RiskHunt3r workshop on uncertainty

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Contents

Introduction

This is a demonstration of Quantitative uncertainty analysis in a Bayesian framework.

Generate an artificial data set for a continuous response variable.

Build and inform a linear model predicting the response given a single covariate.

Demonstrate different ways to use the posterior distribution of the parameters to evaluate the combined impact of parameter uncertainty on an outcome or quantity of interest.

Model

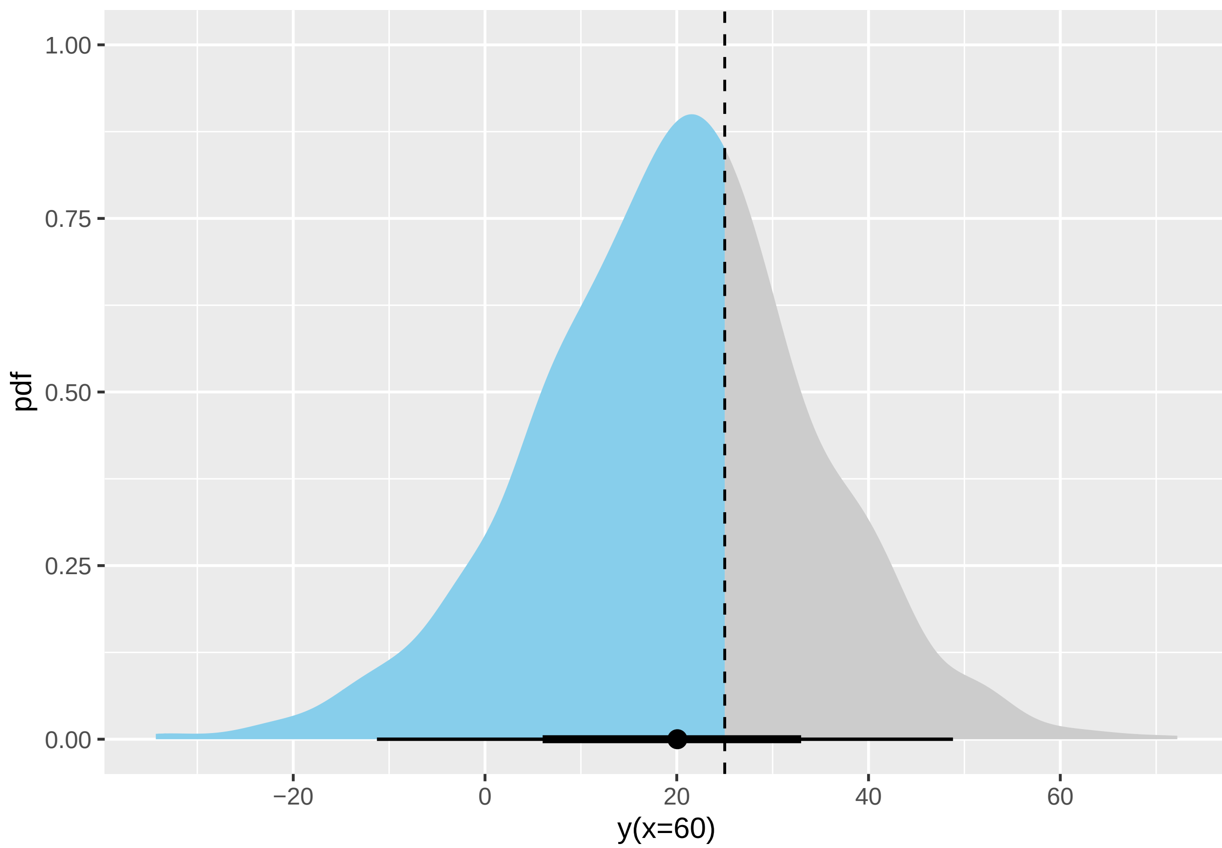
$$Y = a + b \cdot X + e$$

$$e \sim N(0, \sigma)$$

Monte Carlo simulation based on specified probability distributions

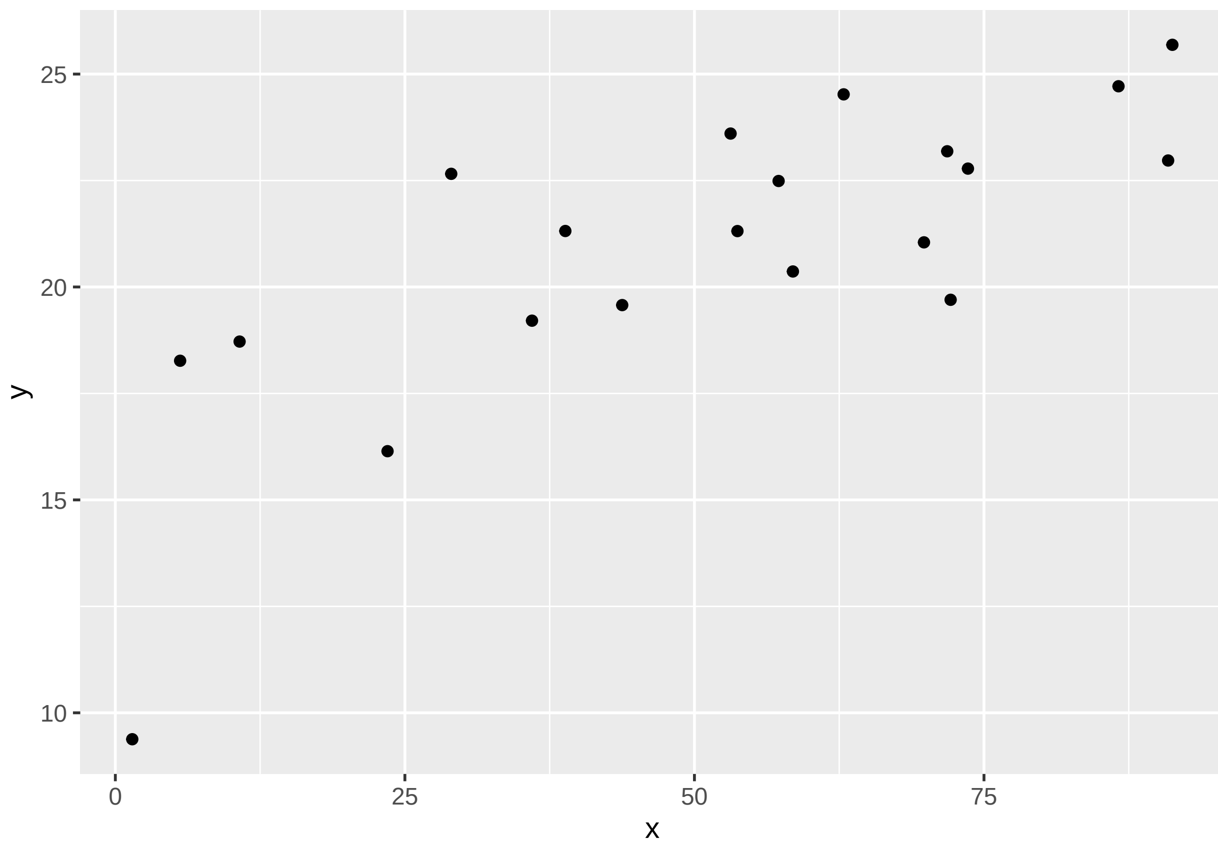
Let us start with a situation where we have uncertainty about parameters

```
n = 10^3 #number of iterations in the MC simulation
a <- rnorm(n,20,10)
b <- rnorm(n,4,0.5)
sigma <- abs(rnorm(n,3,10))
x <- 60
y <- unlist(lapply(1:n,function(i){a[i]+b[i]*(x-50)/50 + rnorm(1,0,sigma[i])}))

df_y <- data.frame(y = y, gr = y<25)

##plot prob density for Y
ggplot(df_y,aes(x = y,fill = stat(x < 25))) +
 stat_halfeye() +
  #stat_dotsinterval() +
  geom_vline(xintercept = c(25), linetype = "dashed") +
  scale_fill_manual(values = c("gray80", "skyblue")) +
  ylab('pdf') +
  xlab('y(x=60)') +
  theme(legend.position='none')
```



Load and plot data set

```
load("demodata.Rdata")

ggplot(df,aes(x=x,y=y))+
  geom_point()
```



Specify a Bayesian model

```
# create a list with data to go into the Bayesian sampler
data_jags <- list(x=df$x, y=df$y, n=nrow(df))

mod_jags <- function(){
    # Priors:
    a ~ dnorm(0, 0.001) # intercept
    b ~ dnorm(0, 0.001) # slope
    sigma ~ dunif(0, 100) # standard deviation
    tau <- 1 / (sigma * sigma) # sigma^2 doesn't work in JAGS

    # Likelihood:
    for (i in 1:n){
        y[i] ~ dnorm(mu[i], tau) # tau is precision (1 / variance)
        mu[i] <- a + b * (x[i]-50)/50
    }

}
```

Run MCMC sampling

```r
# select initial values for the MCMC sampling
init_values <- function(){
    list(a = rnorm(1), b = rnorm(1), sigma = abs(rnorm(1,10,2)))
}

# parameters to save
params <- c("a", "b", "sigma")

# run MCMC sampling using Gibbs sampling (may take some time, but not long)
mcmc_jags <- jags(data = data_jags, inits = init_values, parameters.to.save = params, model.file = mod_
               n.chains = 3, n.iter = 12000, n.burnin = 2000, n.thin = 10)
```

```
## module glm loaded
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 20
##    Unobserved stochastic nodes: 3
##    Total graph size: 131
##
## Initializing model
```

```r
mod_mcmc <- as.mcmc(mcmc_jags)
```

Study summary of the MCMC sample

```r
mcmc_jags
```

```
## Inference for Bugs model at "C:/Users/ekol-usa/AppData/Local/Temp/Rtmp40grAX/model2aa072b24edb.txt",
##  3 chains, each with 12000 iterations (first 2000 discarded), n.thin = 10
##  n.sims = 3000 iterations saved
##          mu.vect sd.vect   2.5%    25%    50%    75%   97.5%  Rhat n.eff
## a         20.729   0.588 19.610 20.348 20.731 21.112  21.923 1.001  3000
## b          5.030   1.110  2.792  4.341  5.038  5.736   7.244 1.001  3000
## sigma      2.603   0.479  1.869  2.261  2.536  2.860   3.696 1.001  3000
## deviance  93.510   2.812 90.375 91.446 92.755 94.802 100.923 1.001  3000
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 4.0 and DIC = 97.5
## DIC is an estimate of expected predictive error (lower deviance is better).
```

Study the convergence of the samples of the parameters

```
#plot(mod_mcmc)
```

Compare model predictions to data

Let us illustrate the model for values on x between 0 and 100.

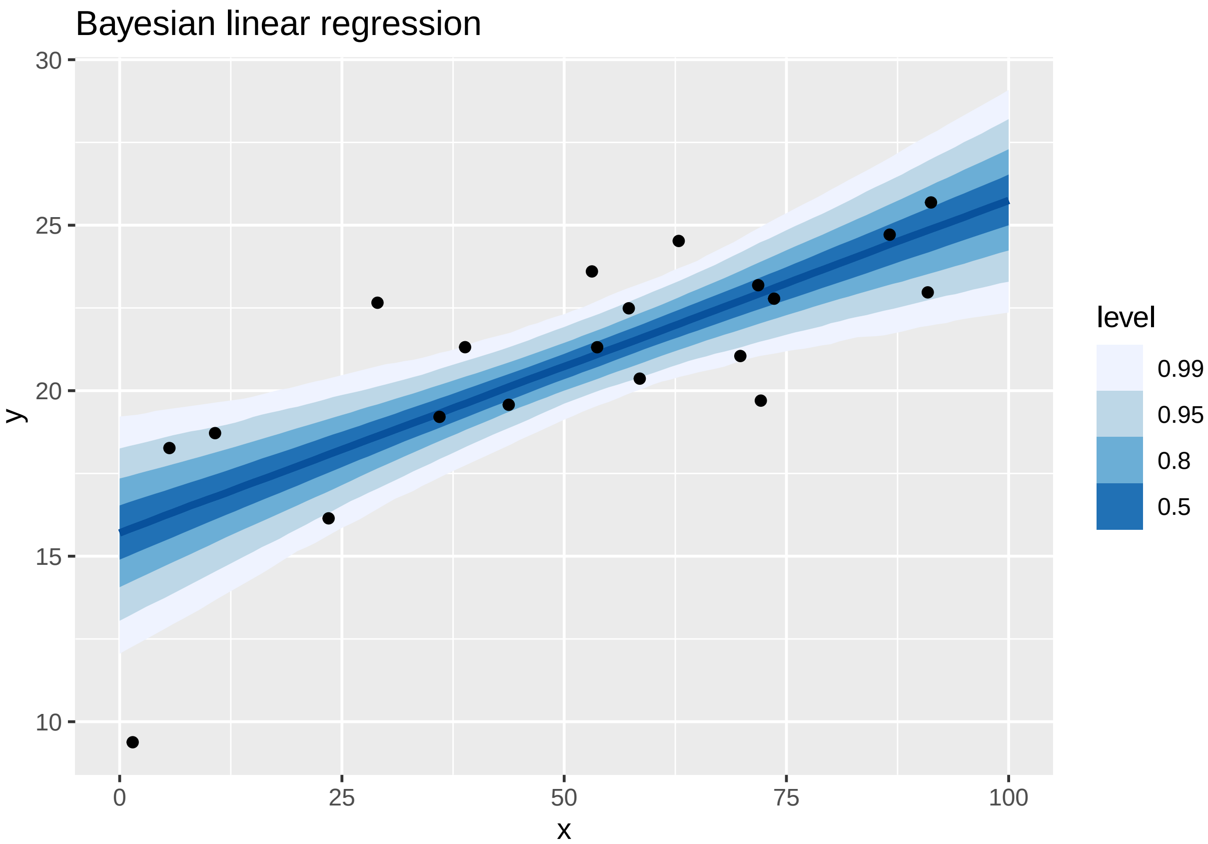
```
# save posterior from three chains into one sample
mcmc_sample <- as.mcmc(rbind(mod_mcmc[[1]], mod_mcmc[[2]], mod_mcmc[[3]]))

# make predictions for different values on x
x_new = seq(0,100,by=1)
```

Uncertainty about the model

```
pred_sample2 <- do.call('rbind',lapply(1:nrow(mcmc_sample),function(i){
data.frame(y=mcmc_sample[i,"a"] + (x_new-50)/50 * mcmc_sample[i,"b"],x=x_new,iter=i)
}))

ggplot(pred_sample2,aes(x=x,y=y)) +
    stat_lineribbon(aes(y = y), .width = c(.99, .95, .8, .5), color = "#08519C") +
  scale_fill_brewer() +
  geom_point(data=df,aes(x=x,y=y)) +
  ggtitle('Bayesian linear regression')
```



