

Confidence Intervals for loess fits and linear/segmented regression models

2022-10-18

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This appendix shows the 95% confidence intervals for the loess and linear/segmented models presented in the main paper.

Data preparation

```
# load packages

library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.6      v purrr   0.3.4
## v tibble  3.1.7      v dplyr   1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

library(glue)

# load data
hmd_lt <- read_rds("https://github.com/JonMinton/change-in-ex/blob/main/data/lifetables.rds?raw=true")

# Labels for codes
country_code_lookup <-
  tribble(
    ~code, ~country,
    "DEUTNP", "Germany",
    "DEUTE", "East Germany",
    "DEUTW", "West Germany",
    "ESP", "Spain",
    "FRATNP", "France",
    "ITA", "Italy",
    "GBRTENW", "England & Wales",
    "GBR_SCO", "Scotland",
    "DEUTSYNTH", "Synthetic Germany",
    "NLD", "Netherlands"
  )
```

```

countries_of_interest <- c(
  "GBRTENW",
  "GBR_SCO",
  "GBR_UK",
  "FRATNP",
  "ESP",
  "ITA",
  "DEUTNP",
  "DEUTE",
  "DEUTW",
  "NLD"
)

source("https://raw.githubusercontent.com/JonMinton/change-in-ex/main/R/make_synthetic_germany_function.R")

source("https://raw.githubusercontent.com/JonMinton/change-in-ex/main/R/make_pop_selection.R")

change_in_ex_selected_countries <-
  hmd_ex_selected_countries_with_synth %>%
    group_by(code, x, sex) %>%
    arrange(year) %>%
    mutate(delta_ex = ex - lag(ex)) %>%
    ungroup()

```

LOESS smoother, confidence intervals

The following shows the LOESS smoother line with confidence intervals for annual changes in life expectancy at birth:

```

p_0_loess <- change_in_ex_selected_countries %>%
  filter(x == 0) %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain"))) %>%
  filter(!is.na(country)) %>%
  filter(between(year, 1980, 2020)) %>%
  mutate(delta_ex = delta_ex * 52.25) %>% # Convert to weeks
  ggplot(aes(x = year, y = delta_ex)) +
  geom_point() +
  stat_smooth(se = TRUE) + # Changed from se = FALSE
  facet_grid(sex~country) +
  geom_hline(yintercept = 0) +
  scale_y_continuous(breaks = seq(-30, 50, by = 10)) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
    x = "Year",
    y = "Change in life expectancy from previous year (in weeks)",
    title = "Annual change in life expectancy at birth, selected countries",
    subtitle = "Line: nonlinear smoother over the points",
    caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population"
  )

```

```
## Joining, by = "code"
```

```
p_0_loess
```

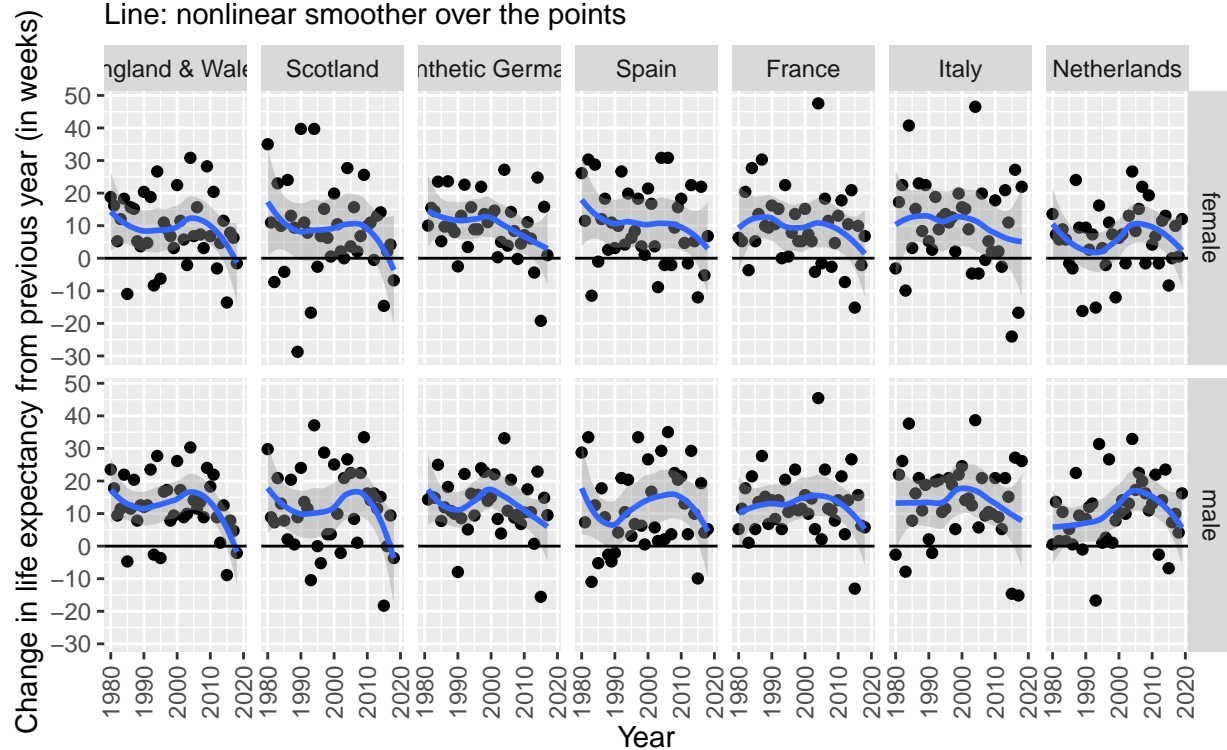
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```

Annual change in life expectancy at birth, selected countries

Line: nonlinear smoother over the points



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

And the following shows the same for life expectancy from age 65 years

```
p_65_loess <- change_in_ex_selected_countries %>%
  filter(x == 65) %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain", "France", "Italy", "Netherlands"))) %>%
  filter(!is.na(country)) %>%
  filter(between(year, 1980, 2020)) %>%
  mutate(delta_ex = delta_ex * 52.25) %>% # Convert to weeks
  ggplot(aes(x = year, y = delta_ex)) +
  geom_point() +
  stat_smooth(se = TRUE) + # changed from se = FALSE
  facet_grid(se~country) +
  geom_hline(yintercept = 0) +
  scale_y_continuous(breaks = seq(-30, 50, by = 10)) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
```

```

x = "Year",
y = "Change in life expectancy from previous year (in weeks)",
title = "Annual change in life expectancy at age 65, selected countries",
subtitle = "Line: nonlinear smoother over the points",
caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German pop
)

