Change Point Regression

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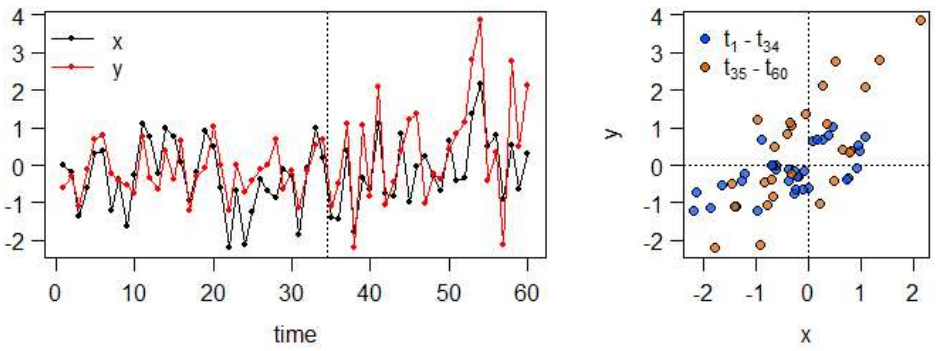
This implementation of change point regression was developed by Julian Stander (University of Plymouth) and first published in Eichenseer et al. (2019).

Assume we want to investigate the relationship between two variables, x and y, that we have collected over a certain period of time. We have reason to believe that the relationship changed at some point, but we don't know when.

Let's generate x and y and plot them. y is linearly dependent on x across the whole time series, but we induce an increase in the intercept, slope and residual variance at the 35^{th} observation:

```
set.seed(10) # change the seed for a different sequence of random numbers
n <- 60 # number of total data points
n_shift <- 35 # the data point at which we introduce a change
x <- rnorm(n,0,1) # generate x
y <- rnorm(n,0,0.5) + 0.5 * x # generate y without a change
y[n_shift:n] <- rnorm(length(n_shift:n),0,1) + 1 * x[n_shift:n] + 0.75 # introduce change
```



The regression model

Now we build a model that can recover the change point and the linear relationship between x and y before and after the change point.

The first part of this model looks like an ordinary least squares regression of y against x:

$$y_i \sim N(\mu_i, \sigma_1^2), \quad \mu_i = \alpha_1 + \beta_1 x_i, \quad i = 1, \ldots, n_{change} - 1$$

Here we have a single intercept (α_1), slope (β_1), and residual variance (σ_1^2). n_{change} - 1 denotes the number of obervations before the change point.

From the change point n_{change} onwards, we add an additional intercept, α_2, to the intercept from the first part (α_1). We do the same for the slope and the residual variance:

$$y_i \sim N(\mu_i, \sigma_1^2 + \sigma_2^2), \quad \mu_i = \alpha_1 + \alpha_2 + (\beta_1 + \beta_2) x_i, \quad i = n_{change}, \ldots, n$$

n denotes the total number of observations, 60 in this case. But how do we actually find the change point n_{change}?

Implementation in JAGS

Here, we turn to the JAGS programming environment. Understanding a model written for JAGS is not easy at first. If you are keen on learning Bayesian modeling from scratch I can highly recommend Richard McElreath's book Statistical Rethinking. We will access JAGS with the R2jags package, so we can keep using R even if we are writing a model for JAGS.

Below, we look at the model. The R code that will be passed to JAGS later is on the left. On the right is an explanation for each line of the model.

```
model_CPR <- function(){

  ### Likelihood or data model part
  for(i in 1:n){

  y[i] ~ dnorm(mu[i], tau[i])



  mu[i] <- alpha_1 +
  alpha_2 * step(i - n_change) +
  (beta_1 + beta_2 * step(i - n_change))*x[i]



  tau[i] <- exp(log_tau[i])

  log_tau[i] <- log_tau_1 + log_tau_2 *
  step(i - n_change)

  }

  ### Priors


  alpha_1 ~ dnorm(0, 1.0E-4)


  alpha_2 ~ dnorm(0, 1.0E-4)

  beta_1 ~ dnorm(0, 1.0E-4)
  beta_2 ~ dnorm(0, 1.0E-4)

  log_tau_1 ~ dnorm(0, 1.0E-4)
  log_tau_2 ~ dnorm(0, 1.0E-4)

  K ~ dcat(p)
  n_change <- possible_change_points[K]

}
```

We save the model as a function named *model_CPR*

Loop over all the data points $1, \ldots, n$

$y_i \sim N(\mu_i, \tau_i)$
note that JAGS uses the precision τ instead of σ^2.
$\tau = 1/\sigma^2$

step takes the value 1 if its argument is $>= 0$,
and 0 otherwise, resulting in
$\mu_i = \alpha_1 + \beta_1 x_i$ before n_{change} and
$\mu_i = \alpha_1 + \alpha_2 + (\beta_1 + \beta_2) x_i$ from n_{change}
onwards

back-transform $log(\tau)$ to τ.

again, the *step* function is used to define $log(\tau)$ before and after n_{change}. Log-transformation is used to ensure that the τ resulting from τ_1 and τ_2 is positive.