Uncertainty about future data points

```
pred_sample3 <- do.call('rbind',lapply(1:nrow(mcmc_sample),function(i){
data.frame(y=mcmc_sample[i,"a"] + (x_new-50)/50 * mcmc_sample[i,"b"] + rnorm(length(x_new),0,mcmc_sampl
}))

ggplot(pred_sample3,aes(x=x,y=y)) +
    stat_lineribbon(aes(y = y), .width = c(.99, .95, .8, .5), color = "#08519C") +
  scale_fill_brewer() +
  geom_point(data=df,aes(x=x,y=y)) +
  ggtitle('Bayesian linear regression')
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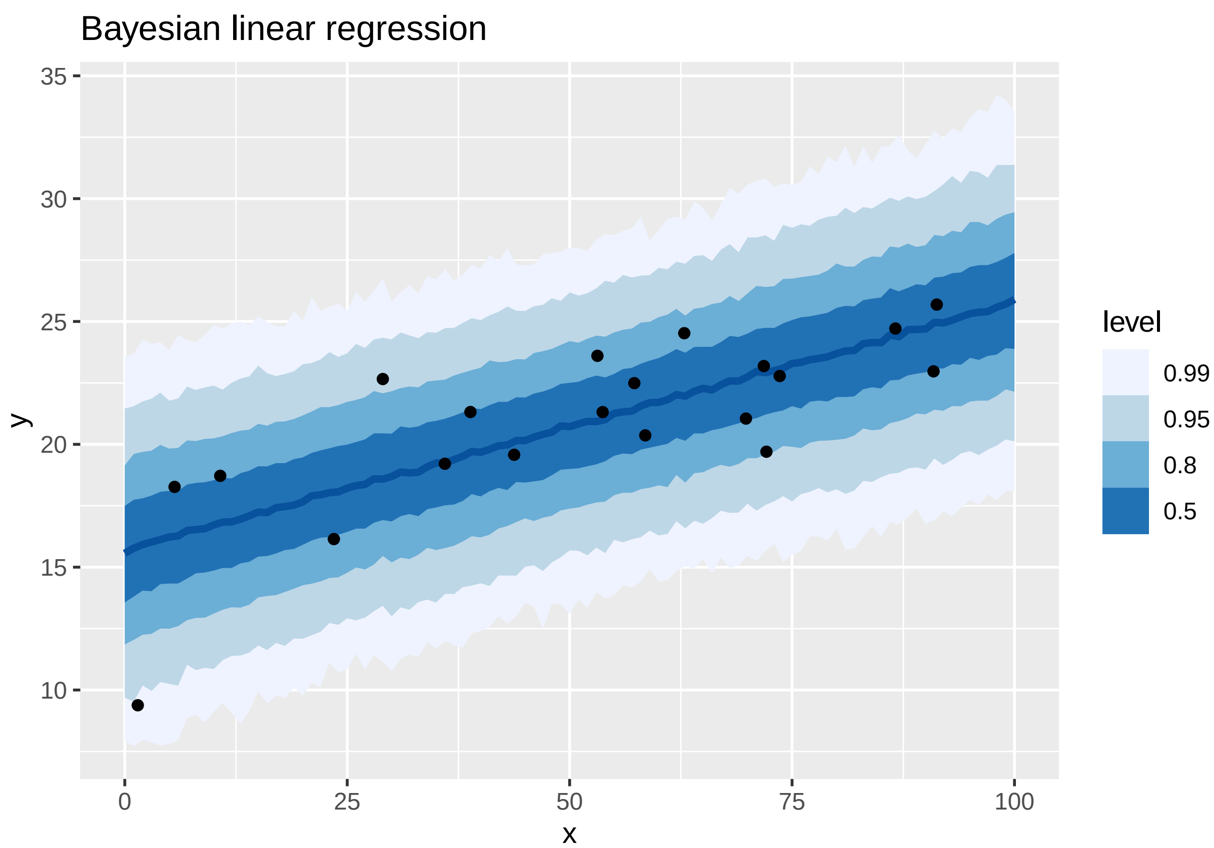
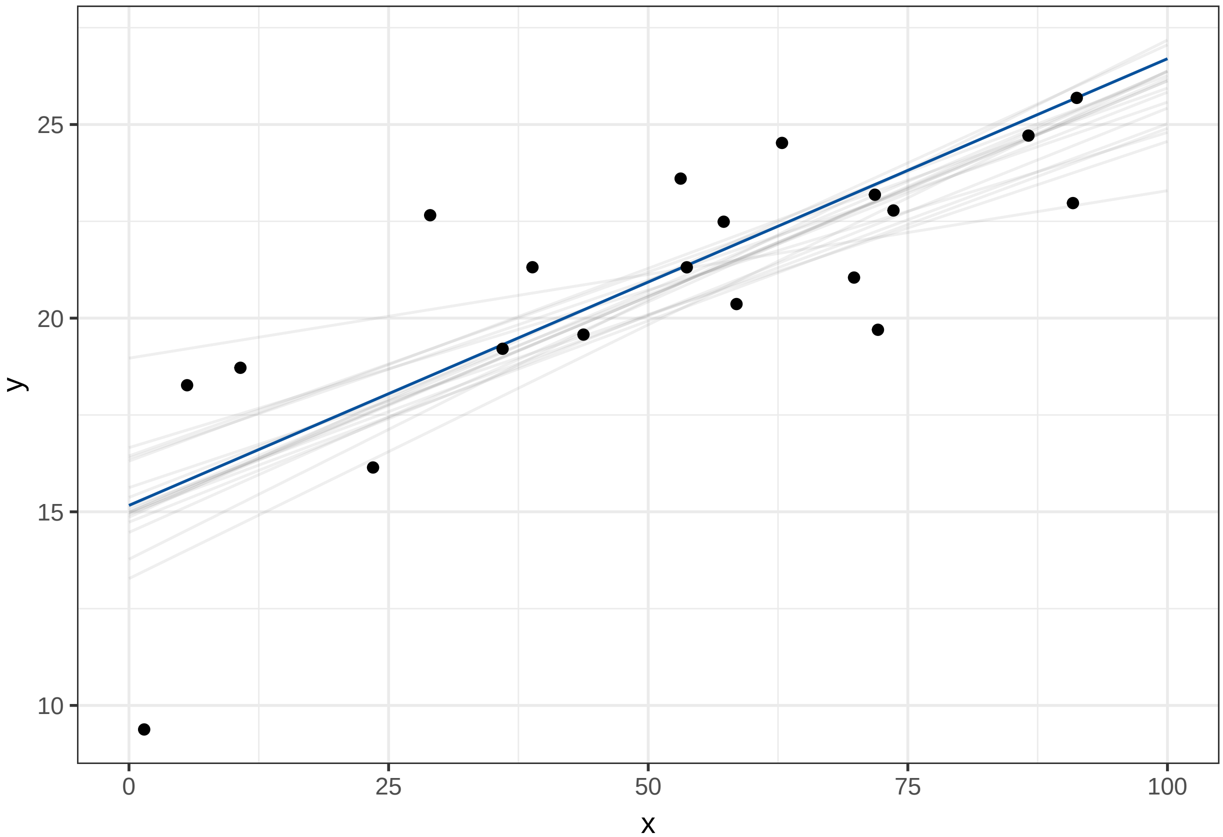


An alternative way to illustrate uncertainty about the model using animated plots

