesred,co2_levels = "412ppm")
#plotTemporal(JULESRED)

CABLEPOP <- get_output_CABLEPOP(site,run = "1",var = var,file.dir.cablepop,co2_levels = "PS_412ppm")
pCABLEPOP <- create_gobj(CABLEPOP)

grid.arrange(pBiomeEP,pLPJGUESS,pJULESRED,pFATES,pBiomeES,pCABLEPOP)

```

Net Primary Production (kgC m⁻² yr⁻¹)



Net Primary Production (kgC m⁻² yr⁻¹)

