

```
library(plyr)
library(dplyr)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:plyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(tidyr)
library(lubridate)

##
## Attaching package: 'lubridate'
## The following object is masked from 'package:plyr':
##
##   here
## The following object is masked from 'package:base':
##
##   date

library(ggplot2)
library(grid)

library(MMWRweek)
library(cdcfluvview)

get_legend_grob <- function(x) {
  data <- ggplot2:::ggplot_build(x)

  plot <- data$plot
  panel <- data$panel
  data <- data$data
  theme <- ggplot2:::plot_theme(plot)
  position <- theme$legend.position
  if (length(position) == 2) {
    position <- "manual"
  }

  legend_box <- if (position != "none") {
    ggplot2:::build_guides(plot$scales, plot$layers, plot$mapping,
      position, theme, plot$guides, plot$labels)
  }
```

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} else {
  ggplot2:::zeroGrob()
}
if (ggplot2:::is.zero(legend_box)) {
  position <- "none"
}
else {
  legend_width <- gtable:::gtable_width(legend_box) + theme$legend.margin
  legend_height <- gtable:::gtable_height(legend_box) + theme$legend.margin
  just <- valid.just(theme$legend.justification)
  xjust <- just[1]
  yjust <- just[2]
  if (position == "manual") {
    xpos <- theme$legend.position[1]
    ypos <- theme$legend.position[2]
    legend_box <- editGrob(legend_box, vp = viewport(x = xpos,
      y = ypos, just = c(xjust, yjust), height = legend_height,
      width = legend_width))
  }
  else {
    legend_box <- editGrob(legend_box, vp = viewport(x = xjust,
      y = yjust, just = c(xjust, yjust)))
  }
}
return(legend_box)
}

```

```

regionflu <- get_flu_data("hhs",
  sub_region = 1:10,
  data_source = "who",
  years=1997:2017)
usflu <- get_flu_data("national",
  sub_region = NA,
  data_source = "who",
  years=1997:2017)

```

```

flu_merged <- rbind.fill(
  usflu[[1]] %>%
    transmute(
      region_type = `REGION TYPE`,
      region = REGION,
      year = YEAR,
      week = WEEK,
      total_specimens = as.numeric(`TOTAL SPECIMENS`),
      total_A = as.numeric(`A (2009 H1N1)` +

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    as.numeric(`A (H1)`) +
    as.numeric(`A (H3)`) +
    as.numeric(`A (Subtyping not Performed)`) +
    as.numeric(`A (Unable to Subtype)`) +
    as.numeric(H3N2v),
total_A_typed = as.numeric(`A (2009 H1N1)`) +
    as.numeric(`A (H1)`) +
    as.numeric(`A (H3)`) +
    as.numeric(H3N2v),
total_A_2009H1N1 = as.numeric(`A (2009 H1N1)`),
total_A_H1 = as.numeric(`A (H1)`),
total_A_H3 = as.numeric(`A (H3)`),
total_A_H3N2v = as.numeric(H3N2v),
total_B = as.numeric(B),
percent_positive = as.numeric(`PERCENT POSITIVE`),
percent_A = total_A / total_specimens * 100,
percent_A_2009H1N1 = as.numeric(`A (2009 H1N1)`) / total_specimens * 100,
percent_A_H1 = as.numeric(`A (H1)`) / total_specimens * 100,
percent_A_H3 = as.numeric(`A (H3)`) / total_specimens * 100,
percent_A_H3N2v = as.numeric(H3N2v) / total_specimens * 100,
percent_B = total_B / total_specimens * 100,
percent_A_2009H1N1_rel_typed_A = as.numeric(`A (2009 H1N1)`) / total_A_typed * 100,
percent_A_H1_rel_typed_A = as.numeric(`A (H1)`) / total_A_typed * 100,
percent_A_H3_rel_typed_A = as.numeric(`A (H3)`) / total_A_typed * 100,
percent_A_H3N2v_rel_typed_A = as.numeric(H3N2v) / total_A_typed * 100
),
regionflu[[1]] %>%
  transmute(
    region_type = `REGION TYPE`,
    region = REGION,
    year = YEAR,
    week = WEEK,
    total_specimens = as.numeric(`TOTAL SPECIMENS`),
    total_A = as.numeric(`A (2009 H1N1)`) +
      as.numeric(`A (H1)`) +
      as.numeric(`A (H3)`) +
      as.numeric(`A (Subtyping not Performed)`) +
      as.numeric(`A (Unable to Subtype)`) +
      as.numeric(H3N2v),
    total_A_typed = as.numeric(`A (2009 H1N1)`) +
      as.numeric(`A (H1)`) +
      as.numeric(`A (H3)`) +
      as.numeric(H3N2v),
    total_A_2009H1N1 = as.numeric(`A (2009 H1N1)`),
    total_A_H1 = as.numeric(`A (H1)`),
    total_A_H3 = as.numeric(`A (H3)`),
    total_A_H3N2v = as.numeric(H3N2v),

```