```
pred_sample_draws <- do.call('rbind',lapply(1:20,function(j){
  i <- sample.int(nrow(mcmc_sample),1)
data.frame(y=mcmc_sample[i,"a"] + (x_new-50)/50 * mcmc_sample[i,"b"],x=x_new,draw=j)
}))
 ggplot(pred_sample_draws,aes(x=x,y=y)) +
  geom_line(aes(group = draw), color = "#08519C") +
  geom_point(data = df) +
  theme_bw() +
  transition_states(draw, 0, 0.2) +
  shadow_mark(past = TRUE, future = TRUE, alpha = 1/8, color = "gray50")
```



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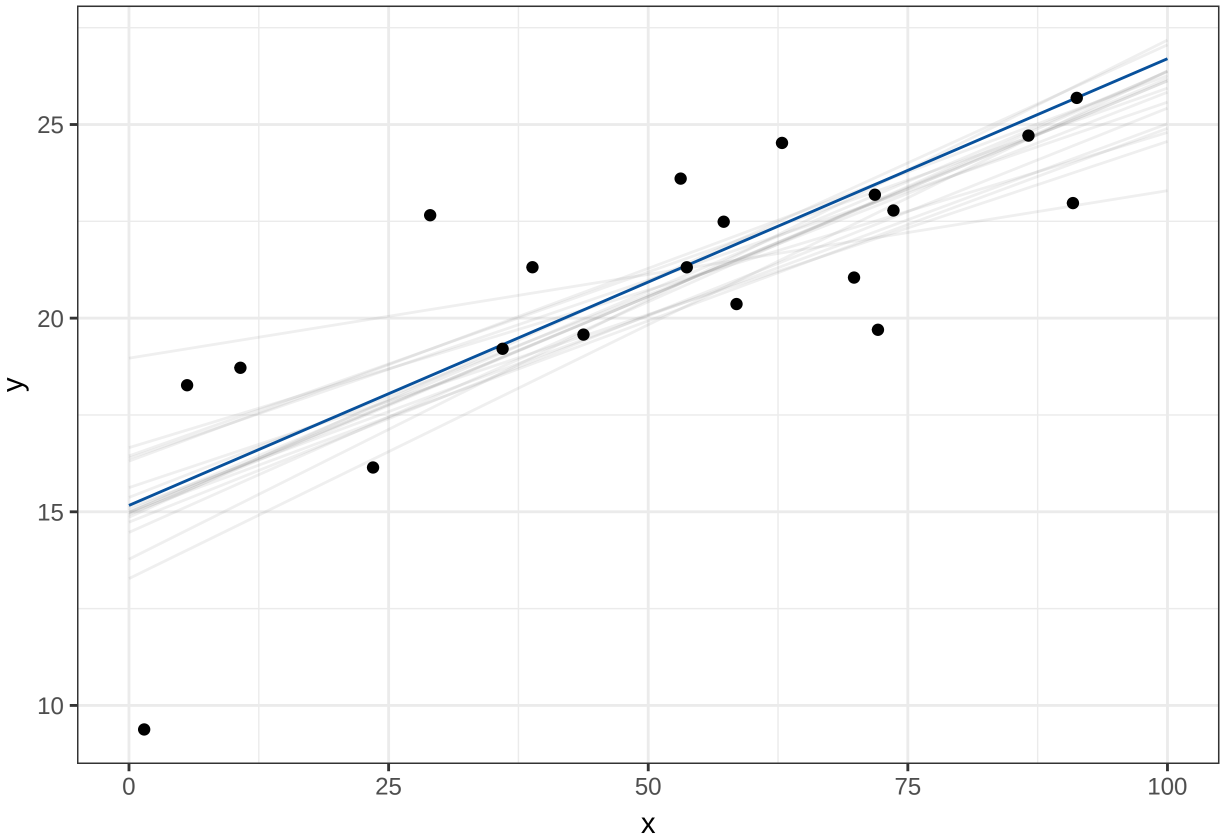