We have to define priors for all parameters that are not specified by data.

$\alpha_1 \sim N(\mu = 0, \tau = 10^{-4})$ That is a normal distribution with mean $\mu = 0$ and standard deviation $\sigma = 100$, because $\sigma = 1/\sqrt{\tau}$
$\alpha_2 \sim N(0, 10^{-4})$

$\beta_1 \sim N(0, 10^{-4})$
$\beta_2 \sim N(0, 10^{-4})$

$log(\tau_1) \sim N(0, 10^{-4})$
$log(\tau_2) \sim N(0, 10^{-4})$

Discrete prior on the change point. K indicates one of the possible change points, based on the probability vector p, which we need to specify beforehand.

Note that we put priors on $log(\tau_1)$ and $log(\tau_2)$, rather than on τ_1 and τ_2 directly, to ensure that the precision τ in the second part of the regression always remains positive. $e^{log(\tau_1)+log(\tau_2)}$ is always > 0, even if the term $log(\tau_1) + log(\tau_2)$ becomes negative.

Prepare the data which we pass to JAGS along with the model:

```
# minimum number of the data points before and after the change
  min_segment_length <- 5

# assign indices to the potential change points we allow
  possible_change_points <- (1:n)[(min_segment_length+1):(n+1-min_segment_length)]

# number of possible change points
  M <- length(possible_change_points)

# probabilities for the discrete uniform prior on the possible change points,
# i.e. all possible change points have the same prior probability
  p <- rep(1 / M, length = M)

# save the data to a list for jags
  data_CPR <- list("x", "y", "n", "possible_change_points", "p")
```

Load the *R2jags* package to access *JAGS* in *R*:

```
  require(R2jags)
```

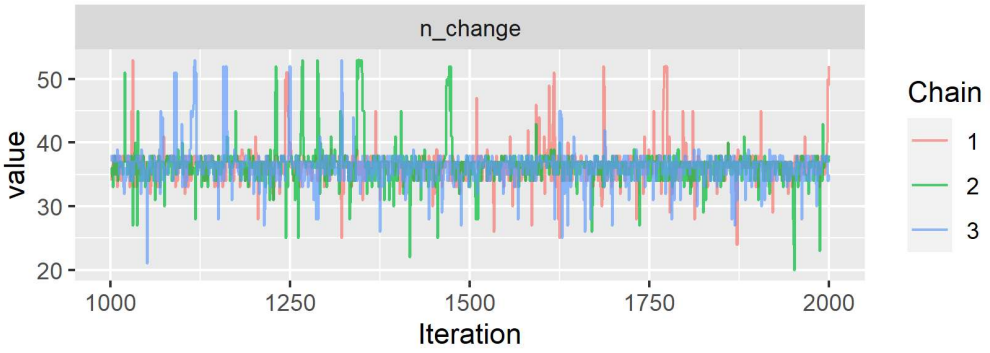
Now we execute the change point regression. We instruct JAGS to run three seperate chains so we can verify that the results are consistent. We allow 2000 iterations for each chain, the first 1000 of each will automatically be discared as burn-in.

```
CPR  <- jags(data = data_CPR,
                         parameters.to.save = c("alpha_1", "alpha_2",
                                                "beta_1","beta_2",
                                                "log_tau_1","log_tau_2",
                                                "n_change"),
                         n.iter = 2000,
                         n.chains = 3,
                         model.file = model_CPR)
```

The results

To visualise the results and inspect the posterior, we are using the *ggmcmc* package, which relies on the *ggplot2* package. For brevity, we just look at the n_{change} parameter here.