```
total_B = as.numeric(B),
percent_positive = as.numeric(`PERCENT POSITIVE`),
percent_A = total_A / total_specimens * 100,
percent_A_2009H1N1 = as.numeric(`A (2009 H1N1)` ) / total_specimens * 100,
percent_A_H1 = as.numeric(`A (H1)` ) / total_specimens * 100,
percent_A_H3 = as.numeric(`A (H3)` ) / total_specimens * 100,
percent_A_H3N2v = as.numeric(H3N2v) / total_specimens * 100,
percent_B = total_B / total_specimens * 100,
percent_A_2009H1N1_rel_typed_A = as.numeric(`A (2009 H1N1)` ) / total_A_typed * 100,
percent_A_H1_rel_typed_A = as.numeric(`A (H1)` ) / total_A_typed * 100,
percent_A_H3_rel_typed_A = as.numeric(`A (H3)` ) / total_A_typed * 100,
percent_A_H3N2v_rel_typed_A = as.numeric(H3N2v) / total_A_typed * 100
)
)%>%
mutate(
  time = MMWRweek2Date(year, week)
)
```

[illegible]

```
flu_merged$season <- ifelse(
  flu_merged$week <= 30,
  paste0(flu_merged$year - 1, "/", flu_merged$year),
  paste0(flu_merged$year, "/", flu_merged$year + 1)
)
```

```
## Season week column: week number within season
## weeks after week 30 get season_week = week - 30
## weeks before week 30 get season_week = week + (number of weeks in previous year) - 30
## This computation relies on the start_date function in package MMWRweek,
## which is not exported from that package's namespace!!!
```

```
flu_merged$season_week <- ifelse(
  flu_merged$week <= 30,
  flu_merged$week + MMWRweek(MMWRweek::start_date(flu_merged$year) - 1)$MMWRweek - 30,
  flu_merged$week - 30
)
```

```
flu_typed <- flu_merged
```

```
regionflu <- get_flu_data("hhs",
  sub_region = 1:10,
  data_source = "ilinet",
  years=1997:2017)
usflu <- get_flu_data("national",
  sub_region = NA,
  data_source = "ilinet",
  years=1997:2017)
```

```

flu_wili <- rbind.fill(usflu, regionflu) %>%
  transmute(
    region_type = `REGION TYPE`,
    region = REGION,
    year = YEAR,
    week = WEEK,
    wILI = as.numeric(`% WEIGHTED ILI`),
    ILI = as.numeric(`%UNWEIGHTED ILI`),
    total_ILI = as.numeric(ILITOTAL),
    total_patients = as.numeric(`TOTAL PATIENTS`)
  )

## Warning in evalq(as.numeric(c("1.10148", "1.20007", "1.37876", "1.1992", : NAs introduced by coercion
## Warning in evalq(as.numeric(c("1.21686", "1.28064", "1.23906", "1.14473", : NAs introduced by coercion
## Warning in evalq(as.numeric(c("570", "615", "681", "653", "700", "655", : NAs introduced by coercion
## Warning in evalq(as.numeric(c("46842", "48023", "54961", "57044", "55506", : NAs introduced by coercion

flu <- left_join(flu_typed, flu_wili,
  by = c("region_type", "region", "year", "week"))

```

```

flu$wILI_times_4 <- flu$wILI * 4

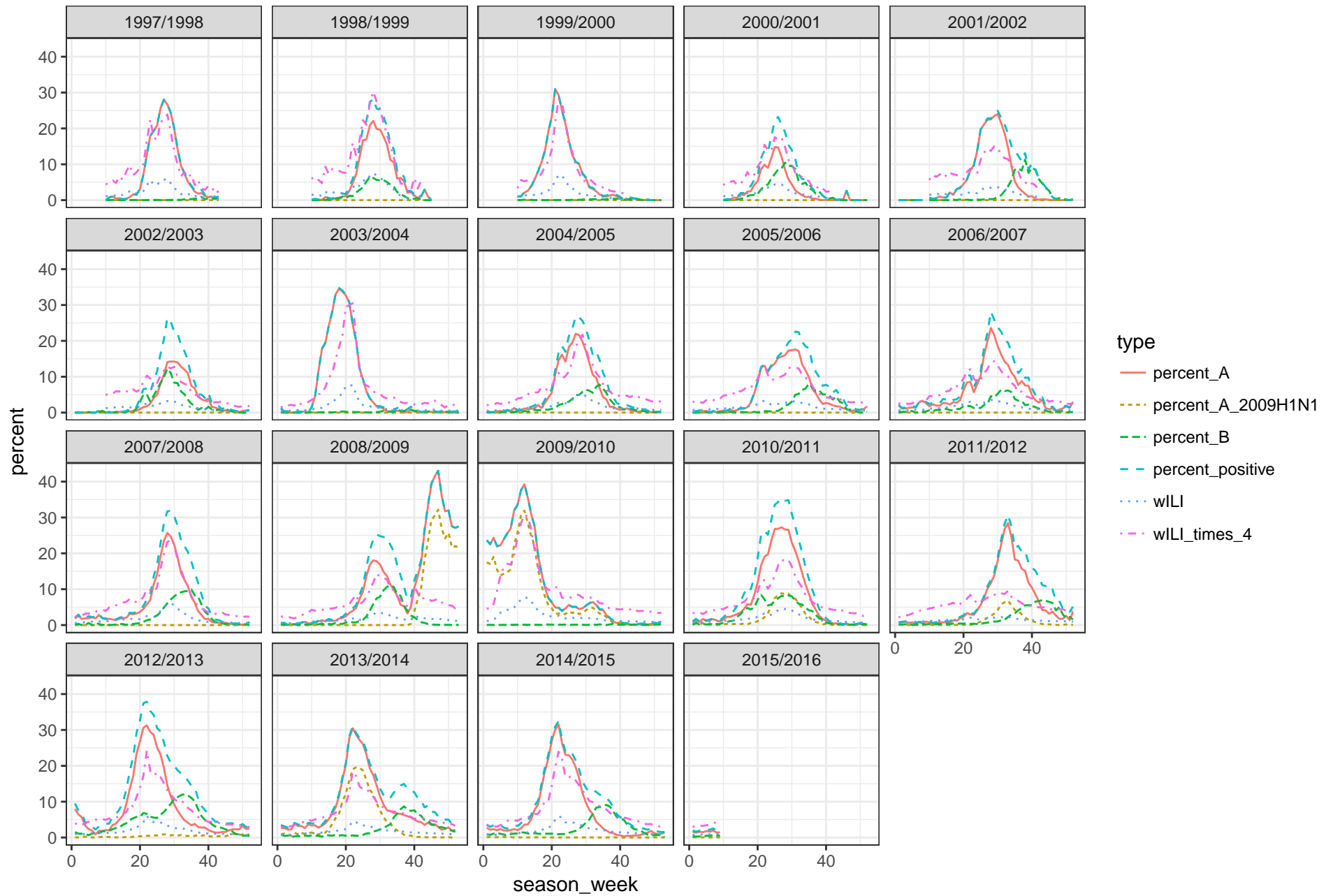
for(region_val in unique(flu$region)) {
  region_flu <- flu %>% filter(region == region_val)