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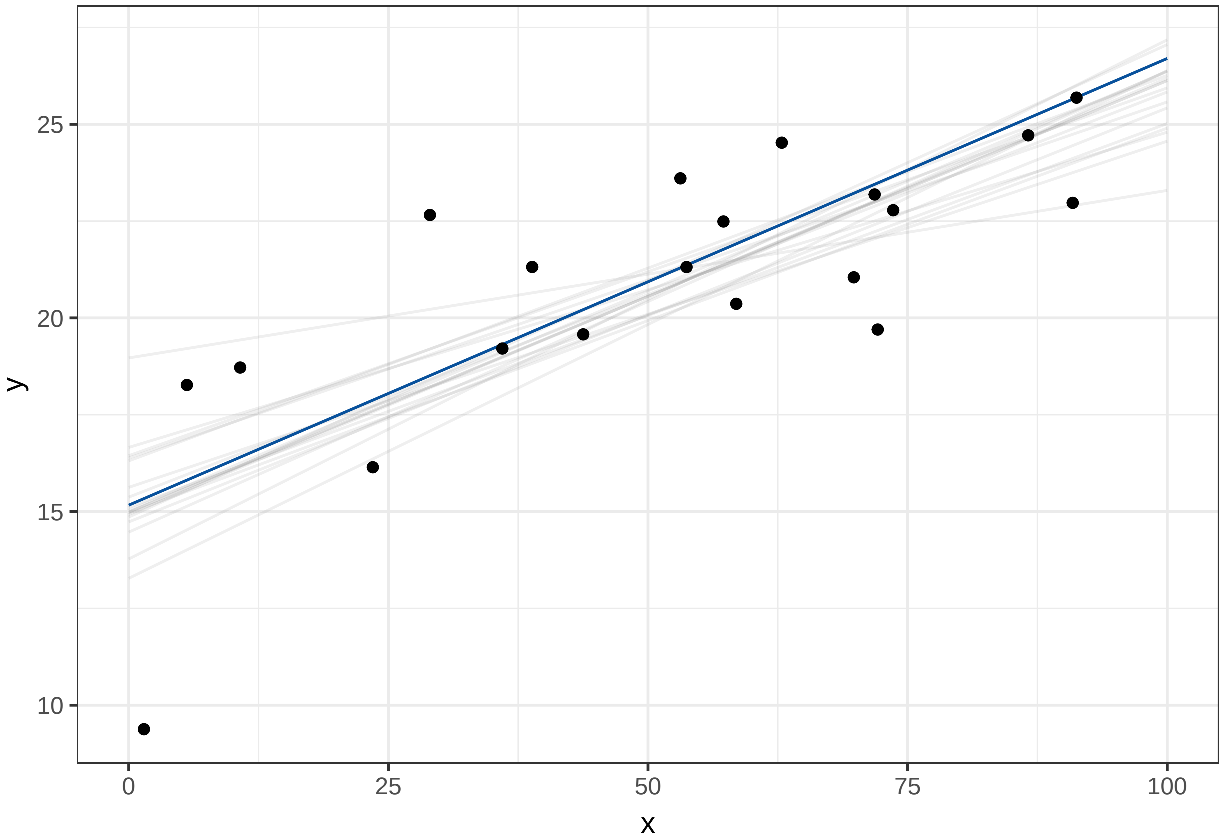

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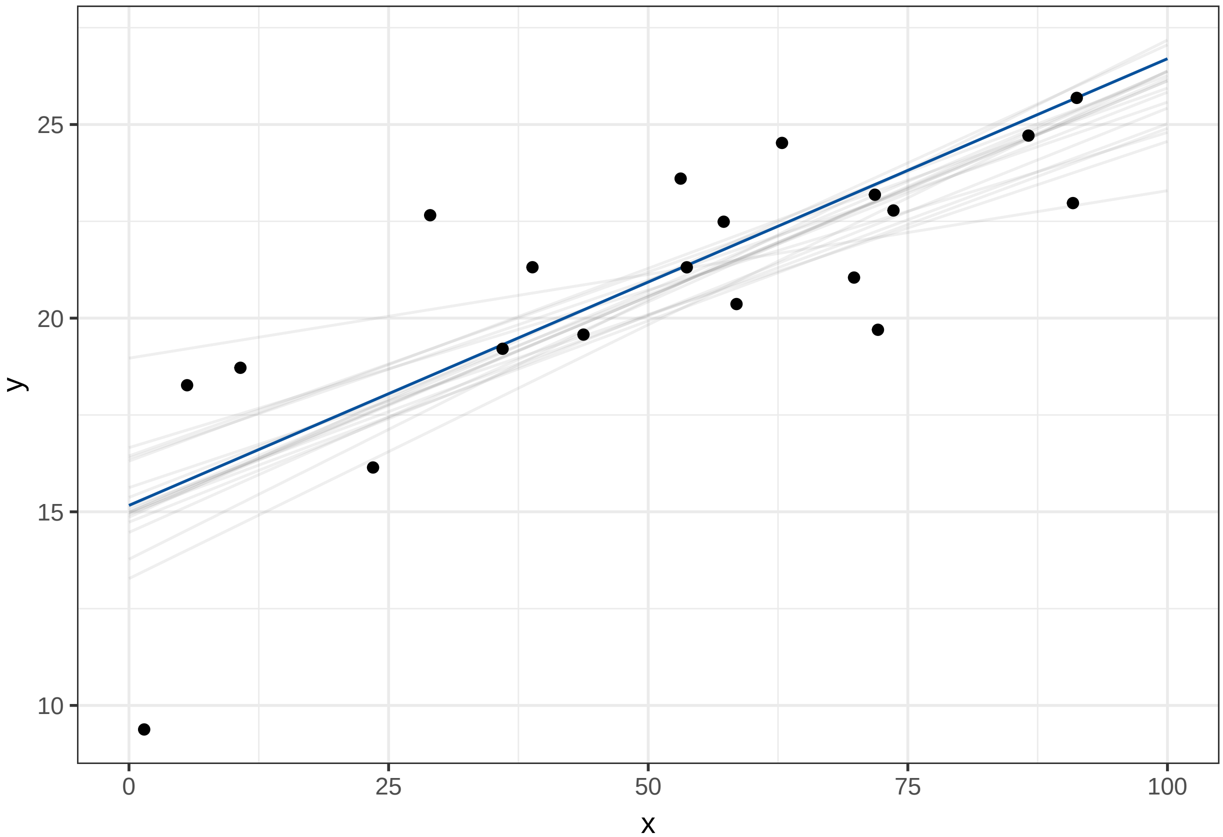

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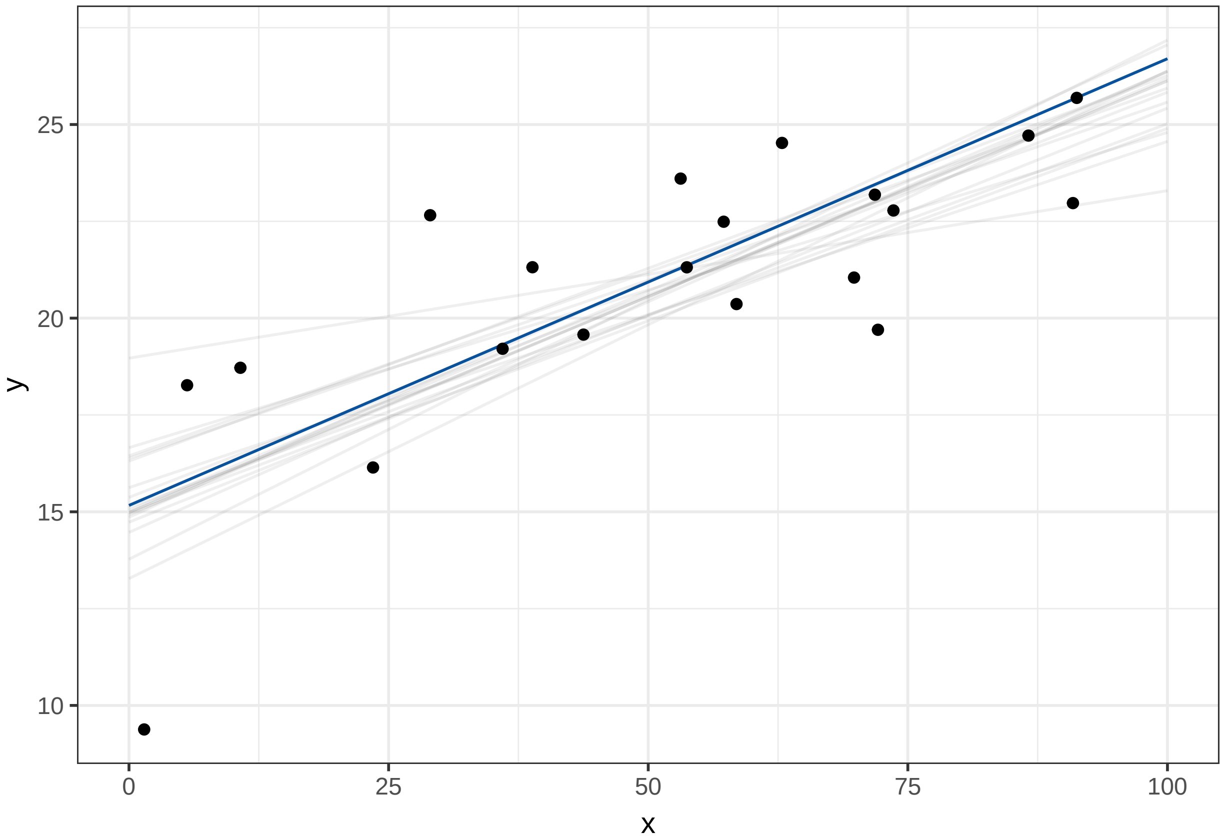
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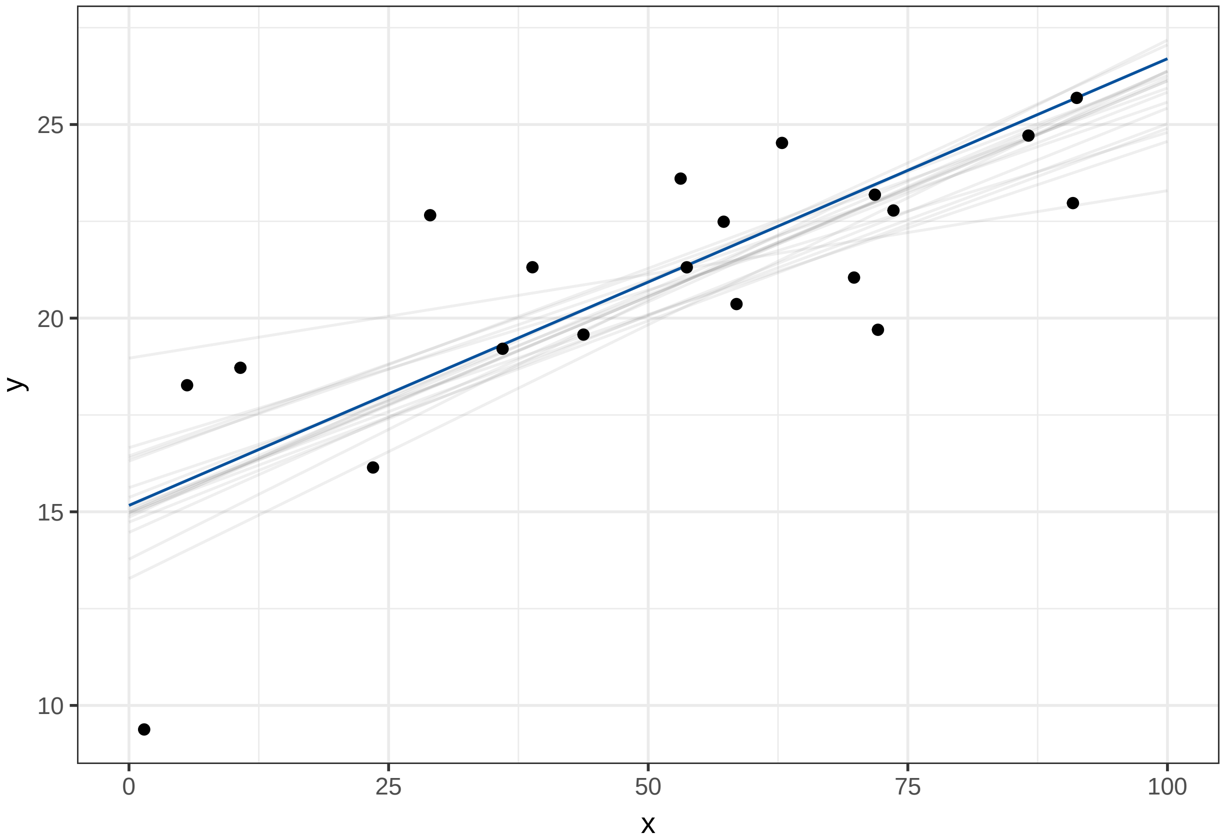

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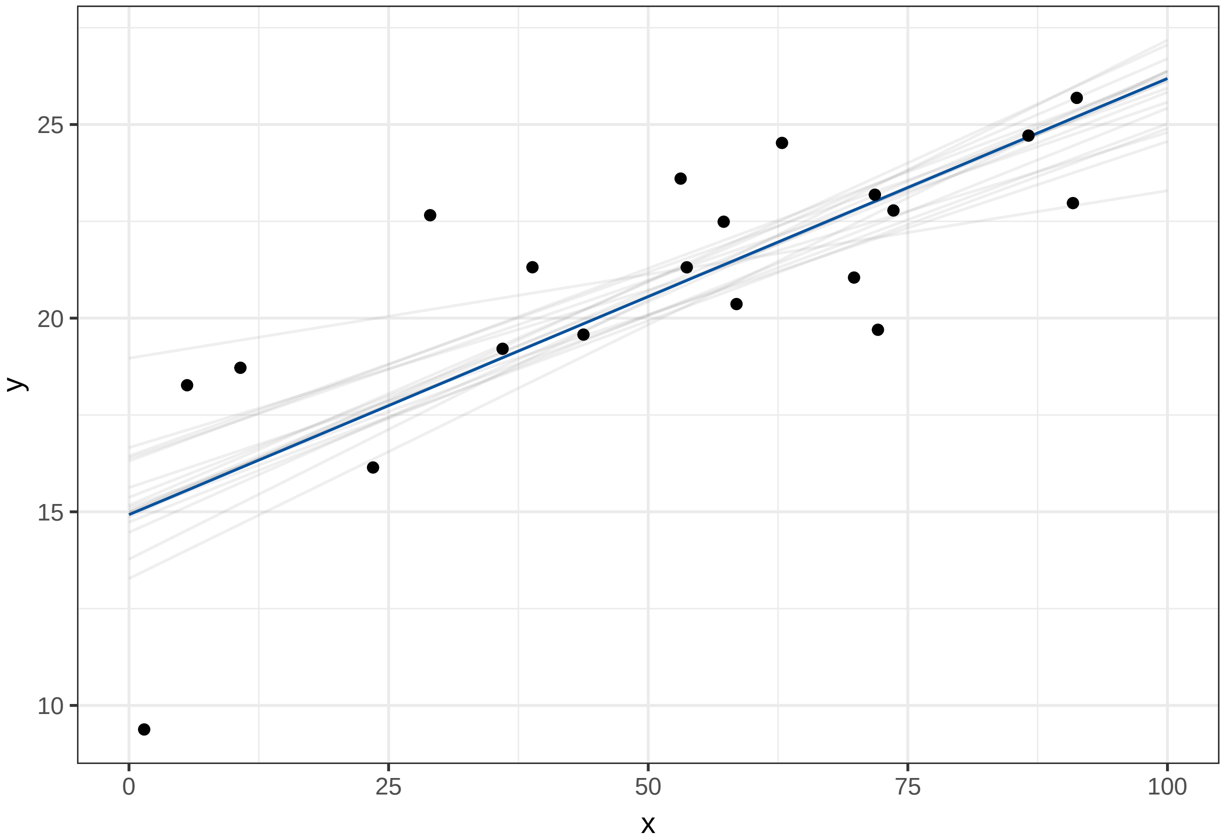

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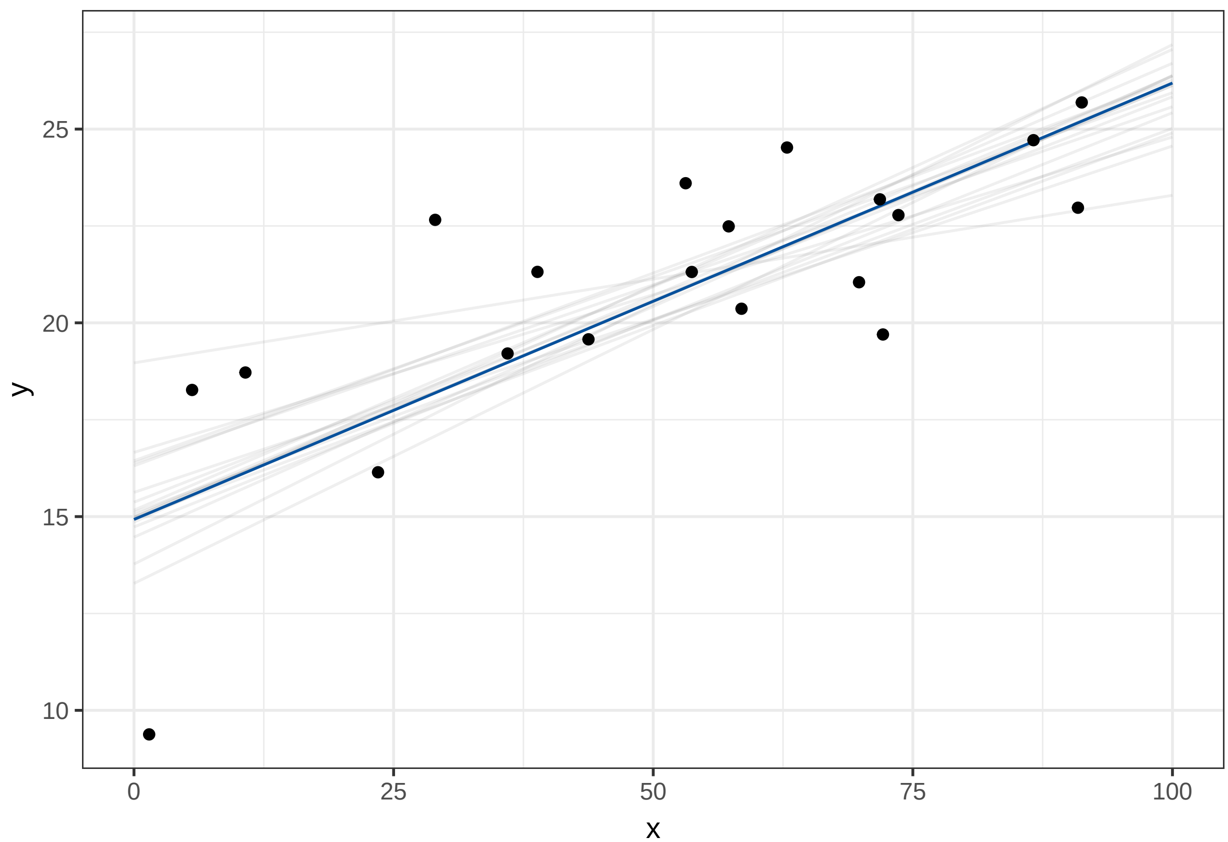