```

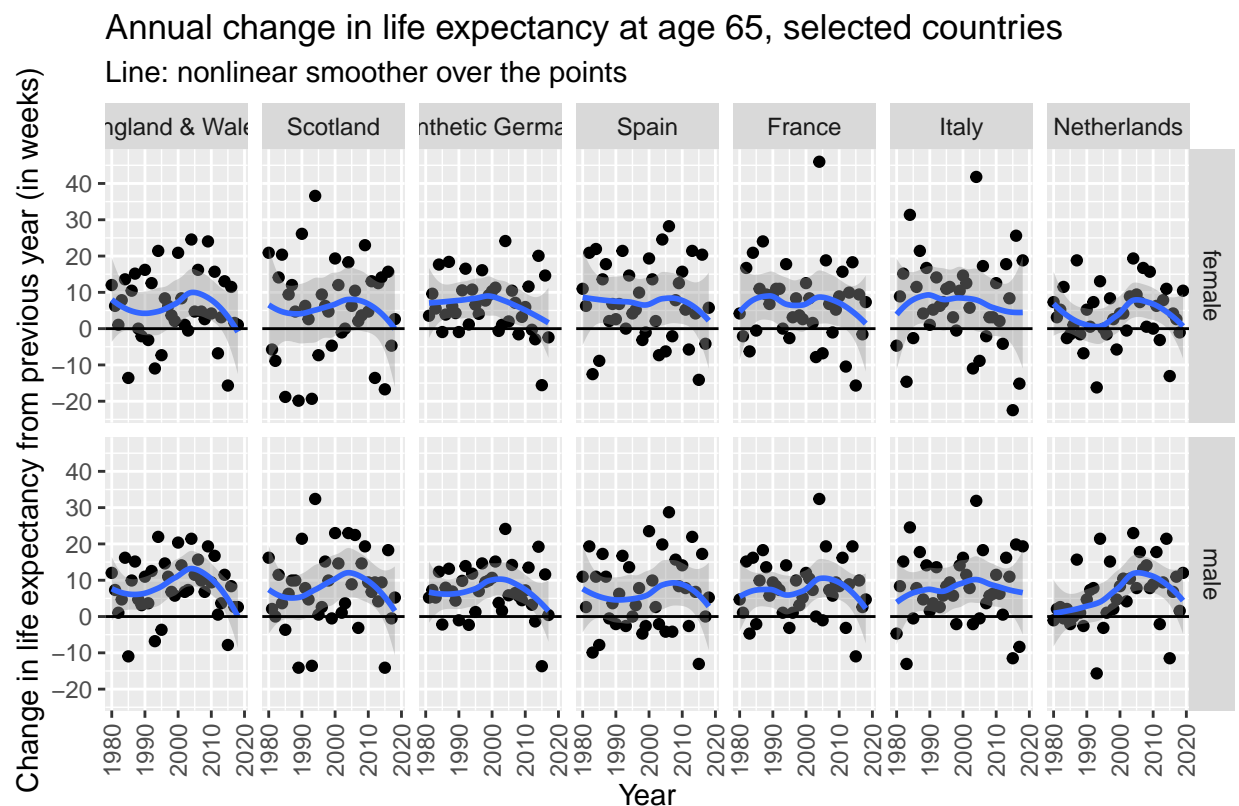
```
## Joining, by = "code"
```

```
p_65_loess
```

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

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```



ce: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

We can see that the 95% CI on the smoother includes values below zero for a number of populations.

Within the above, and in the main paper, the LOESS smoother is called in ggplot2's `stat_smooth` function, which uses slightly different parameterisation than if the `loess` function in the `stats` packages were called directly. For consistency with the main paper we can extract the point estimate, lower and upper CIs, and standard error, directly from the above ggplot objects. The following function does this:

```

extract_loess_ci <- function(p){
  b <- ggplot_build(p)
  panel_lookup <- b$layout$layout

  # get smoother values

```

```

p_loess <- b$data[[2]]

# Join and simplify

sm <- p_loess %>%
  select(x, y, ymin, ymax, se, PANEL) %>%
  left_join(panel_lookup)

# find last year for each country

max_years <- p$data %>%
  group_by(country, sex) %>%
  filter(year == max(year)) %>%
  select(country, sex, max_year = year)

sm %>%
  select(x, y, ymin, ymax, se, sex, country) %>%
  left_join(max_years) %>%
  filter(x == max_year)
}

```

And the following code applies the function to the two previously created ggplot2 objects

```

loess_lastyear_x0 <-
extract_loess_ci(p_0_loess) %>%
  rename(year = x, y_point = y,
         y_lower = ymin, y_upper = ymax, y_se = se) %>%
  mutate(x = 0) %>% # x now starting age
  select(year, x, sex, country, everything(), -max_year)

```

```

## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
## Joining, by = "PANEL"
## Joining, by = c("sex", "country")

```

```

loess_lastyear_x65 <-
extract_loess_ci(p_65_loess) %>%
  rename(year = x, y_point = y,
         y_lower = ymin, y_upper = ymax, y_se = se) %>%
  mutate(x = 65) %>% # x now starting age
  select(year, x, sex, country, everything(), -max_year)

```

```

## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
## Joining, by = "PANEL"
## Joining, by = c("sex", "country")

```

```

loess_lastyear_both <-
  bind_rows(loess_lastyear_x0, loess_lastyear_x65)

```

```
loess_lastyear_both
```

```

##   year  x   sex      country  y_point  y_lower  y_upper  y_se
## 1  2018  0 female England & Wales -1.37085831 -13.530072 10.788356 5.983454