  # for(season_val in unique(region_flu$season)) {
  p_typed <- ggplot(region_flu %>%
    # filter(season == season_val) %>%
    gather_("type", "percent", c("percent_A", "percent_A_2009H1N1", "percent_B", "percent_positive", "wILI", "wILI_times_4"))) +
    geom_line(aes(x = season_week, y = percent, colour = type, linetype = type)) +
    facet_wrap(~ season) +
    ggtitle(region_val) +
    theme_bw()

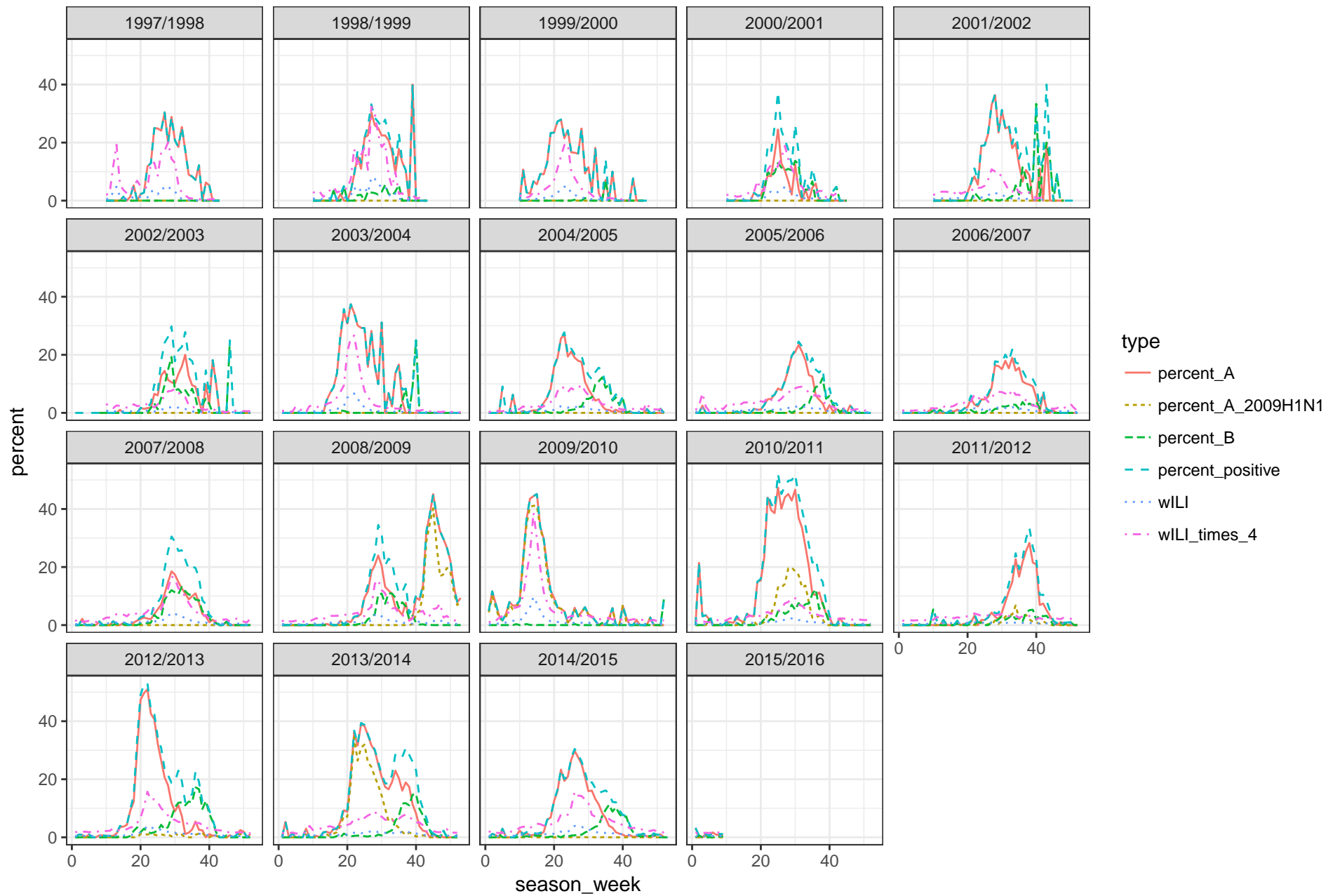