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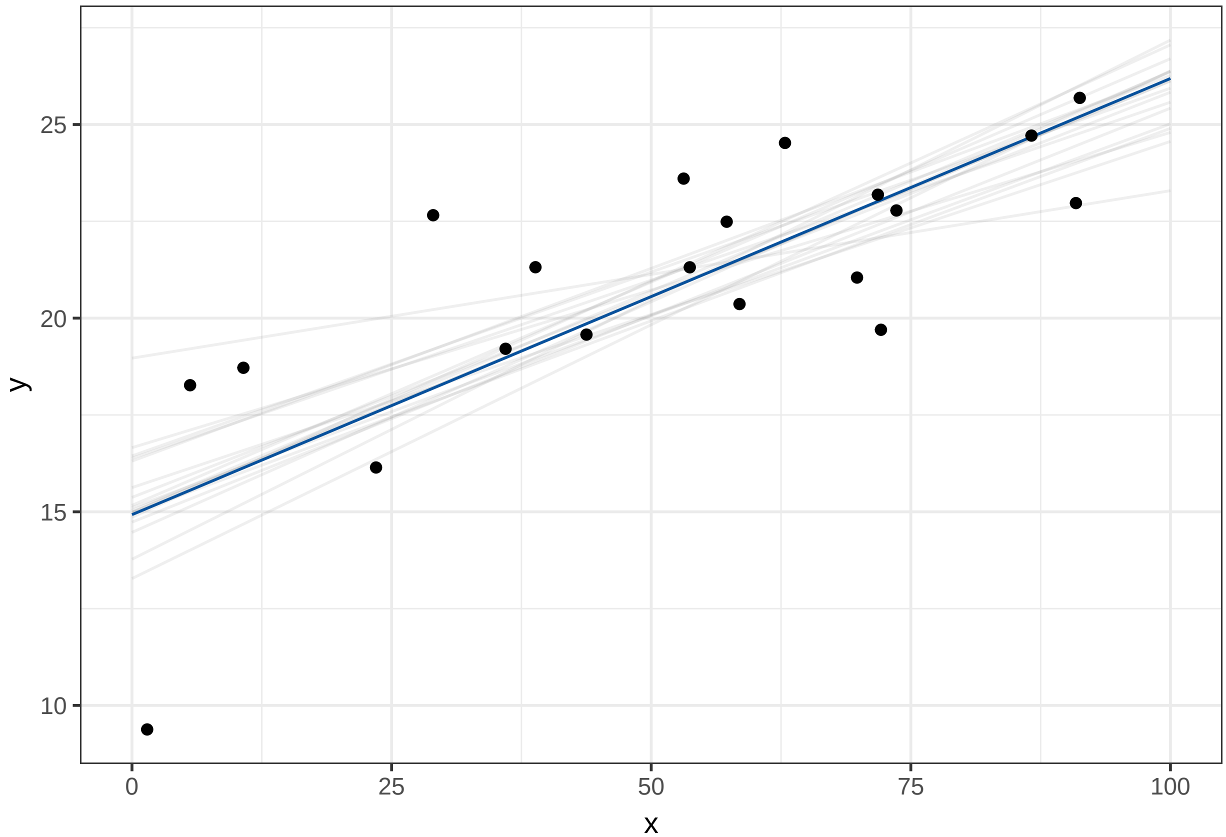

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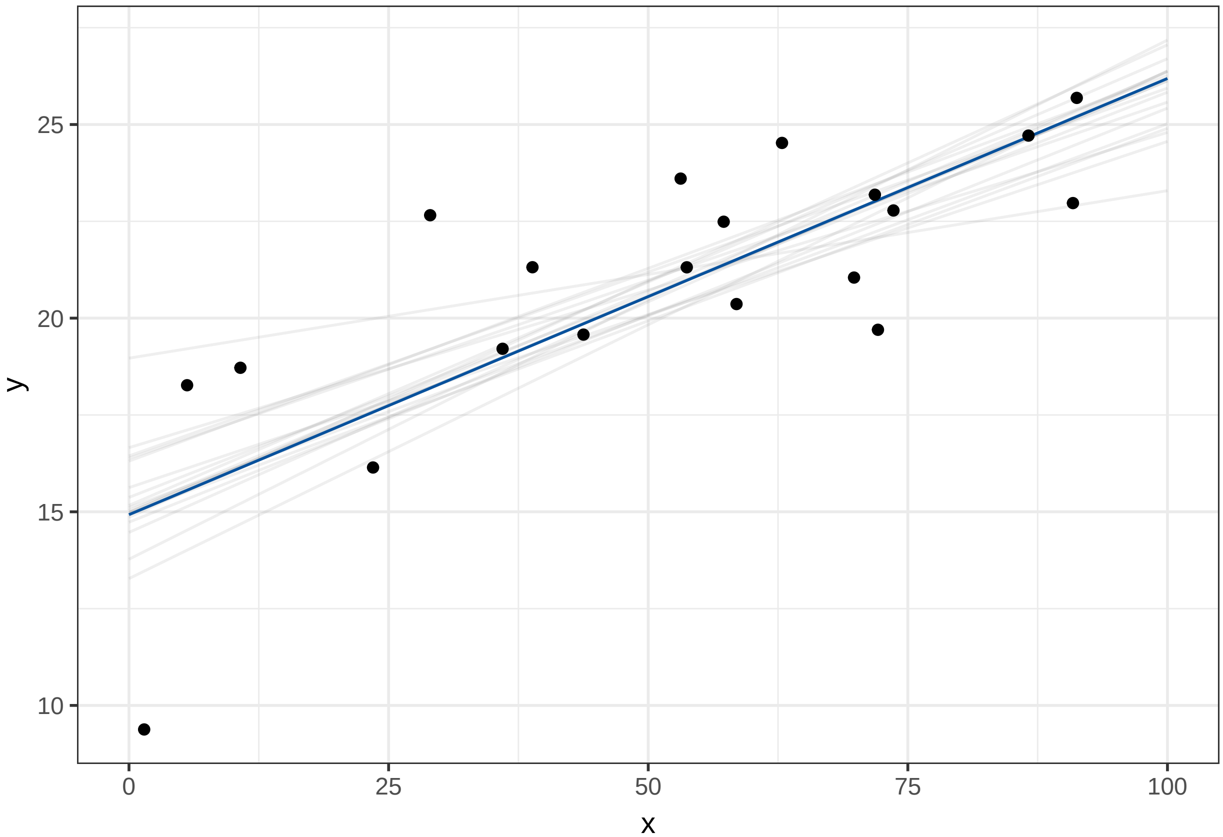

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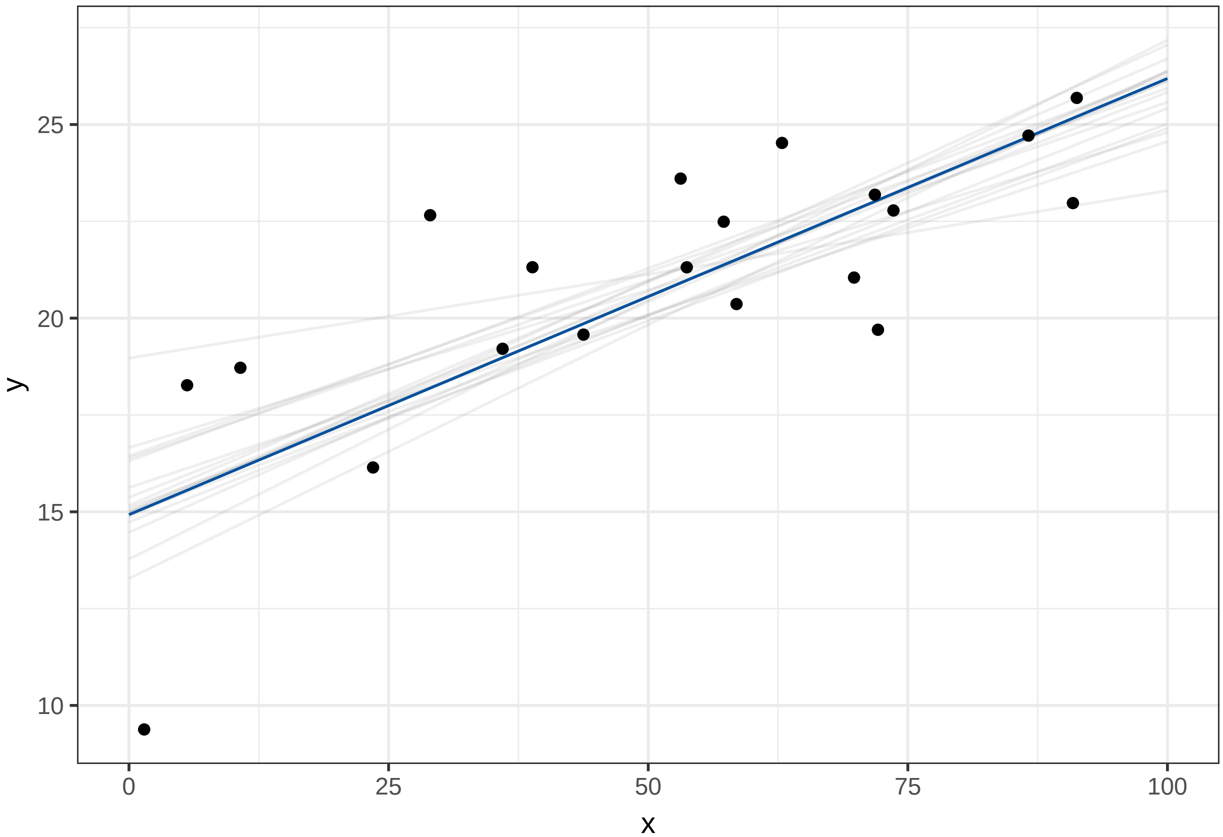

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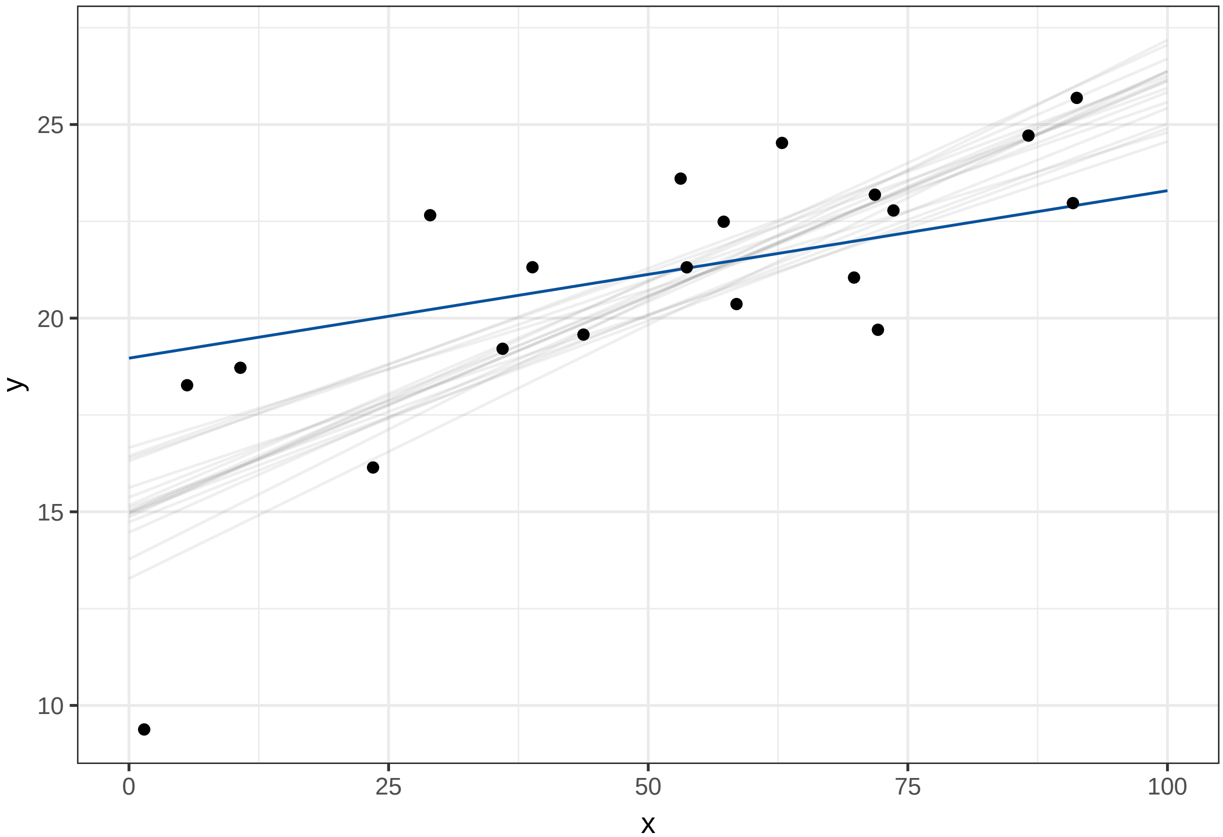

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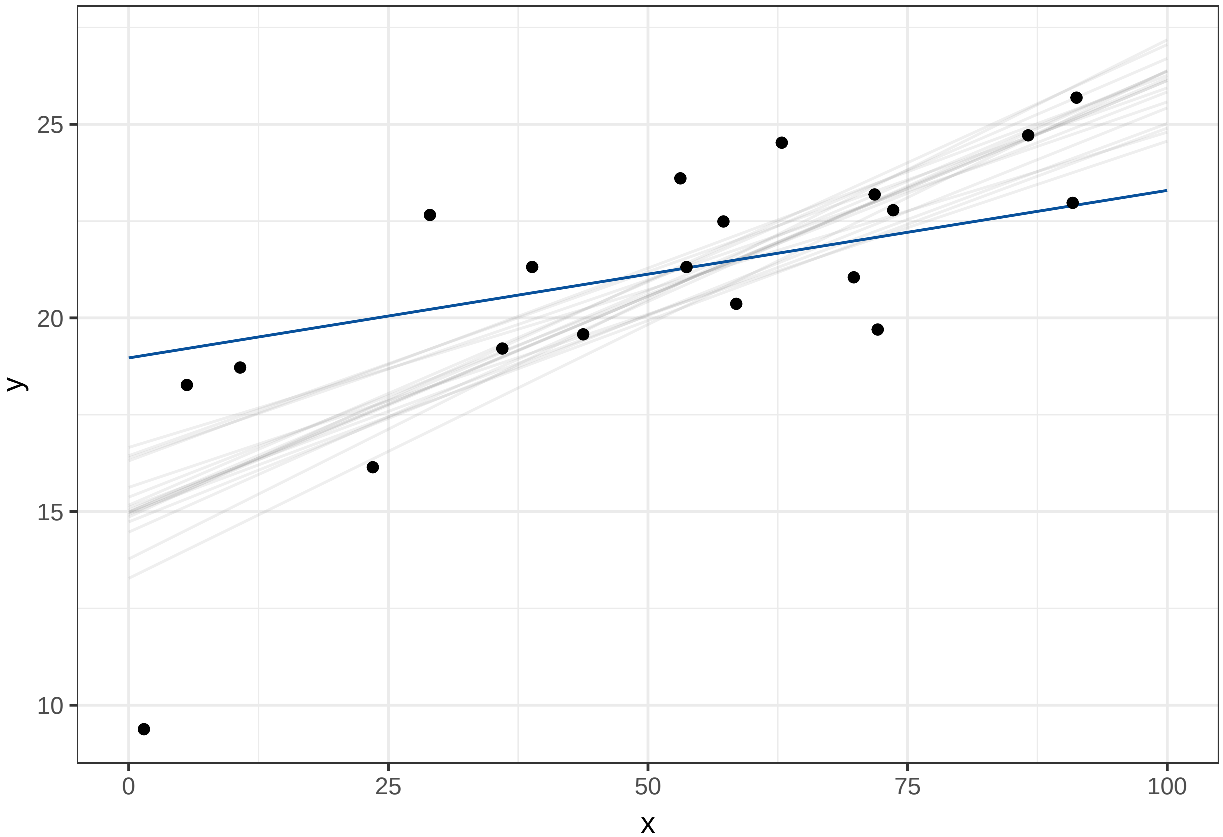
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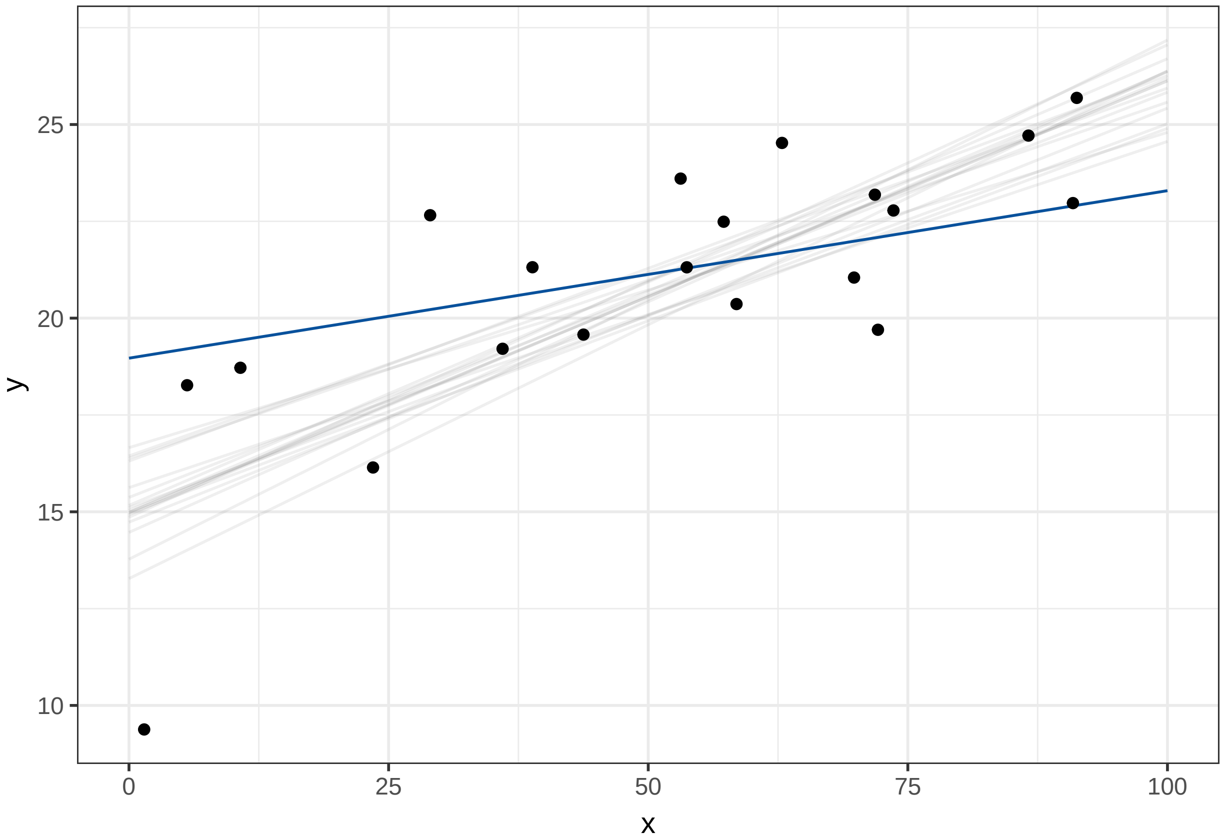