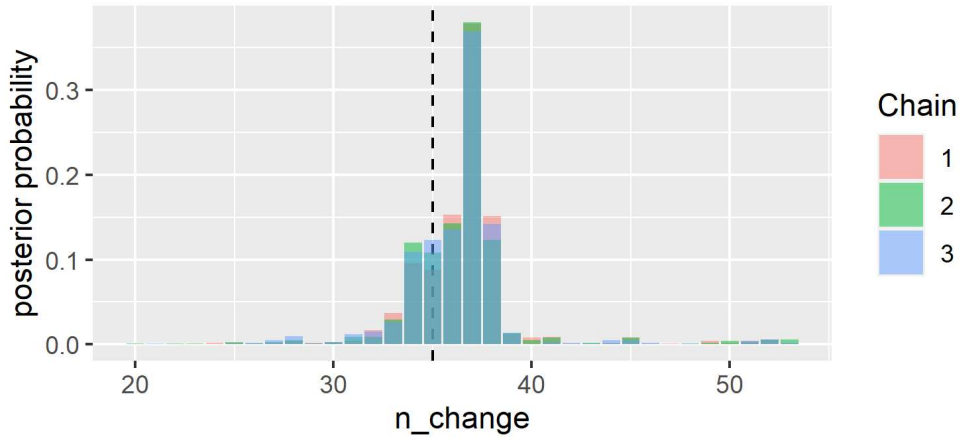
```
library(ggmcmc)
CPR.ggs <- ggs(as.mcmc(CPR)) # convert to ggs object
ggs_traceplot(CPR.ggs, family = "n_change")
```



Looks like the chains converge and mix nicely. We can already see that our model locates the change point somewhere between 30 and 40, although the chains occasionally explore regions further away.

Let's look at the posterior probabilities for the possible change points:

```
ggplot(data = CPR.ggs %>% filter(Parameter == "n_change"),
  aes(x=value, y = 3*(..count..)/sum(..count..), fill = as.factor(Chain))) +
  geom_vline(xintercept = 35,lty = 2) + geom_bar(position = "identity", alpha = 0.5) +
  ylab("posterior probability") + xlab("n_change") + labs(fill='Chain')
```



The 37^{th} point has the highest probability of being the change point. That is not far off from where we introduced the change, at the 35^{th} point (dashed line). The random generation of x and y has led to 37 being favoured. We also note that there are only minor differences between the three chains, and those differences would likely further dwindle if we were to let the chains run for longer.

Using the posterior distribution, we can answer questions like: "In which interval does the change point fall with 90 % probability?"

```
quantile(CPR$BUGSoutput$sims.list$n_change, probs = c(0.05, 0.95))
```

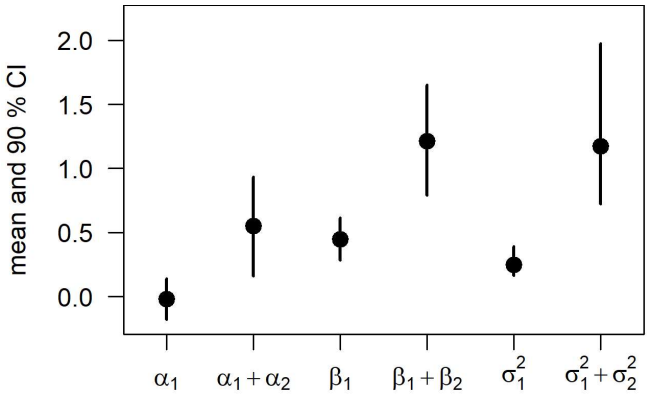
```
##  5% 95%
##  33  39
```

We can also inquire about the probability that the change point falls in the interval 34 to 38:

```
round(length(which(CPR$BUGSoutput$sims.list$n_change %in% 34:38))/
            (CPR$BUGSoutput$n.sims),2)
```

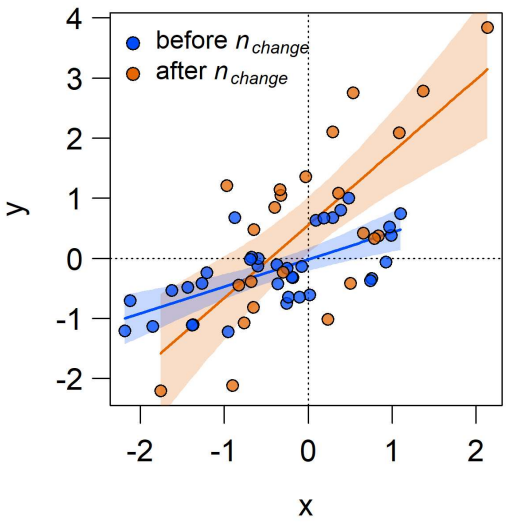
```
## [1] 0.87
```

Finally, let's have a look at the regression parameters and plot the resulting regressions before and after the most likely change point.



The intercept, slope, and residual variance all increase after the change point.

This can be immediately seen when plotting the change point regression:



The shaded areas denote 95 % credible intervals around the regression lines.

You can find the full R code for this analysis at
https://github.com/KEichenseer/Methods/blob/main/Change_point_regression.R

Get in touch if you have any comments or questions!

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