    print(p_typed)
  # }
}

```

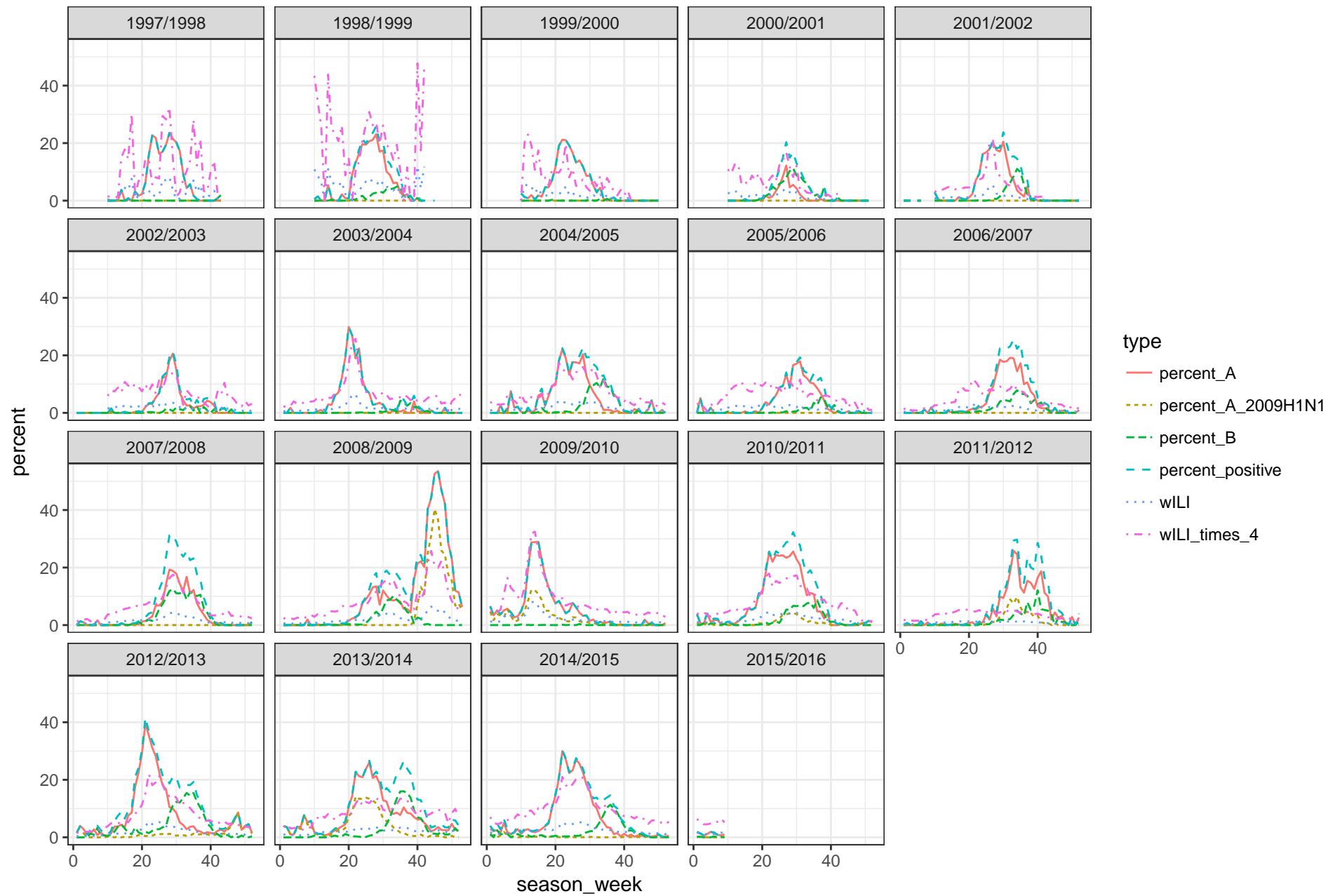
X



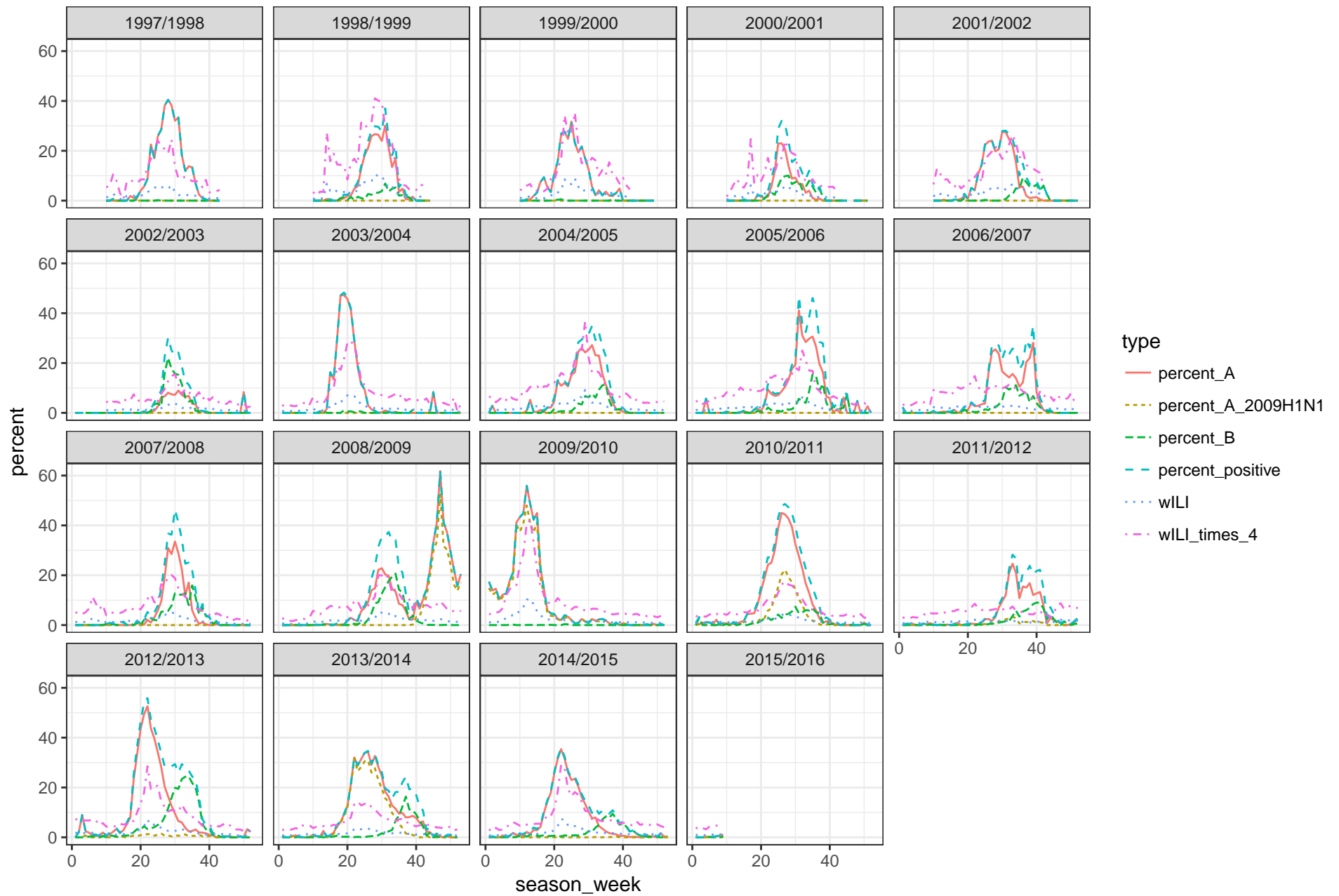
Region 1