```

## 2	2018	0	female	Scotland	-3.61707693	-20.509289	13.275135	8.312525
## 3	2017	0	female	Synthetic Germany	2.96747333	-8.062811	13.997757	5.414911
## 4	2018	0	female	Spain	2.94139772	-11.305593	17.188389	7.010833
## 5	2018	0	female	France	1.37863909	-12.054318	14.811596	6.610253
## 6	2018	0	female	Italy	5.10750796	-11.526141	21.741157	8.185288
## 7	2019	0	female	Netherlands	2.36725240	-8.638790	13.373295	5.422197
## 8	2018	0	male	England & Wales	-1.77259987	-11.851773	8.306573	4.959882
## 9	2018	0	male	Scotland	-3.64395051	-17.511375	10.223474	6.824051
## 10	2017	0	male	Synthetic Germany	5.96684307	-4.694271	16.627957	5.233681
## 11	2018	0	male	Spain	4.51381577	-9.686210	18.713842	6.987722
## 12	2018	0	male	France	5.32872389	-5.947412	16.604860	5.548898
## 13	2018	0	male	Italy	7.76595659	-6.604990	22.136904	7.071830
## 14	2019	0	male	Netherlands	5.69252174	-5.722116	17.107159	5.623494
## 15	2018	65	female	England & Wales	-0.90447135	-12.535858	10.726915	5.723714
## 16	2018	65	female	Scotland	-0.06883654	-16.054439	15.916766	7.866390
## 17	2017	65	female	Synthetic Germany	1.60189046	-8.061272	11.265053	4.743773
## 18	2018	65	female	Spain	2.19830409	-11.023504	15.420112	6.506348
## 19	2018	65	female	France	1.39777068	-11.805226	14.600767	6.497091
## 20	2018	65	female	Italy	4.47429730	-10.963447	19.912041	7.596793
## 21	2019	65	female	Netherlands	0.65630234	-8.168485	9.481090	4.347588
## 22	2018	65	male	England & Wales	0.03630923	-8.724677	8.797295	4.311213
## 23	2018	65	male	Scotland	1.54944773	-10.702427	13.801322	6.029051
## 24	2017	65	male	Synthetic Germany	1.51214525	-6.944740	9.969031	4.151596
## 25	2018	65	male	Spain	2.76986201	-9.287731	14.827455	5.933447
## 26	2018	65	male	France	2.23048158	-7.404687	11.865650	4.741391
## 27	2018	65	male	Italy	6.56582403	-4.980548	18.112196	5.681879
## 28	2019	65	male	Netherlands	4.38609383	-4.768505	13.540692	4.510071

The estimates are in weeks of increase per year. The following function produces summary statements for each population

```
summarise_loess <- function(df, cntry, dp = 2){
  df <- df %>% filter(country == cntry)

  last_year <- df$year[1]

  y_x0_pt_m <- df %>% filter(x == 0, sex == "male") %>% pull("y_point") %>% round(dp)
  y_x65_pt_m <- df %>% filter(x == 65, sex == "male") %>% pull("y_point") %>% round(dp)
  y_x0_pt_f <- df %>% filter(x == 0, sex == "female") %>% pull("y_point") %>% round(dp)
  y_x65_pt_f <- df %>% filter(x == 65, sex == "female") %>% pull("y_point") %>% round(dp)

  y_x0_lwr_m <- df %>% filter(x == 0, sex == "male") %>% pull("y_lower") %>% round(dp)
  y_x65_lwr_m <- df %>% filter(x == 65, sex == "male") %>% pull("y_lower") %>% round(dp)
  y_x0_lwr_f <- df %>% filter(x == 0, sex == "female") %>% pull("y_lower") %>% round(dp)
  y_x65_lwr_f <- df %>% filter(x == 65, sex == "female") %>% pull("y_lower") %>% round(dp)

  y_x0_upr_m <- df %>% filter(x == 0, sex == "male") %>% pull("y_upper") %>% round(dp)
  y_x65_upr_m <- df %>% filter(x == 65, sex == "male") %>% pull("y_upper") %>% round(dp)
  y_x0_upr_f <- df %>% filter(x == 0, sex == "female") %>% pull("y_upper") %>% round(dp)
  y_x65_upr_f <- df %>% filter(x == 65, sex == "female") %>% pull("y_upper") %>% round(dp)

  y_x0_se_m <- df %>% filter(x == 0, sex == "male") %>% pull("y_se") %>% round(dp)
  y_x65_se_m <- df %>% filter(x == 65, sex == "male") %>% pull("y_se") %>% round(dp)
  y_x0_se_f <- df %>% filter(x == 0, sex == "female") %>% pull("y_se") %>% round(dp)
```

```

y_x65_se_f <- df %>% filter(x == 65, sex == "female") %>% pull("y_se") %>% round(dp)

pfall_x0_m <- pnorm(0, y_x0_pt_m, y_x0_se_m) %>% round(dp)
pfall_x65_m <- pnorm(0, y_x65_pt_m, y_x65_se_m) %>% round(dp)
pfall_x0_f <- pnorm(0, y_x0_pt_f, y_x0_se_f) %>% round(dp)
pfall_x65_f <- pnorm(0, y_x65_pt_f, y_x65_se_f) %>% round(dp)

glue::glue("{cntry} in {last_year}: \nFor males, LOESS estimated annual changes of {y_x0_pt_m} (95% CI: {y_x0_se_m}, {y_x65_pt_m}, {y_x65_se_m})")
}

```

The following are descriptive summaries of life expectancy trends in the last observed year, as estimated through the LOESS method:

```

unique(loess_lastyear_both$country) %>% as.character() %>%
  map(summarise_loess, df = loess_lastyear_both)

```

```

## [[1]]
## England & Wales in 2018:
## For males, LOESS estimated annual changes of -1.77 (95% CI -11.85 to 8.31) weeks/year for life expectancy
## For females, LOESS estimated annual changes of -1.37 (95% CI -13.53 to 10.79) weeks/year for life expectancy
##
## [[2]]
## Scotland in 2018:
## For males, LOESS estimated annual changes of -3.64 (95% CI -17.51 to 10.22) weeks/year for life expectancy
## For females, LOESS estimated annual changes of -3.62 (95% CI -20.51 to 13.28) weeks/year for life expectancy
##
## [[3]]
## Synthetic Germany in 2017:
## For males, LOESS estimated annual changes of 5.97 (95% CI -4.69 to 16.63) weeks/year for life expectancy
## For females, LOESS estimated annual changes of 2.97 (95% CI -8.06 to 14) weeks/year for life expectancy
##
## [[4]]
## Spain in 2018:
## For males, LOESS estimated annual changes of 4.51 (95% CI -9.69 to 18.71) weeks/year for life expectancy
## For females, LOESS estimated annual changes of 2.94 (95% CI -11.31 to 17.19) weeks/year for life expectancy
##
## [[5]]
## France in 2018:
## For males, LOESS estimated annual changes of 5.33 (95% CI -5.95 to 16.6) weeks/year for life expectancy
## For females, LOESS estimated annual changes of 1.38 (95% CI -12.05 to 14.81) weeks/year for life expectancy
##
## [[6]]
## Italy in 2018:
## For males, LOESS estimated annual changes of 7.77 (95% CI -6.6 to 22.14) weeks/year for life expectancy
## For females, LOESS estimated annual changes of 5.11 (95% CI -11.53 to 21.74) weeks/year for life expectancy
##
## [[7]]
## Netherlands in 2019:
## For males, LOESS estimated annual changes of 5.69 (95% CI -5.72 to 17.11) weeks/year for life expectancy
## For females, LOESS estimated annual changes of 2.37 (95% CI -8.64 to 13.37) weeks/year for life expectancy

```

We can see from the above summaries that the confidence intervals for all populations tend to include negative values, and that the resulting estimated probabilities that the true value in the last observed year (conditional on the model) is below zero, i.e. falling, is substantial (at least 12%) for populations and starting ages considered. For England & Wales, and Scotland (except males from age 65), it is more probable than

not that life expectancy fell in the last observed year.