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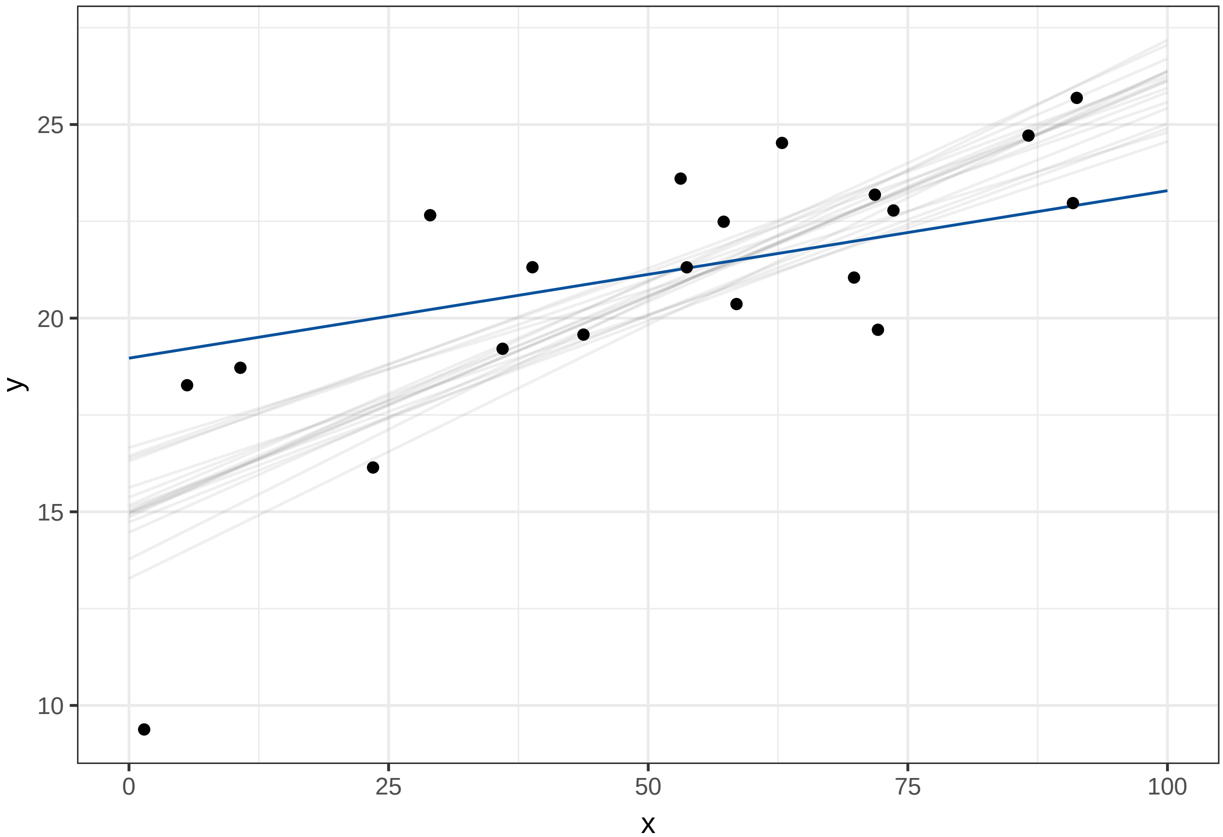
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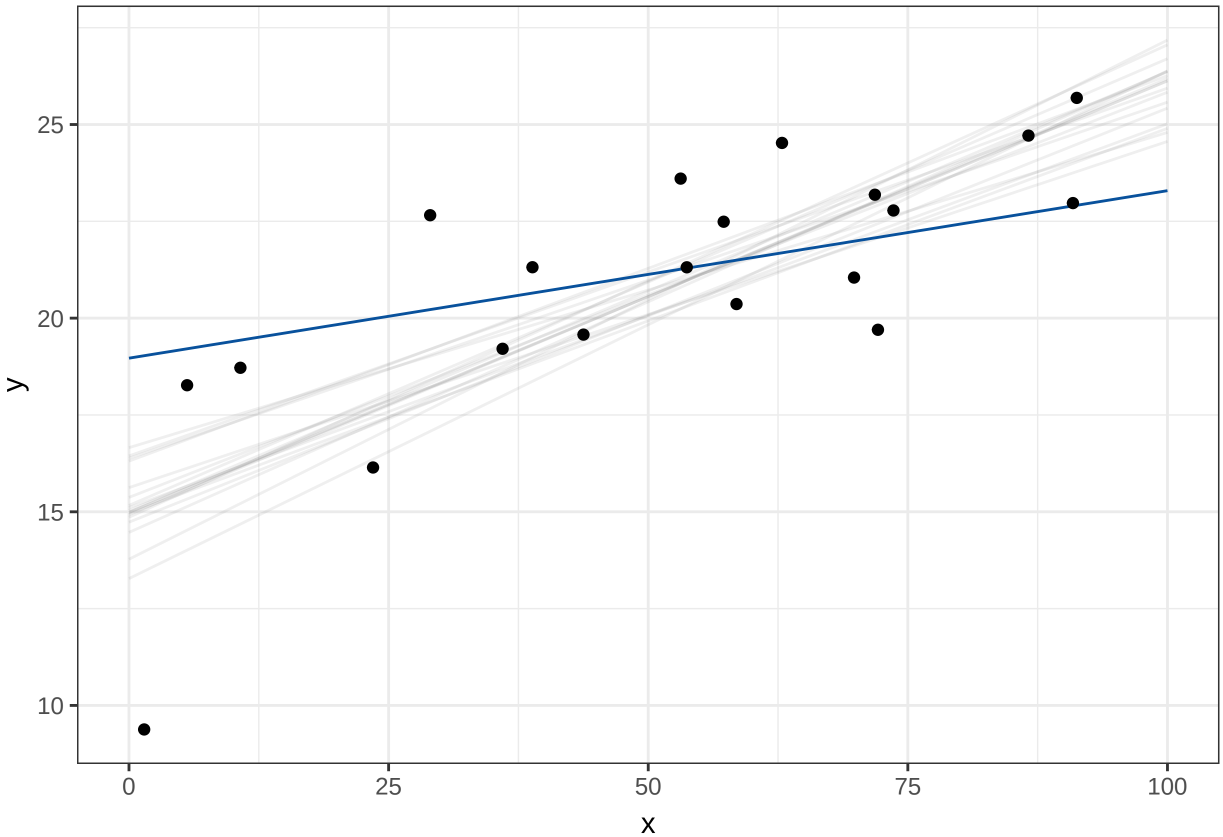
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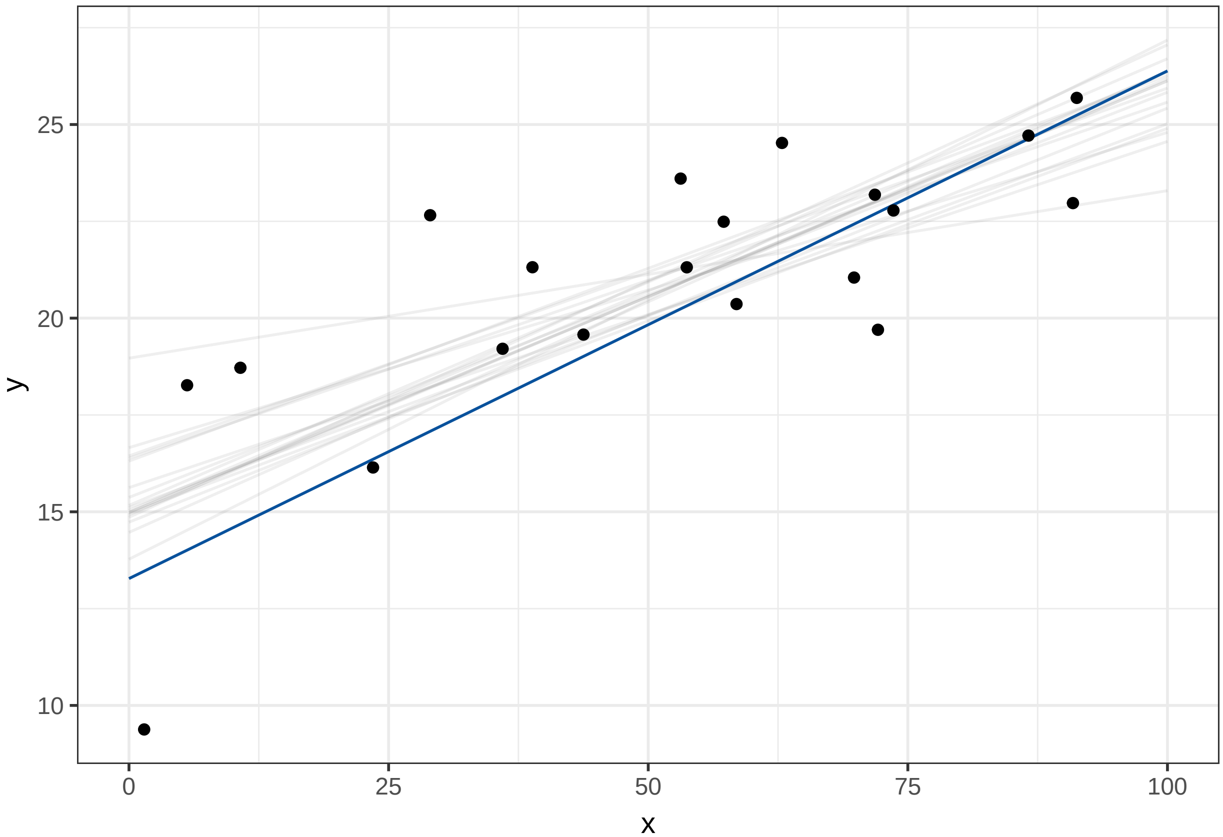

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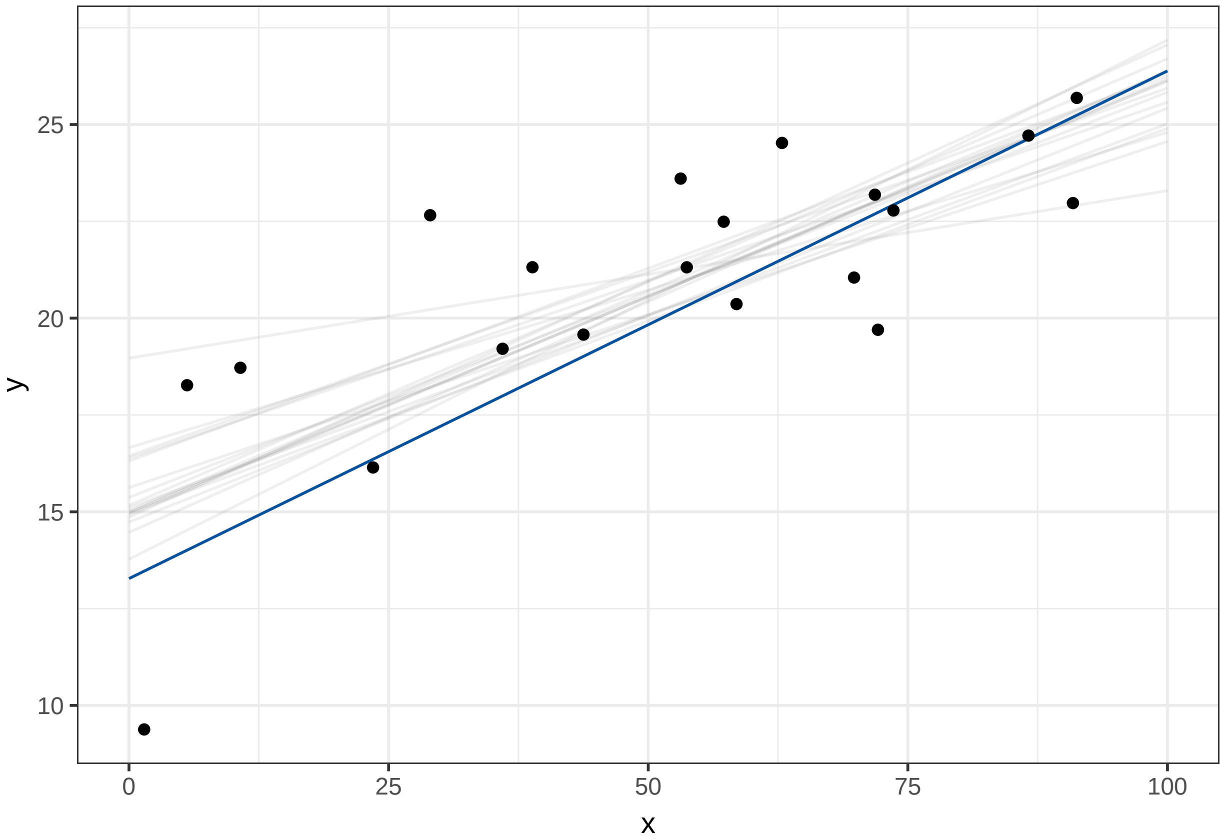

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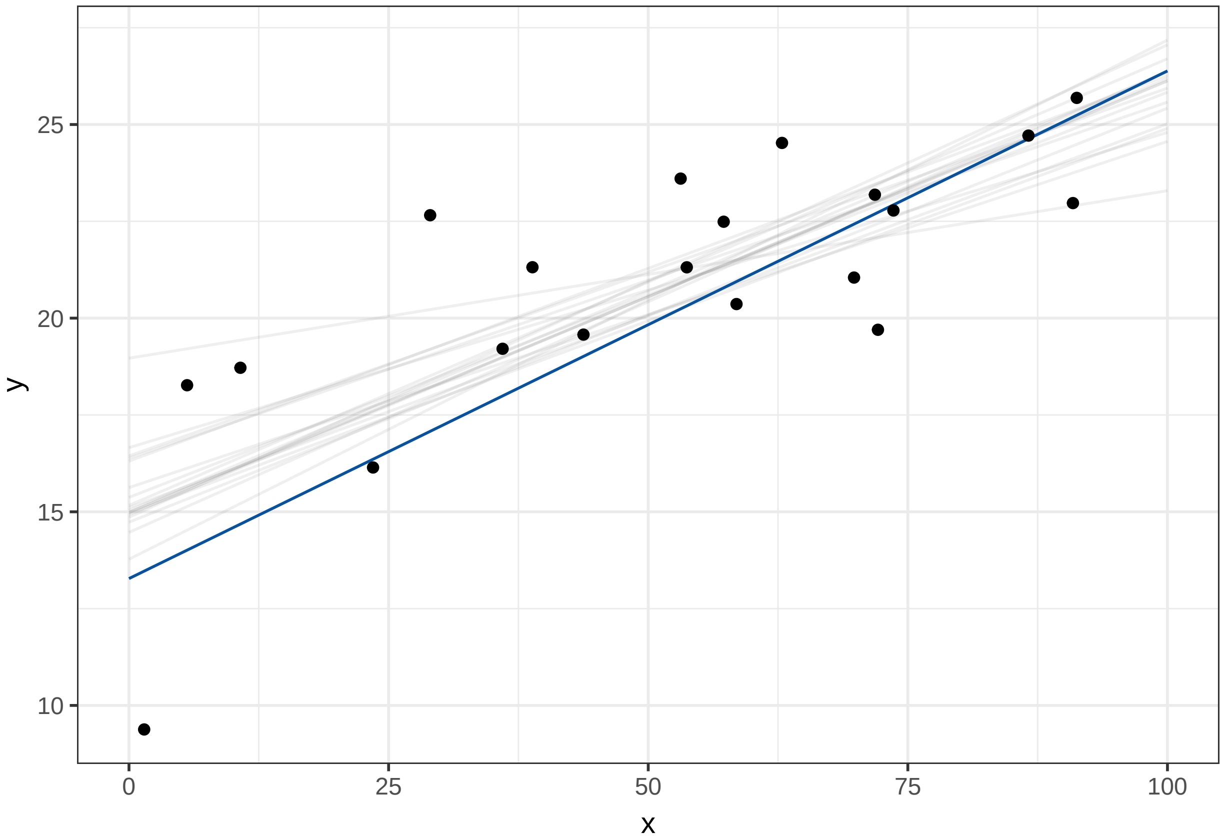

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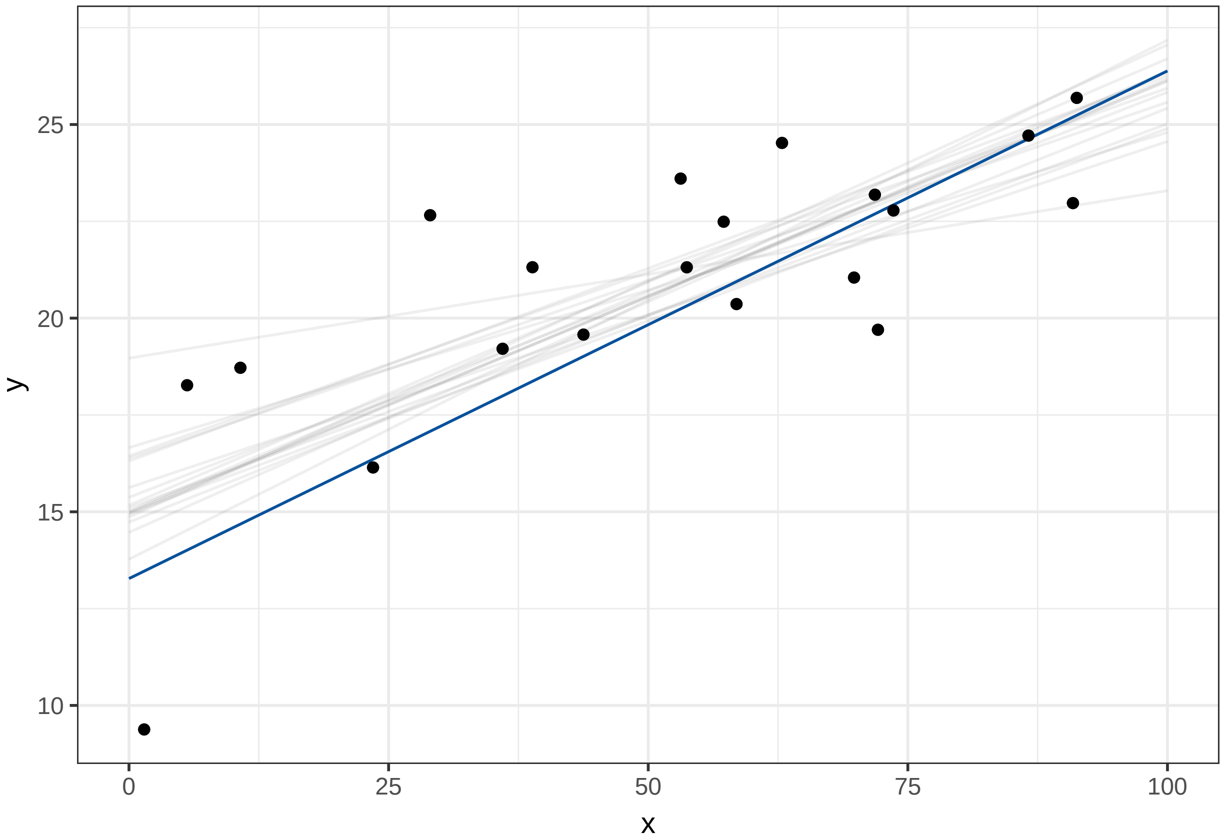