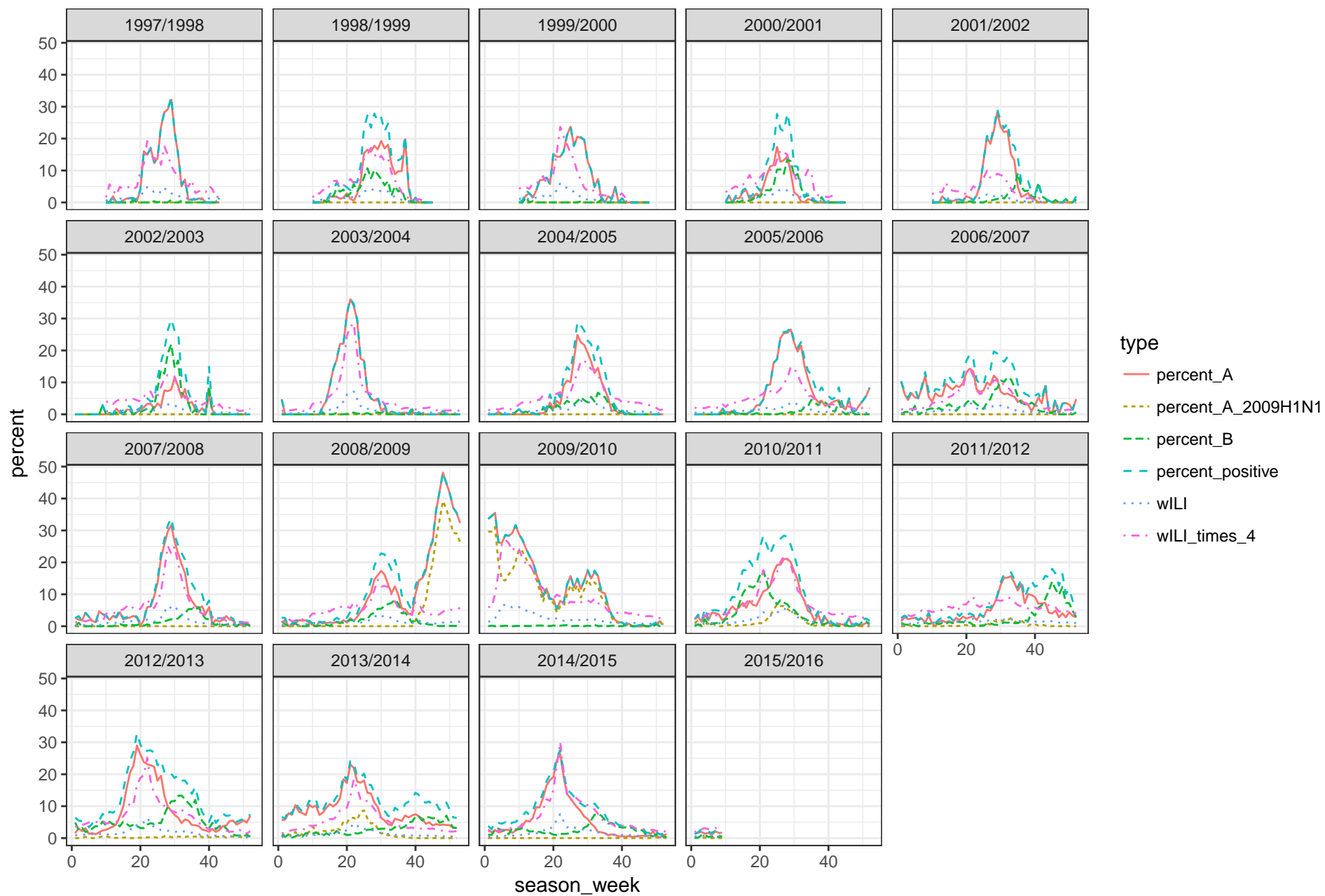
Region 2



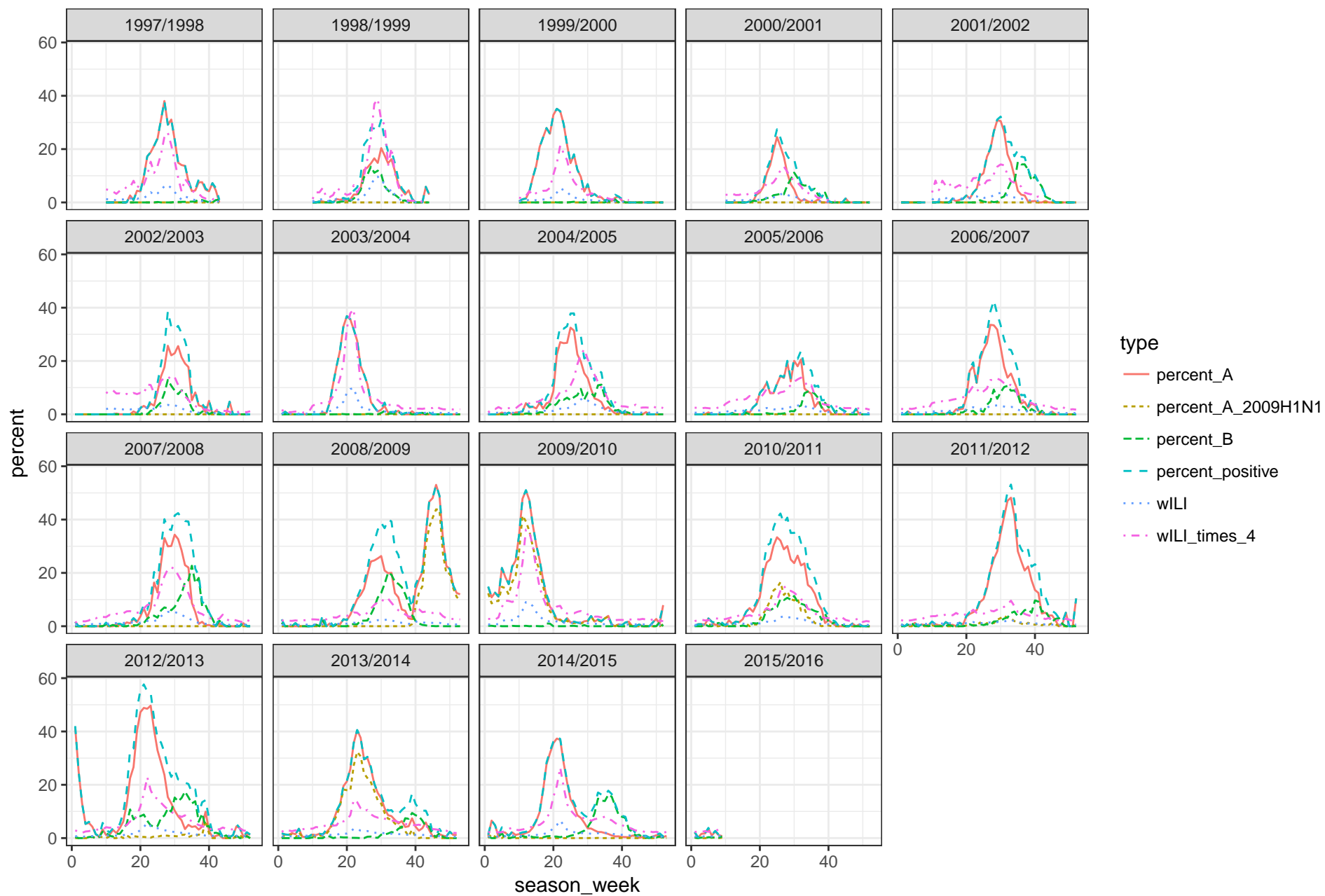
Region 3



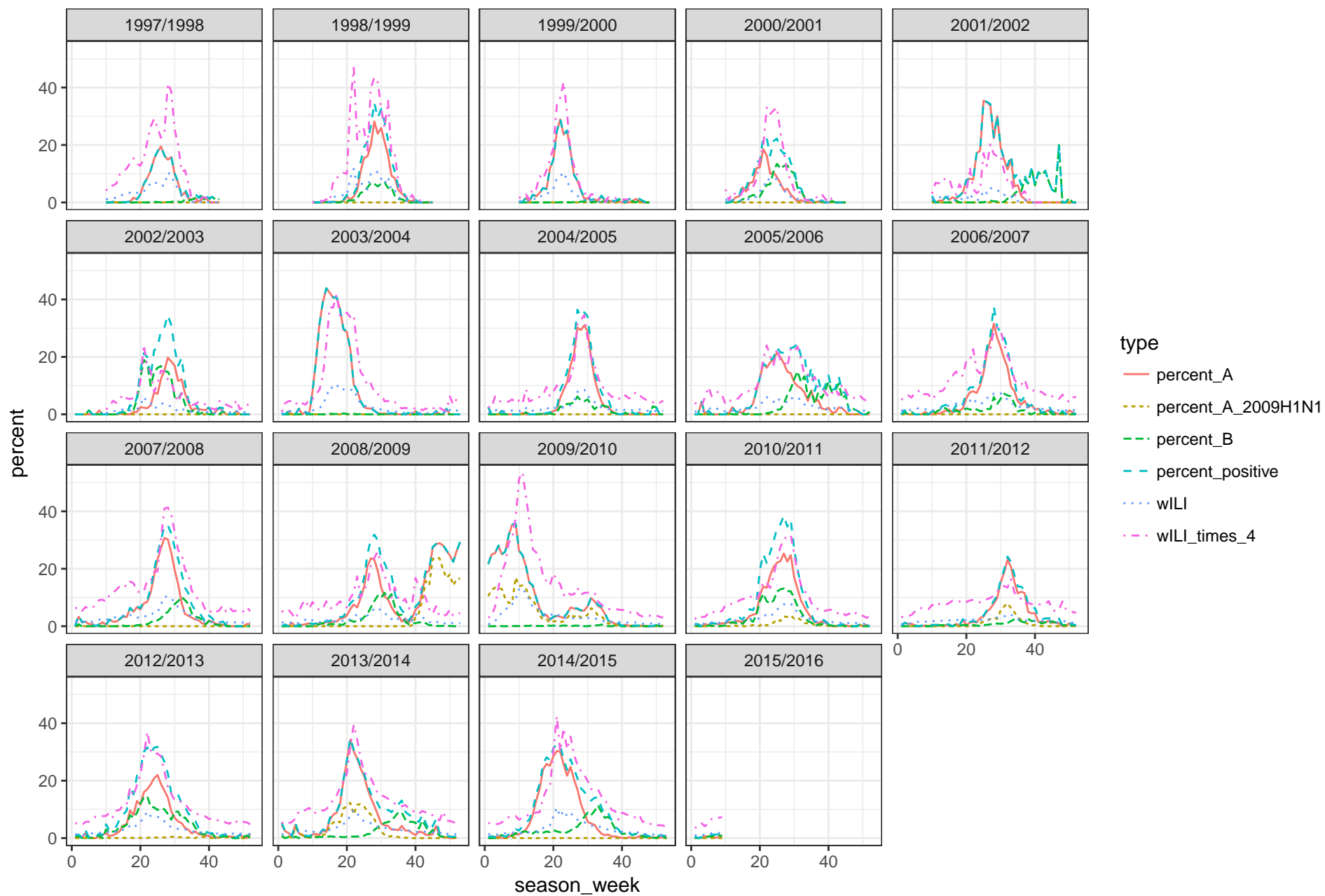
Region 4