Linear regression and Breakpoint confidence intervals

```
estimate_breakpoints_and_pval <- function(df){
  null_mdl <- lm(ex ~ year, data = df)
  seg_mdl <- segmented::segmented(null_mdl, seg.Z= ~year, psi = 2010)
  seg2_mdl <- segmented::segmented(null_mdl, seg.z= ~year, psi= c(1985, 2010)) # added to test

  list(
    null = null_mdl,
    seg = seg_mdl,
    seg2 = seg2_mdl
  )
}

segmented_breakpoints_models <-
  hmd_ex_selected_countries_with_synt %>%
  filter(code != "DEUTNP") %>%
  filter(year >= 1979) %>%
  group_by(code, x, sex) %>%
  nest() %>%
  mutate(
    mdl_outputs = map(data, estimate_breakpoints_and_pval)
  ) %>%
  unnest_longer(mdl_outputs)

# Now let's get the BIC for each model

make_predictions <- function(mdl, dta = tibble(year = 1980:2020)){
  tibble(
    year = dta$year,
    ex_pred = predict(mdl, newdata = dta)
  )
}

best_model_predictions_descriptions <-
segmented_breakpoints_models %>%
  mutate(bic = map_dbl(mdl_outputs, BIC)) %>%
  group_by(code, x, sex) %>%
  mutate(rank_bic = rank(bic)) %>%
  filter(rank_bic == 1) %>%
  mutate(
    best_model = case_when(
      mdl_outputs_id == 'seg2' ~ "Two breakpoints",
      mdl_outputs_id == 'seg' ~ "One breakpoint",
      mdl_outputs_id == 'null' ~ "No breakpoints"
    )
  ) %>%
  mutate(
    first_breakpoint = map2_dbl(
      mdl_outputs_id, mdl_outputs,
```



```

function(x, y){
  if (x == 'null' ) {NA_real_} else {
    y[["psi"]][1,2]
  }
}
),
first_breakpoint_se = map2_dbl(
  mdl_outputs_id, mdl_outputs,
  function(x, y){
    if (x == 'null' ) {NA_real_} else {
      y[["psi"]][1,3]
    }
  }
),
second_breakpoint = map2_dbl(
  mdl_outputs_id, mdl_outputs,
  function(x, y){
    if (x == 'seg2') {
      y[["psi"]][2,2]
    } else {
      NA_real_
    }
  }
),
second_breakpoint_se = map2_dbl(
  mdl_outputs_id, mdl_outputs,
  function(x, y){
    if (x == 'seg2') {
      y[["psi"]][2,3]
    } else {
      NA_real_
    }
  }
)
) %>% # let's add predictions too
mutate(
  pred_data = map(mdl_outputs, make_predictions),
  joined_data = map2(data, pred_data, left_join)
) %>%
select(code, x, sex, joined_data, first_breakpoint:second_breakpoint_se) %>%
unnest(joined_data)

```

```

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```

```
best_breakpoint_model_predictions <-
  segmented_breakpoints_models %>%
    mutate(bic = map_dbl mdl_outputs, BIC)) %>%
    group_by(code, x, sex) %>%
    filter(bic == min(bic)) %>%
    mutate(predictions = map2(mdl_outputs, data, predict, interval = "confidence", level = 0.95)) %>%
    mutate(data_augmented = map2(data, predictions, bind_cols)) %>%
    select(code, x, sex, data_augmented) %>%
    ungroup() %>%
    unnest(data_augmented)
```

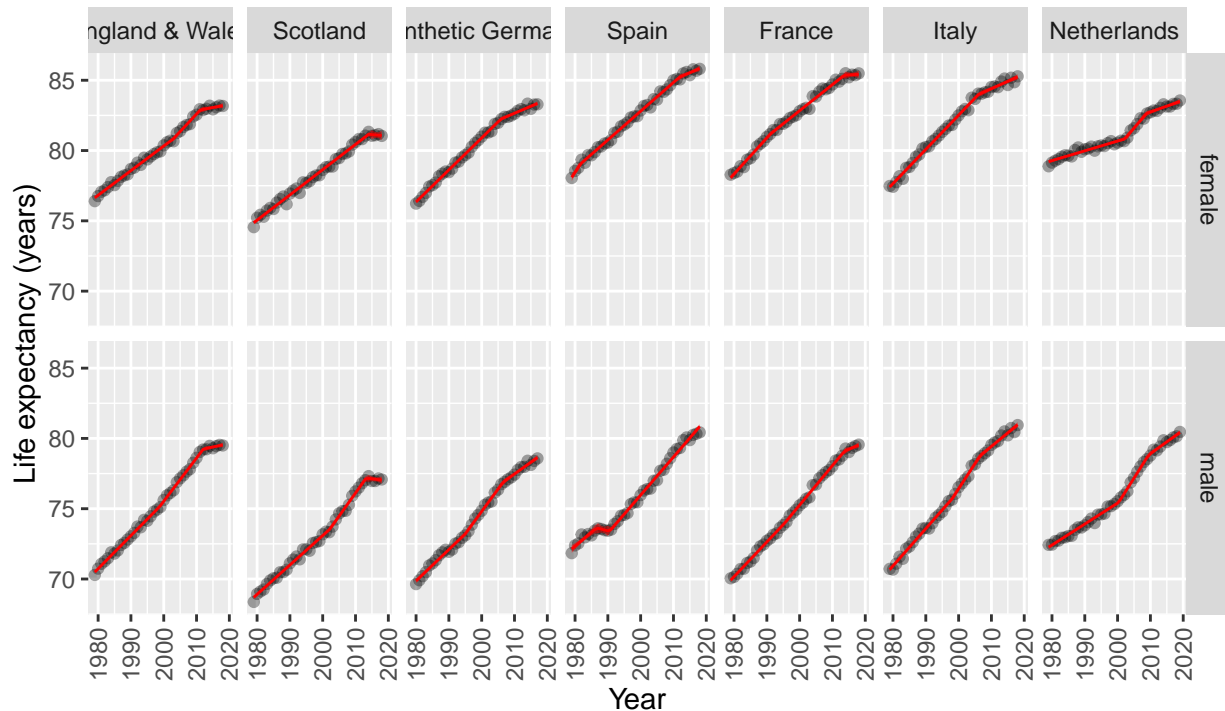
```
best_breakpoint_model_predictions %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain"))
  filter(!is.na(country)) %>%
  filter(x == 0) %>%
  ggplot(aes(x = year)) +
  facet_grid(sex ~ country) +
  geom_point(aes(y = ex), alpha = 0.35) +
  geom_line(aes(y = fit), colour = "red") +
  geom_ribbon(aes(ymin = lwr, ymax = upr), fill = "red", colour = NA, alpha = 0.5) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
    x = "Year",
    y = "Life expectancy (years)",
    title = "Predicted and observed life expectancy at birth, selected countries",
    subtitle = "Line: Best segmented regression model for the country",
```