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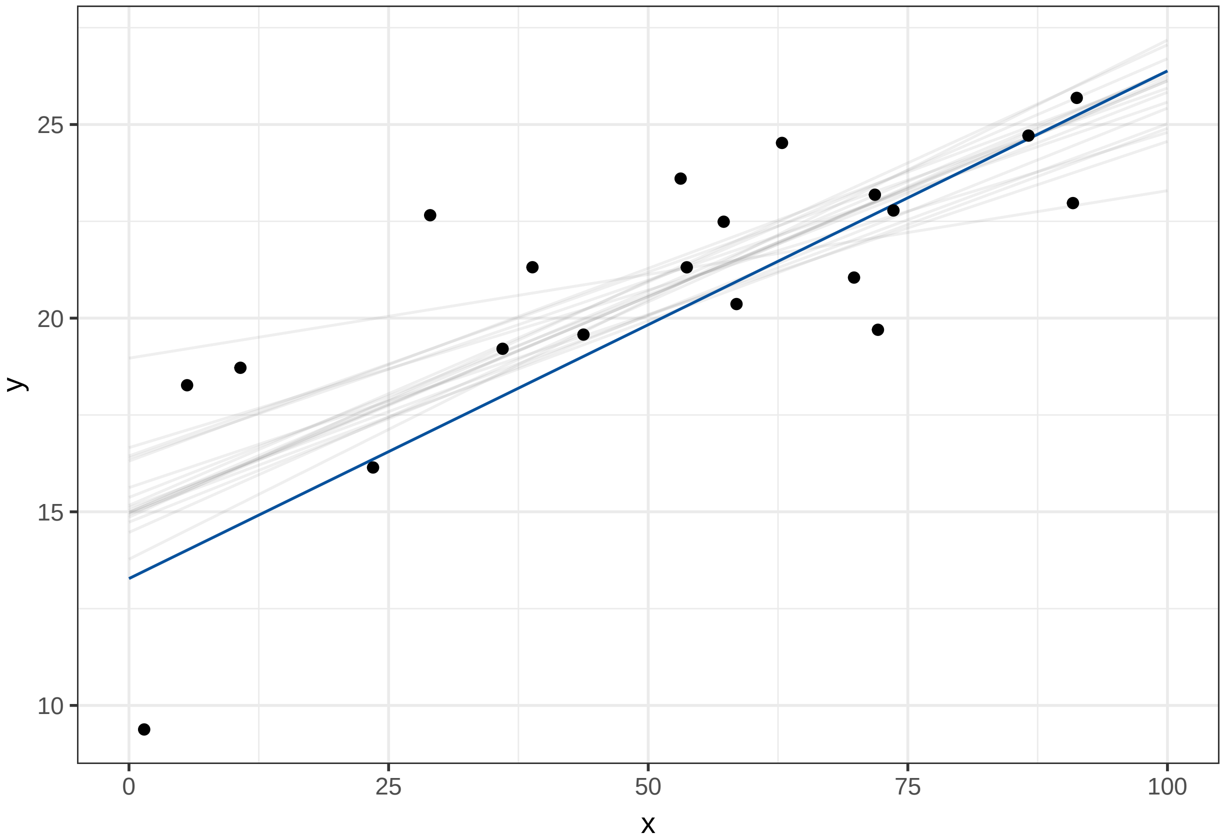

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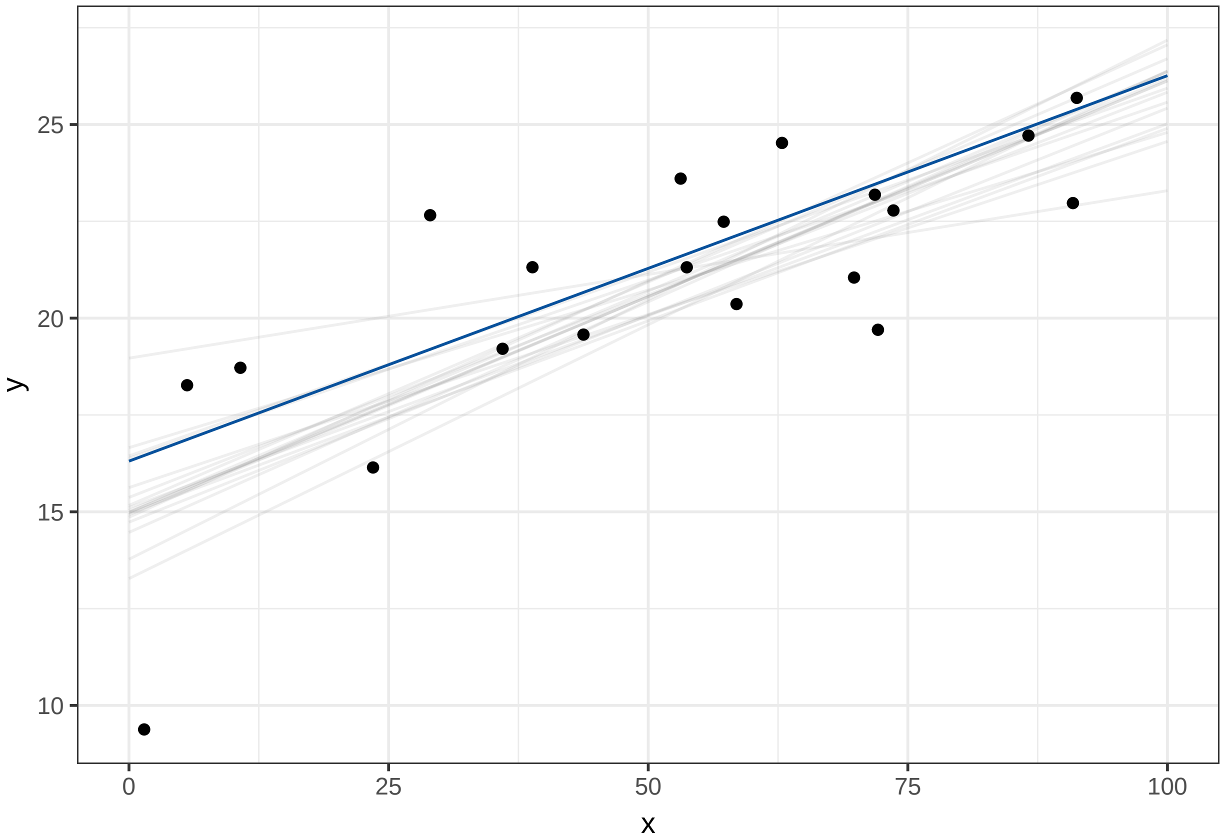
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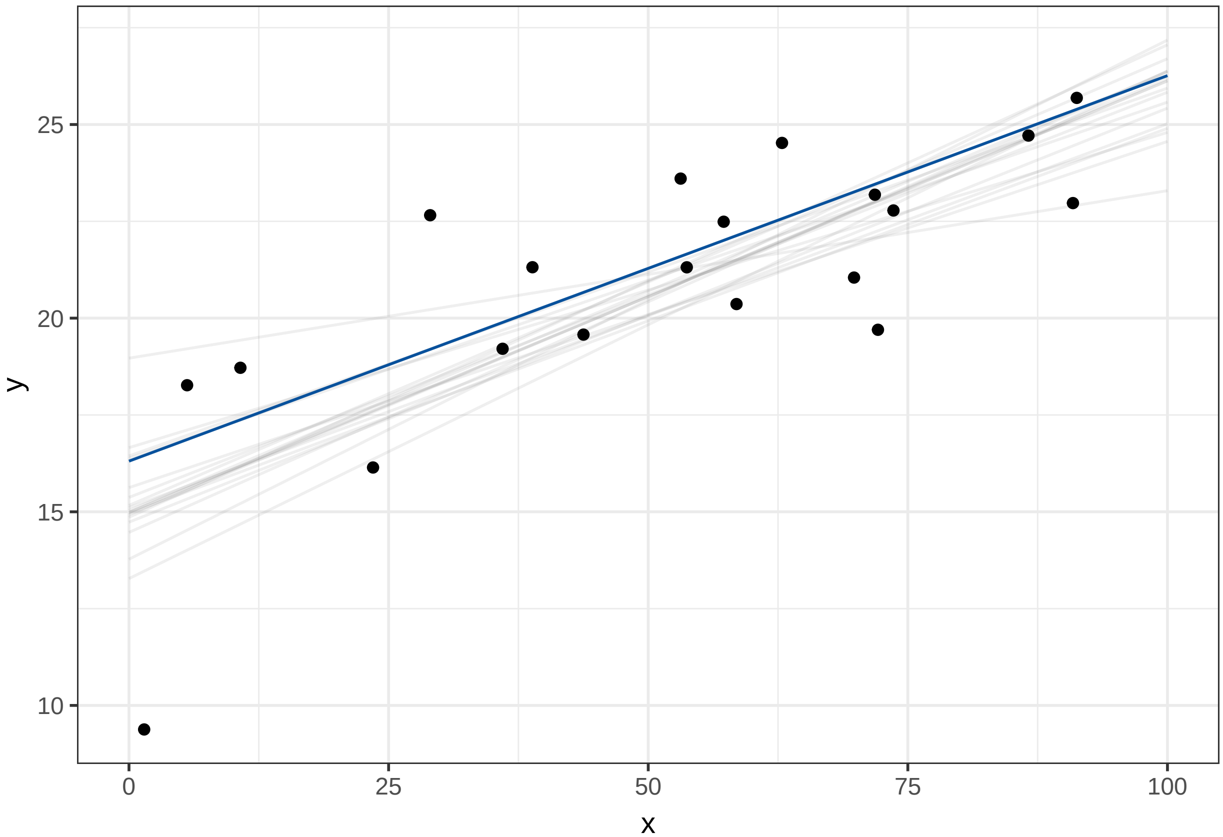

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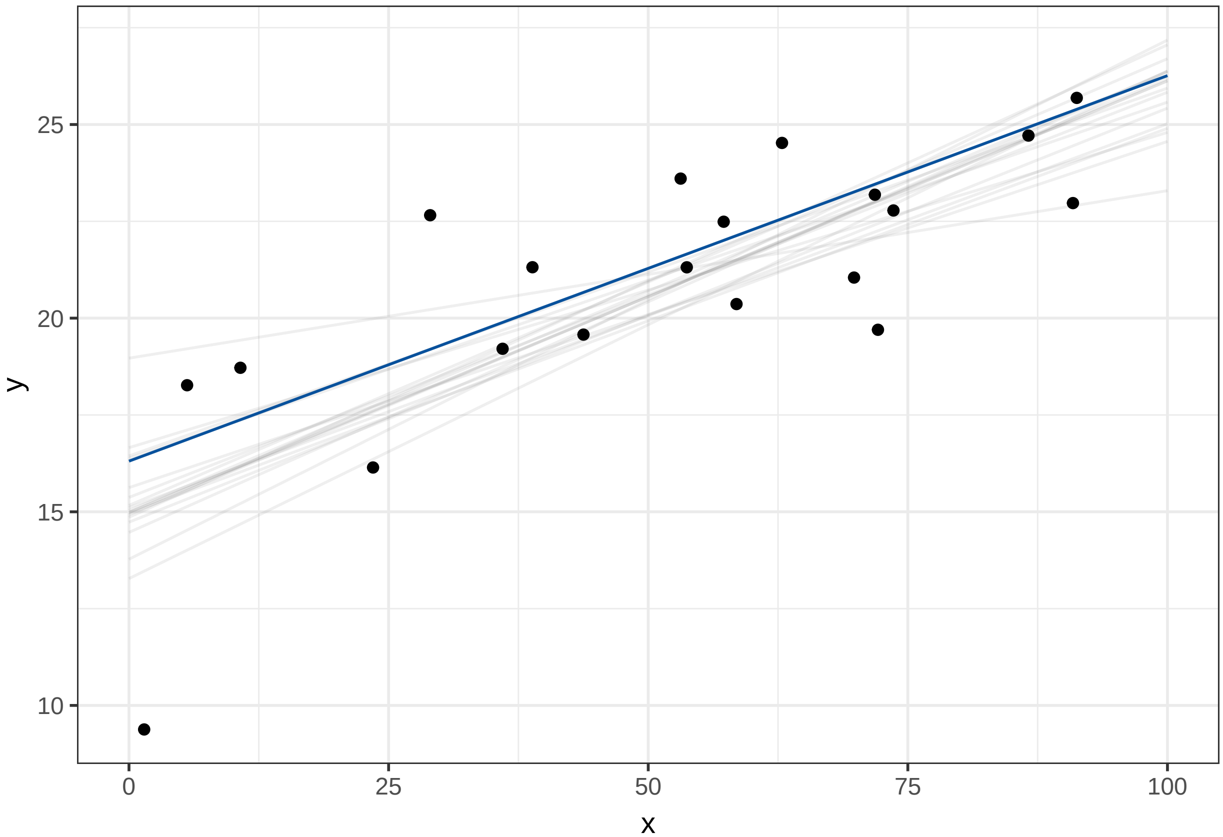

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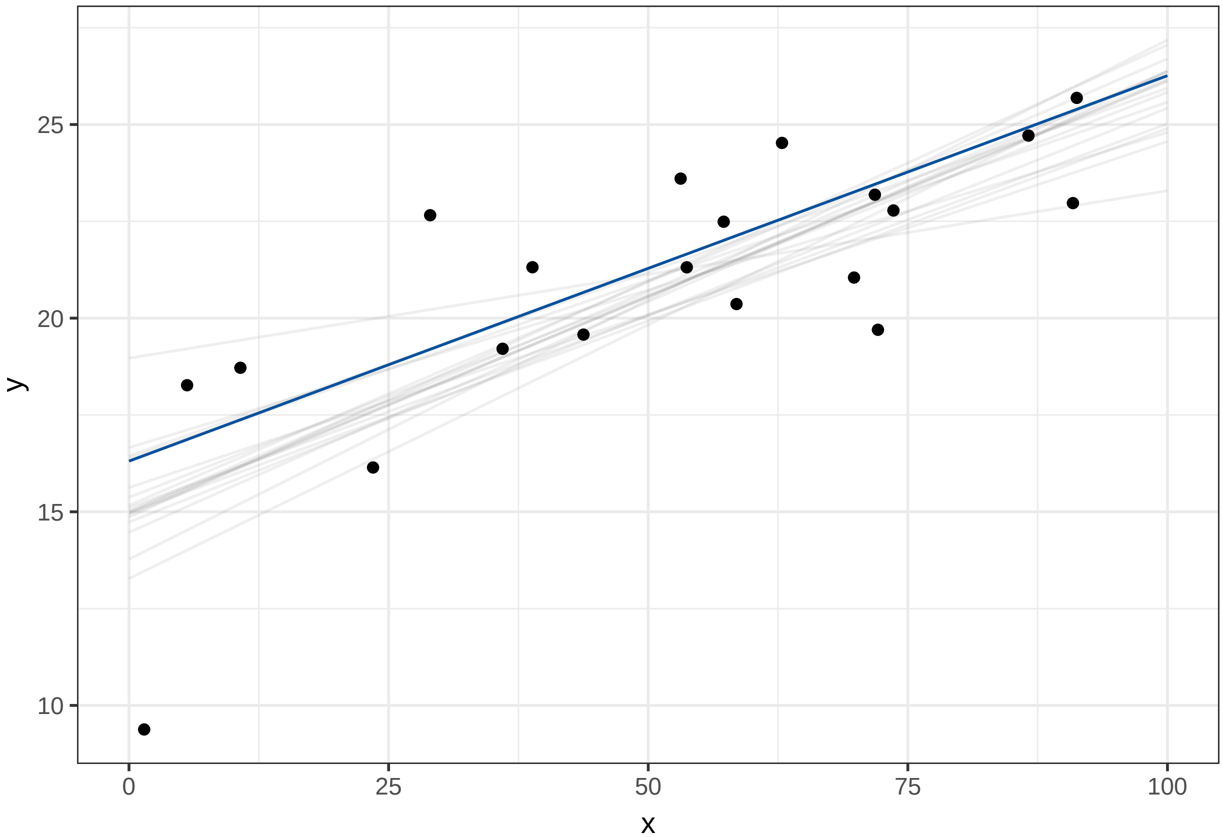

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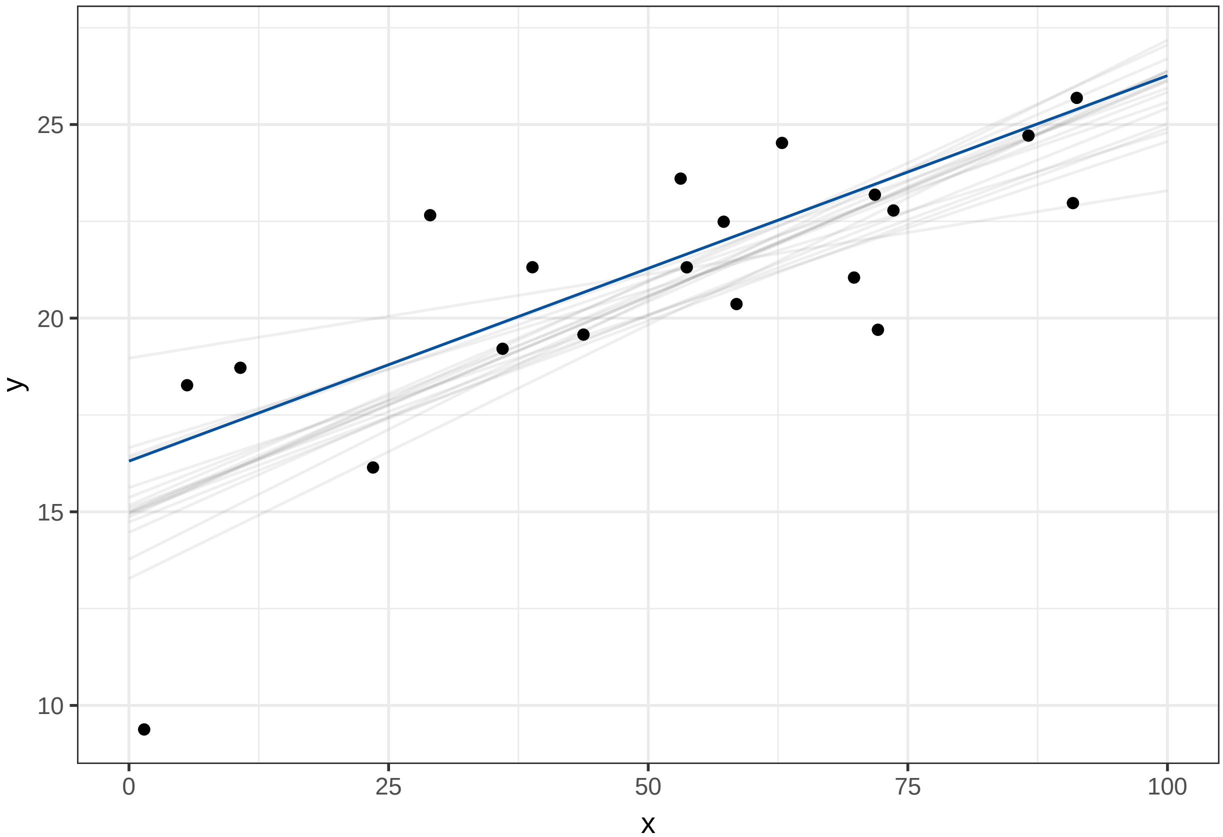