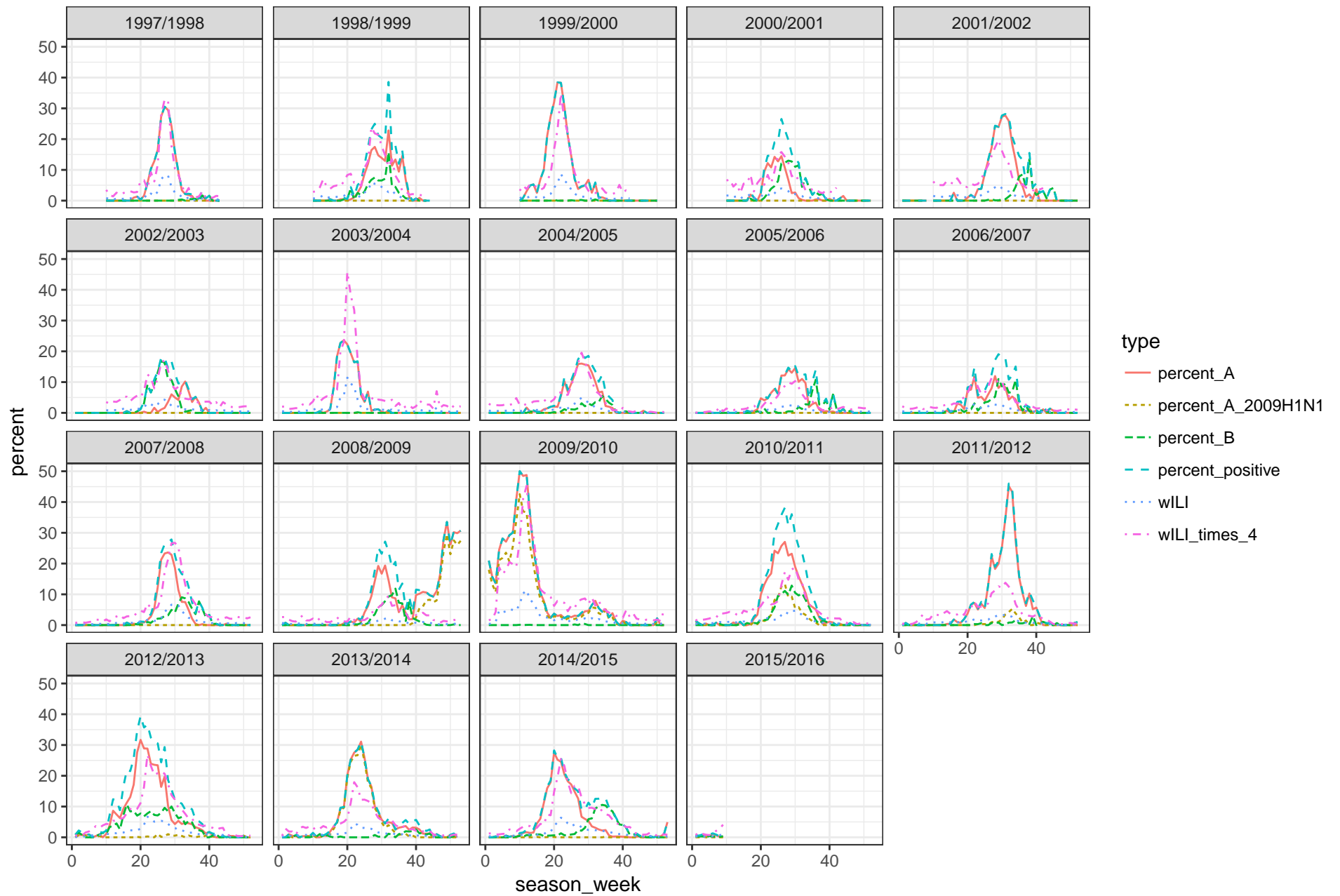
Region 5



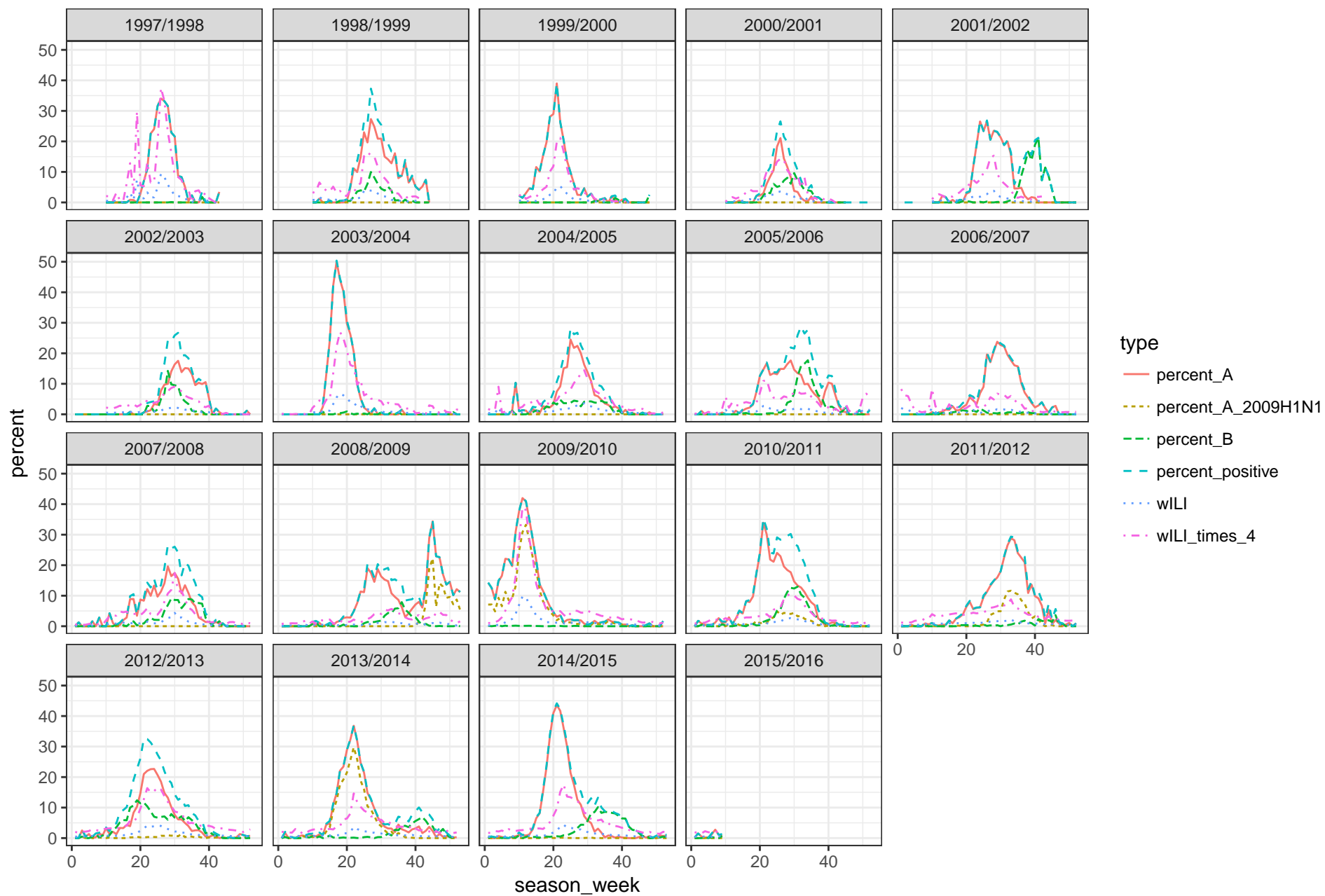
Region 6



Region 7



Region 8



Region 9



Region 10