```
caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting"
)
```

```
## Joining, by = "code"
```

Predicted and observed life expectancy at birth, selected countries

Line: Best segmented regression model for the country



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

The confidence intervals are quite hard to see given the data points. In the figure below they are shown without the points

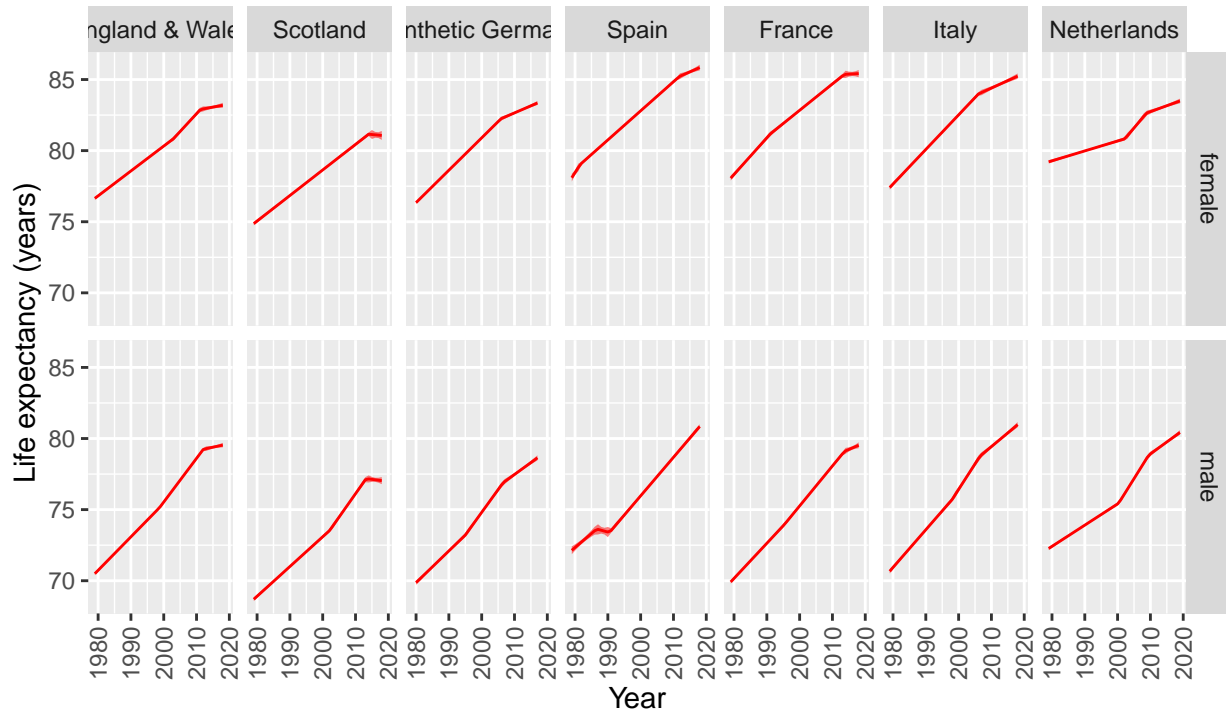
```
best_breakpoint_model_predictions %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain", "France", "Italy", "Netherlands"))) %>%
  filter(!is.na(country)) %>%
  filter(x == 0) %>%
  ggplot(aes(x = year)) +
  facet_grid(sex ~ country) +
  # geom_point(aes(y = ex), alpha = 0.35) +
  geom_line(aes(y = fit), colour = "red") +
  geom_ribbon(aes(ymin = lwr, ymax = upr), fill = "red", colour = NA, alpha = 0.5) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
    x = "Year",
    y = "Life expectancy (years)",
    title = "Predicted and observed life expectancy at birth, selected countries",
    subtitle = "Line: Best segmented regression model for the country",
    caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting"
  )
```

)

```
## Joining, by = "code"
```

Predicted and observed life expectancy at birth, selected countries

Line: Best segmented regression model for the country



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

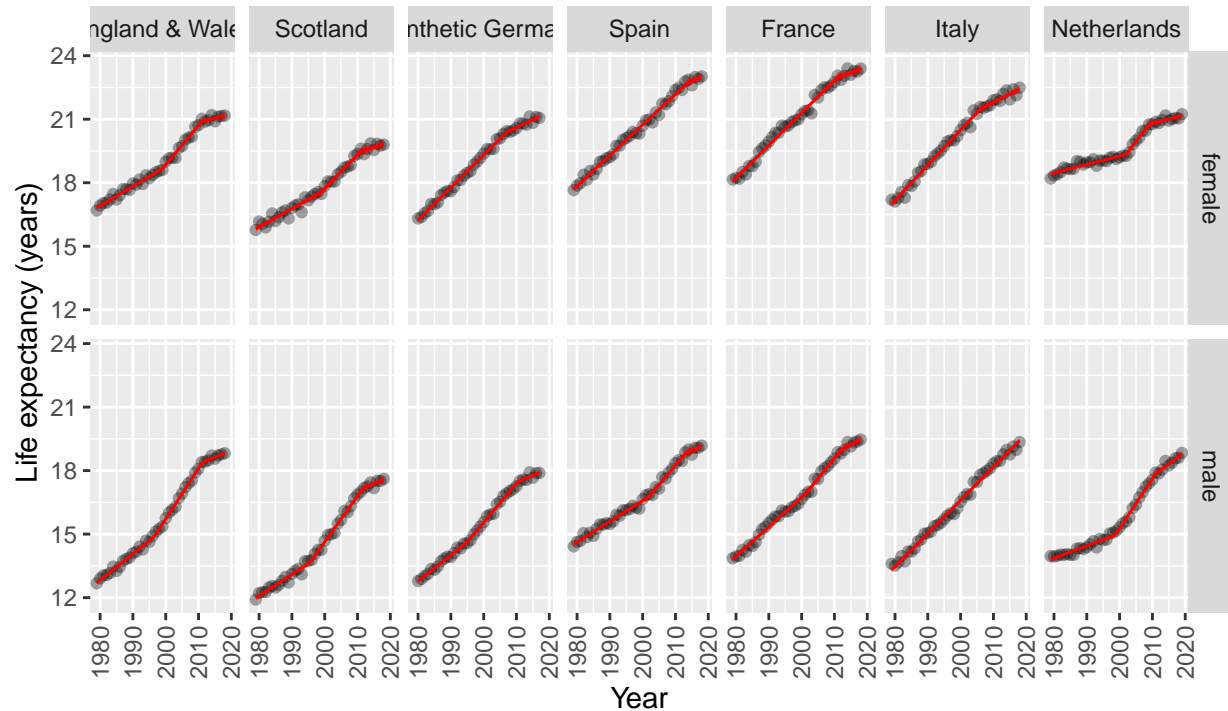
They are repeated, with and then without points, for life expectancy from age 65 below:

```
best_breakpoint_model_predictions %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain", "France", "Italy", "Netherlands"))) %>%
  filter(!is.na(country)) %>%
  filter(x == 65) %>%
  ggplot(aes(x = year)) +
  facet_grid(sex ~ country) +
  geom_point(aes(y = ex), alpha = 0.35) +
  geom_line(aes(y = fit), colour = "red") +
  geom_ribbon(aes(ymin = lwr, ymax = upr), fill = "red", colour = NA, alpha = 0.5) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
    x = "Year",
    y = "Life expectancy (years)",
    title = "Predicted and observed life expectancy at age 65, selected countries",
    subtitle = "Line: Best segmented regression model for the country",
    caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting"
  )
```

```
## Joining, by = "code"
```

Predicted and observed life expectancy at age 65, selected countries

Line: Best segmented regression model for the country



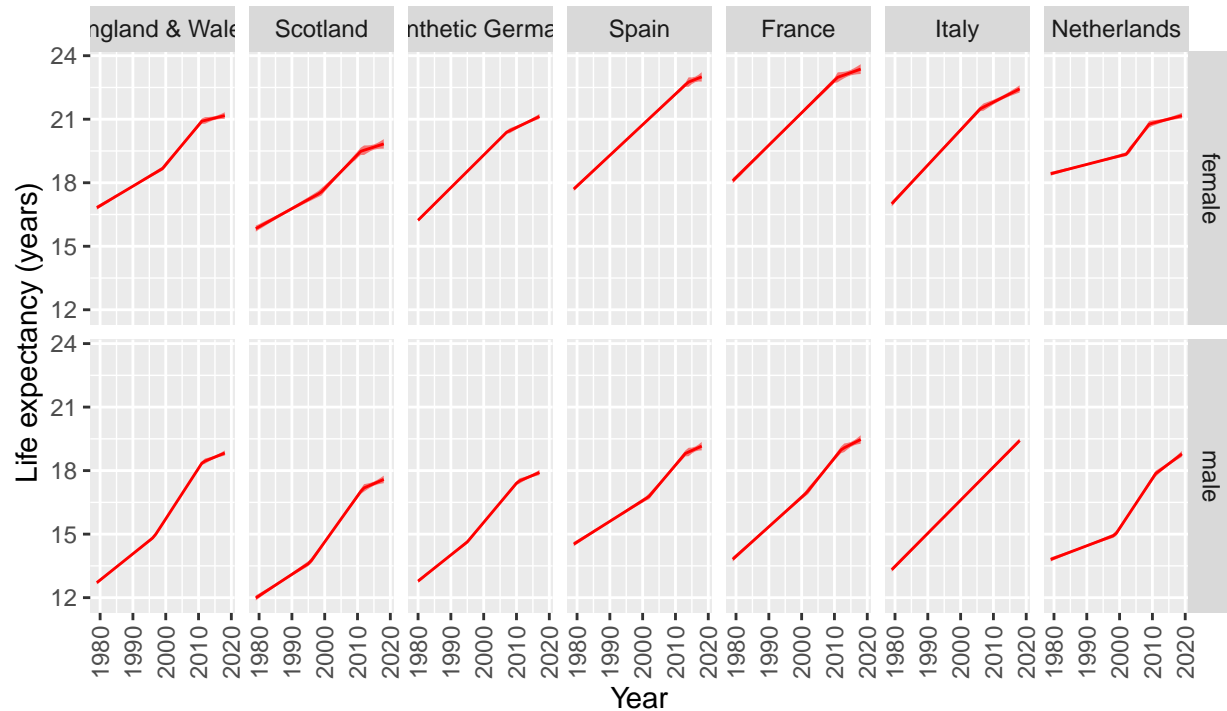
Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

```
best_breakpoint_model_predictions %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain", "France", "Italy", "Netherlands"))) %>%
  filter(!is.na(country)) %>%
  filter(x == 65) %>%
  ggplot(aes(x = year)) +
  facet_grid(sex ~ country) +
  # geom_point(aes(y = ex), alpha = 0.35) +
  geom_line(aes(y = fit), colour = "red") +
  geom_ribbon(aes(ymin = lwr, ymax = upr), fill = "red", colour = NA, alpha = 0.5) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  ) +
  labs(
    x = "Year",
    y = "Life expectancy (years)",
    title = "Predicted and observed life expectancy at age 65, selected countries",
    subtitle = "Line: Best segmented regression model for the country",
    caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting"
  )
```

```
## Joining, by = "code"
```

Predicted and observed life expectancy at age 65, selected countries

Line: Best segmented regression model for the country



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

```
pred_differenced <-
  best_breakpoint_model_predictions %>%
  left_join(country_code_lookup) %>%
  mutate(country = factor(country, levels = c("England & Wales", "Scotland", "Synthetic Germany", "Spain"))) %>%
  filter(!is.na(country)) %>%
  group_by(country, sex, x) %>%
  arrange(year) %>%
  mutate(
    diff_ex = 52.25 * (ex - lag(ex)),
    diff_fit = 52.25 * (fit - lag(fit)),
    adj_upr = 52.25 * (upr - fit),
    adj_lwr = 52.25 * (lwr - fit),
    diff_upr = diff_fit + adj_upr,
    diff_lwr = diff_fit + adj_lwr
  ) %>%
  filter(!is.na(diff_fit))
```

Joining, by = "code"

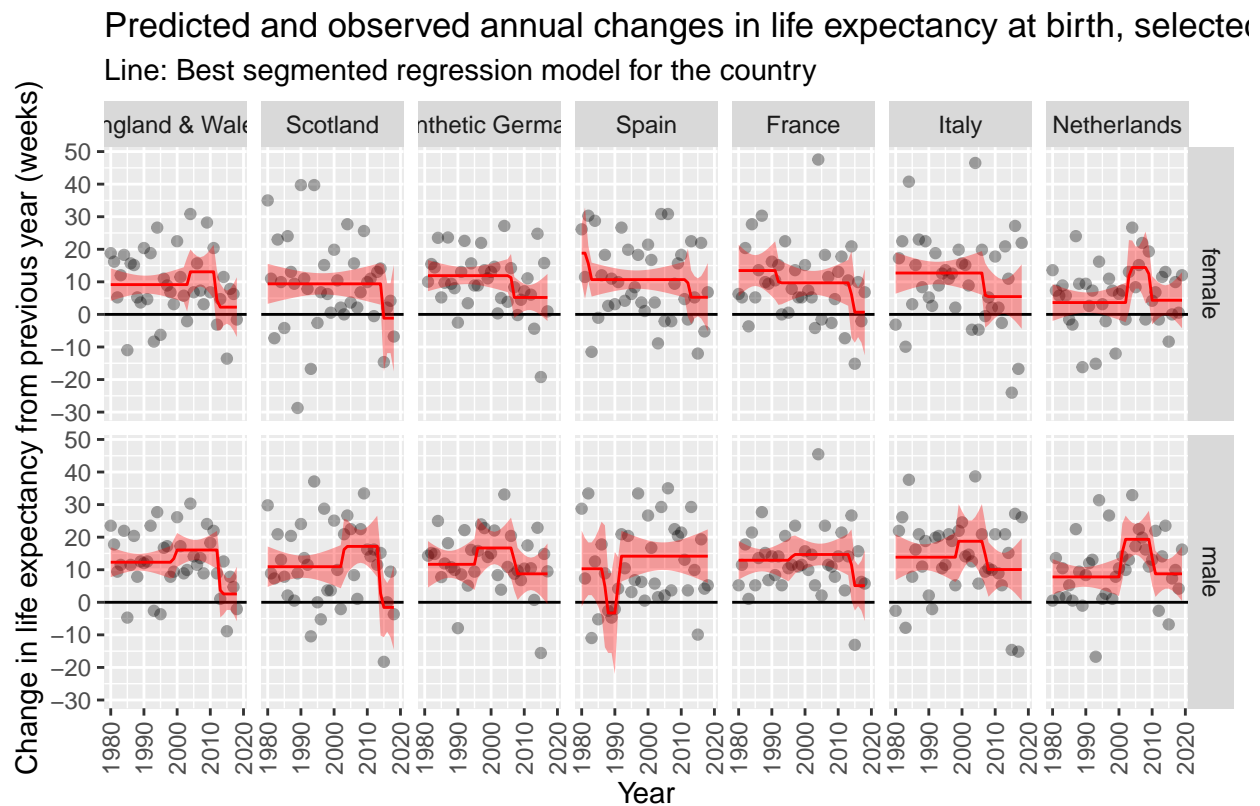
The following shows differences with confidence intervals for life expectancy from birth:

```
pred_differenced %>%
  filter(x == 0) %>%
  ggplot(aes(year)) +
  geom_point(aes(y = diff_ex), alpha = 0.35) +
  facet_grid(sex ~ country) +
  geom_hline(yintercept = 0) +
```

```

geom_line(aes(y = diff_fit), colour = "red") +
geom_ribbon(aes(ymin = diff_lwr, ymax = diff_upr), colour = NA, fill = "red", alpha = 0.35) +
theme(
  axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
) +
scale_y_continuous(breaks = seq(-30, 50, by = 10)) +
labs(
  x = "Year",
  y = "Change in life expectancy from previous year (weeks)",
  title = "Predicted and observed annual changes in life expectancy at birth, selected countries",
  subtitle = "Line: Best segmented regression model for the country",
  caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population"
)

```



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

And the following shows the same for life expectancy changes from age 65

```

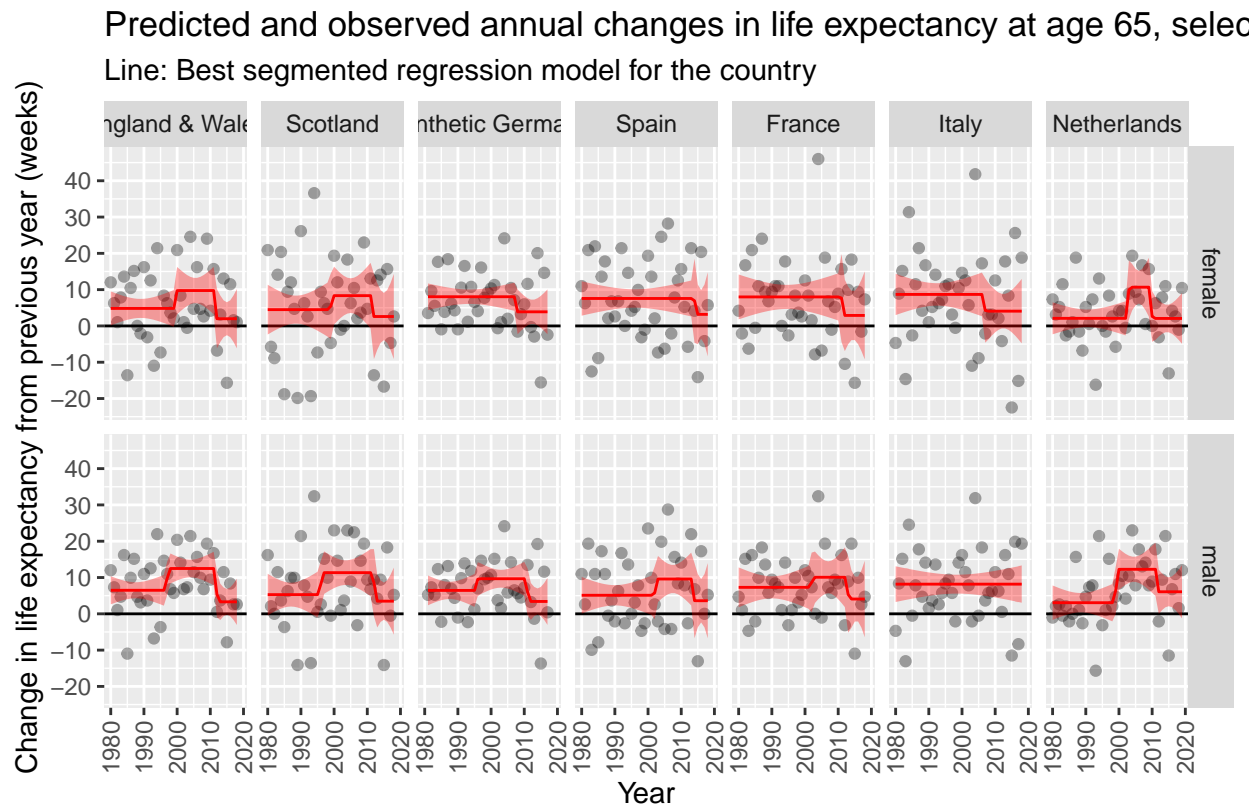
pred_differenced %>%
  filter(x == 65) %>%
  ggplot(aes(year)) +
  geom_point(aes(y = diff_ex), alpha = 0.35) +
  facet_grid(sex ~ country) +
  geom_hline(yintercept = 0) +
  geom_line(aes(y = diff_fit), colour = "red") +
  geom_ribbon(aes(ymin = diff_lwr, ymax = diff_upr), colour = NA, fill = "red", alpha = 0.35) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)
  )

```

```

) +
scale_y_continuous(breaks = seq(-30, 50, by = 10)) +
labs(
  x = "Year",
  y = "Change in life expectancy from previous year (weeks)",
  title = "Predicted and observed annual changes in life expectancy at age 65, selected countries",
  subtitle = "Line: Best segmented regression model for the country",
  caption = "Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German pop
)

```



Source: Human Mortality Database. Synthetic Germany based on 20% East/80% West German population weighting

As with the LOESS model, we can present the point estimates, 95% CIs, and implied probabilities that the values in the last observed year are below zero.

```

summarise_reg_seg <- function(df, cntry, dp = 2){
  df <- df %>%
    filter(country == cntry) %>%
    filter(year == max(year))

  last_year <- max(df$year)

  y_x0_pt_m <- df %>% filter(x == 0, sex == "male") %>% pull("diff_fit")
  y_x65_pt_m <- df %>% filter(x == 65, sex == "male") %>% pull("diff_fit")
  y_x0_pt_f <- df %>% filter(x == 0, sex == "female") %>% pull("diff_fit")
  y_x65_pt_f <- df %>% filter(x == 65, sex == "female") %>% pull("diff_fit")

  y_x0_lwr_m <- df %>% filter(x == 0, sex == "male") %>% pull("diff_lwr")
  y_x65_lwr_m <- df %>% filter(x == 65, sex == "male") %>% pull("diff_lwr")

```



```

y_x0_lwr_f <- df %>% filter(x == 0, sex == "female") %>% pull("diff_lwr")
y_x65_lwr_f <- df %>% filter(x == 65, sex == "female") %>% pull("diff_lwr")

y_x0_upr_m <- df %>% filter(x == 0, sex == "male") %>% pull("diff_upr")
y_x65_upr_m <- df %>% filter(x == 65, sex == "male") %>% pull("diff_upr")
y_x0_upr_f <- df %>% filter(x == 0, sex == "female") %>% pull("diff_upr")
y_x65_upr_f <- df %>% filter(x == 65, sex == "female") %>% pull("diff_upr")

y_x0_se_m <- c(y_x0_upr_m - y_x0_pt_m, y_x0_pt_m - y_x0_lwr_m) %>% `/(1.96)` %>% mean() %>% round(dp)
y_x65_se_m <- c(y_x65_upr_m - y_x65_pt_m, y_x65_pt_m - y_x65_lwr_m) %>% `/(1.96)` %>% mean() %>% round(dp)
y_x0_se_f <- c(y_x0_upr_f - y_x0_pt_f, y_x0_pt_f - y_x0_lwr_f) %>% `/(1.96)` %>% mean() %>% round(dp)
y_x65_se_f <- c(y_x65_upr_f - y_x65_pt_f, y_x65_pt_f - y_x65_lwr_f) %>% `/(1.96)` %>% mean() %>% round(dp)

y_x0_lwr_m <- y_x0_lwr_m %>% round(dp)
y_x65_lwr_m <- y_x65_lwr_m %>% round(dp)
y_x0_lwr_f <- y_x0_lwr_f %>% round(dp)
y_x65_lwr_f <- y_x65_lwr_f %>% round(dp)

y_x0_upr_m <- y_x0_upr_m %>% round(dp)
y_x65_upr_m <- y_x65_upr_m %>% round(dp)
y_x0_upr_f <- y_x0_upr_f %>% round(dp)
y_x65_upr_f <- y_x65_upr_f %>% round(dp)

y_x0_pt_m <- y_x0_pt_m %>% round(dp)
y_x65_pt_m <- y_x65_pt_m %>% round(dp)
y_x0_pt_f <- y_x0_pt_f %>% round(dp)
y_x65_pt_f <- y_x65_pt_f %>% round(dp)

pfall_x0_m <- pnorm(0, y_x0_pt_m, y_x0_se_m) %>% round(dp)
pfall_x65_m <- pnorm(0, y_x65_pt_m, y_x65_se_m) %>% round(dp)
pfall_x0_f <- pnorm(0, y_x0_pt_f, y_x0_se_f) %>% round(dp)
pfall_x65_f <- pnorm(0, y_x65_pt_f, y_x65_se_f) %>% round(dp)

glue::glue("{cntry} in {last_year}: \nFor males, segmented/linear estimated annual changes of {y_x0_pt_m}
}

```

As before, we can produce summary statements for each country as follows:

```

unique(pred_differenced$country) %>% as.character() %>%
  map(summarise_reg_seg , df = pred_differenced)

## [[1]]
## Spain in 2018:
## For males, segmented/linear estimated annual changes of 14.16 (95% CI 5.92 to 22.4) weeks/year for 1
## For females, segmented/linear estimated annual changes of 5.26 (95% CI -5.23 to 15.76) weeks/year for
##
## [[2]]
## France in 2018:
## For males, segmented/linear estimated annual changes of 5.12 (95% CI -5.76 to 16) weeks/year for lif
## For females, segmented/linear estimated annual changes of 0.68 (95% CI -12.57 to 13.93) weeks/year f
##
## [[3]]
## Italy in 2018:

```

```

## For males, segmented/linear estimated annual changes of 10.06 (95% CI 0.47 to 19.66) weeks/year for 1
## For females, segmented/linear estimated annual changes of 5.46 (95% CI -4.45 to 15.37) weeks/year for 1
##
## [[4]]
## Netherlands in 2019:
## For males, segmented/linear estimated annual changes of 8.75 (95% CI 0.38 to 17.11) weeks/year for 1
## For females, segmented/linear estimated annual changes of 4.35 (95% CI -4.25 to 12.95) weeks/year for 1
##
## [[5]]
## England & Wales in 2018:
## For males, segmented/linear estimated annual changes of 2.55 (95% CI -5.8 to 10.91) weeks/year for 1
## For females, segmented/linear estimated annual changes of 2.23 (95% CI -6.95 to 11.41) weeks/year for 1
##
## [[6]]
## Scotland in 2018:
## For males, segmented/linear estimated annual changes of -1.57 (95% CI -14.52 to 11.39) weeks/year for 1
## For females, segmented/linear estimated annual changes of -1.15 (95% CI -17.55 to 15.25) weeks/year for 1
##
## [[7]]
## Synthetic Germany in 2017:
## For males, segmented/linear estimated annual changes of 8.74 (95% CI -0.57 to 18.05) weeks/year for 1
## For females, segmented/linear estimated annual changes of 5.2 (95% CI -2.03 to 12.43) weeks/year for 1

```