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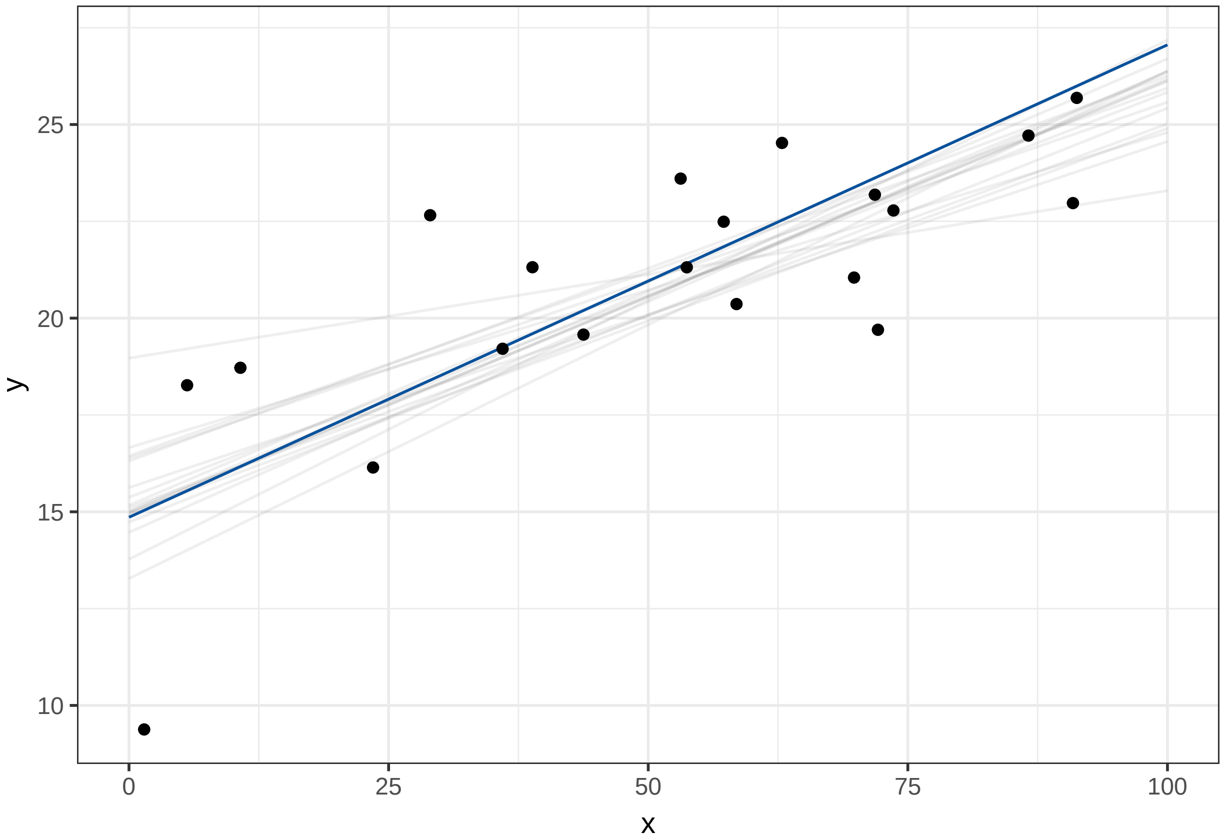
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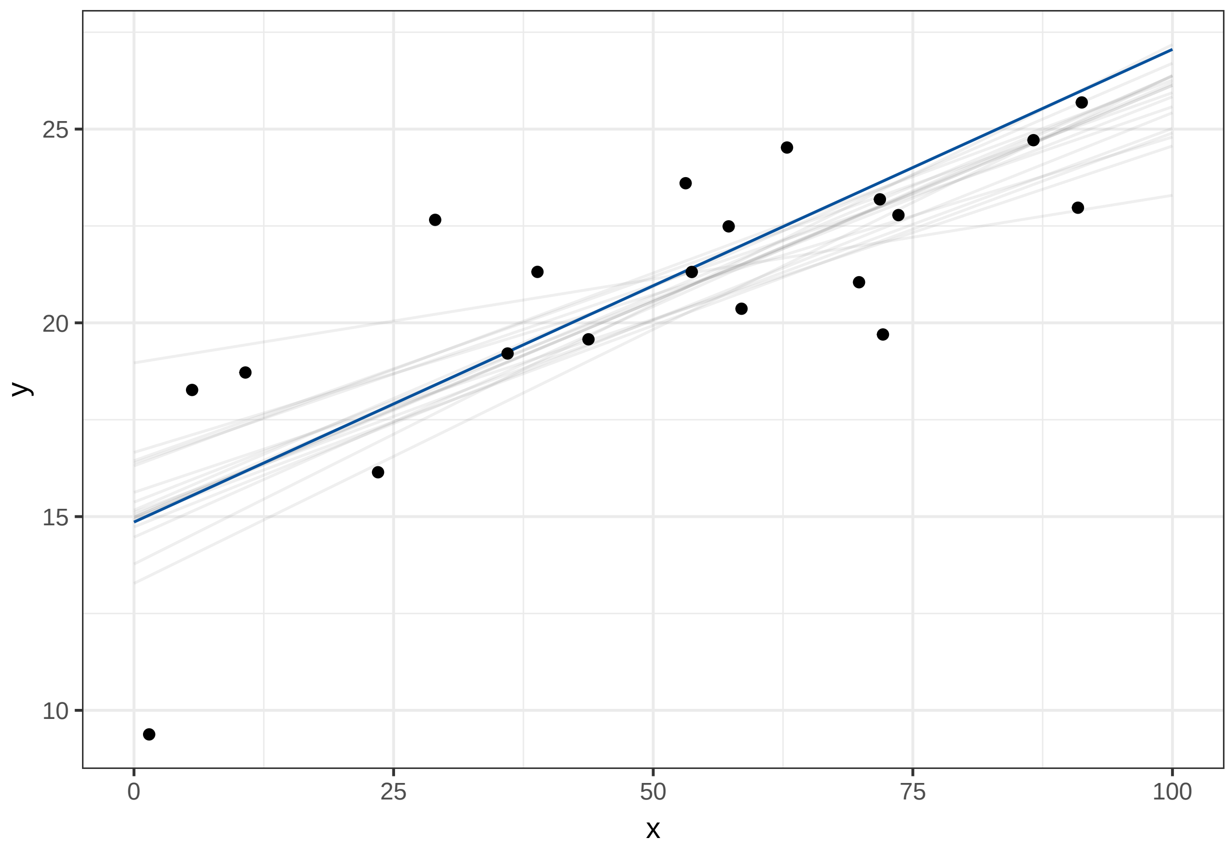
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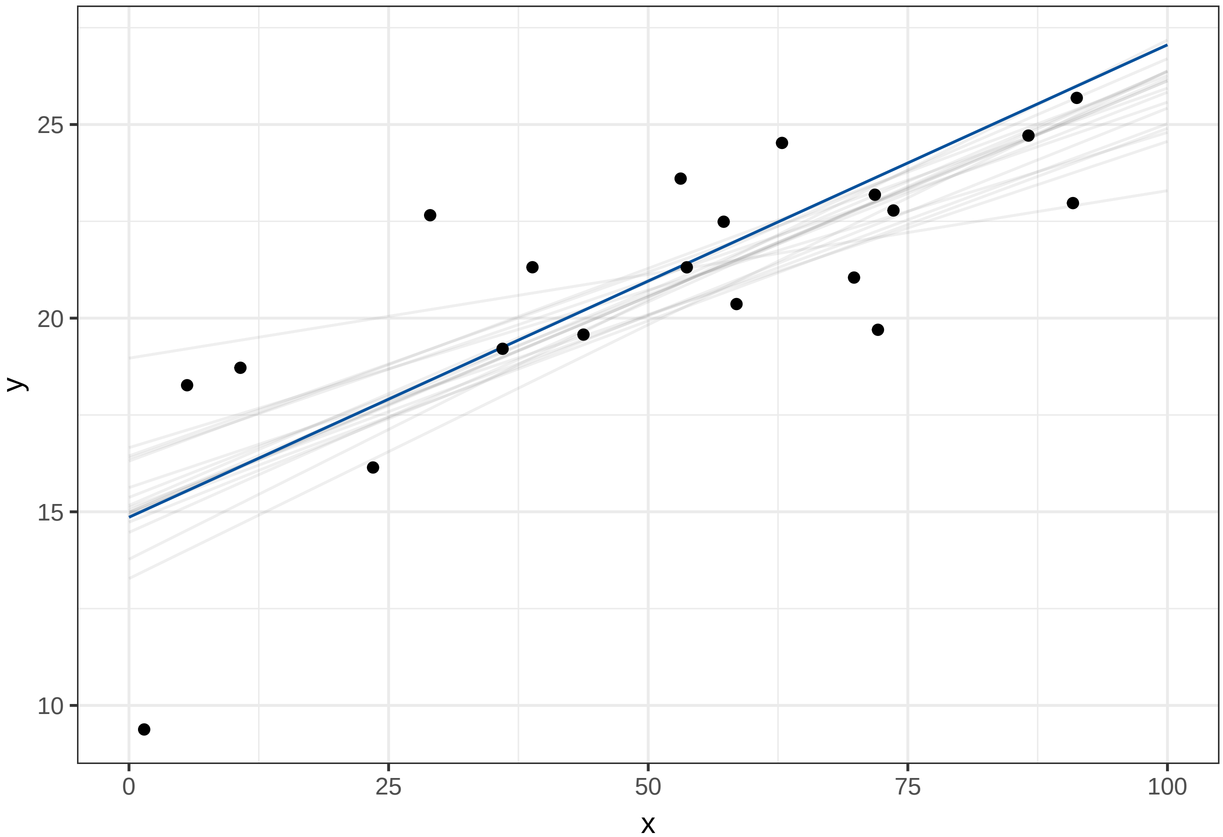
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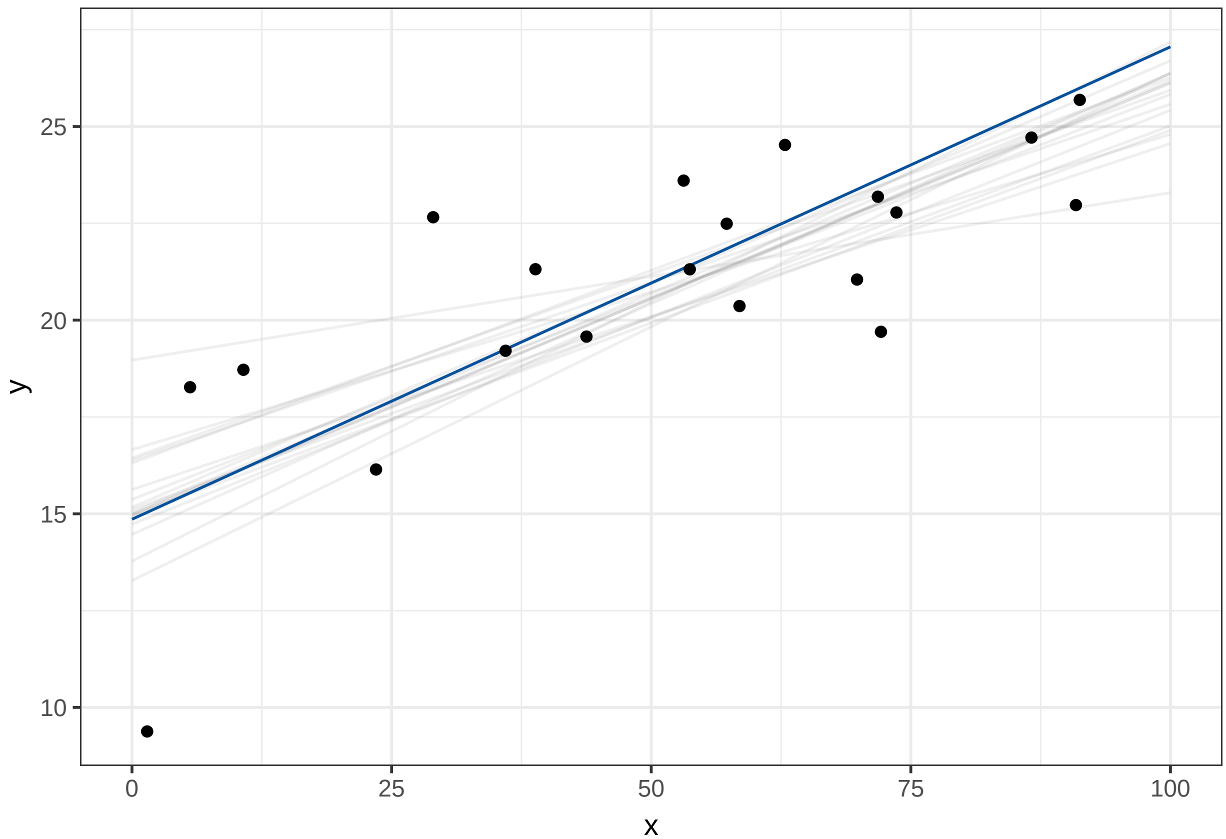
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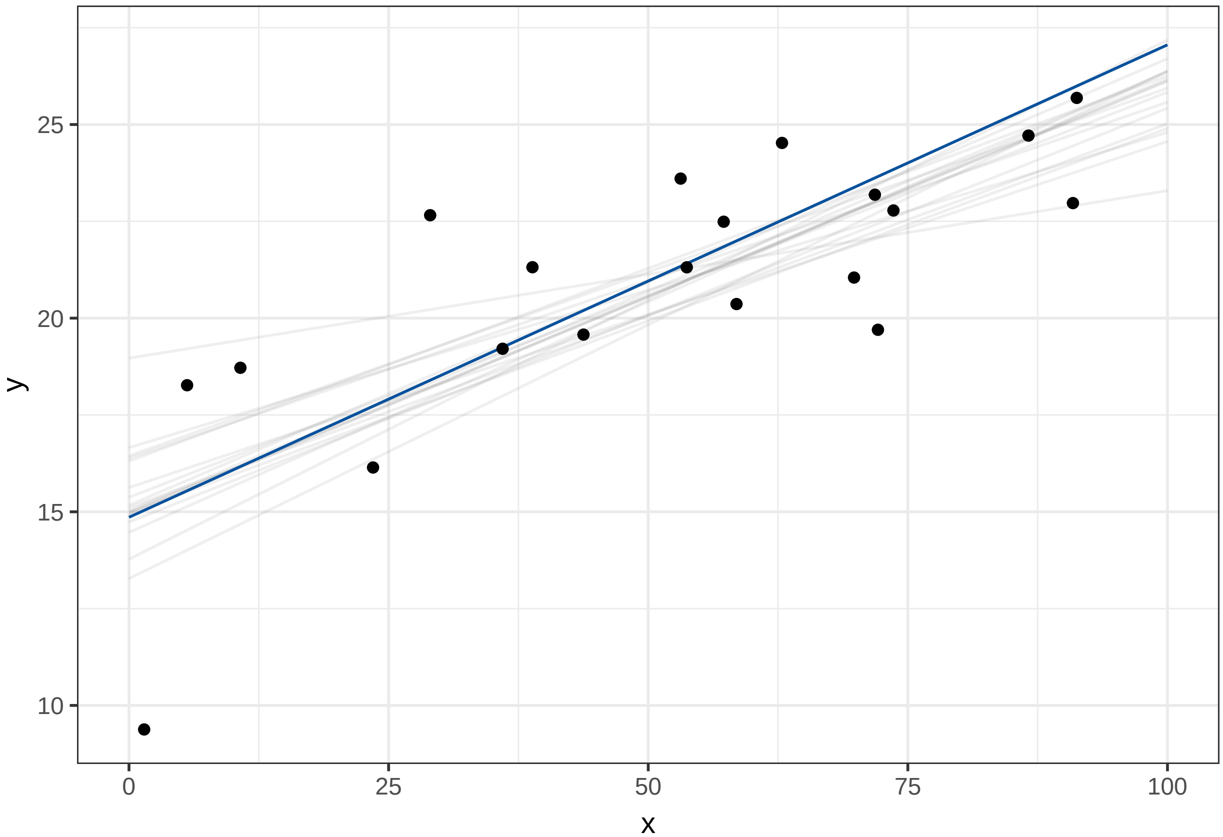
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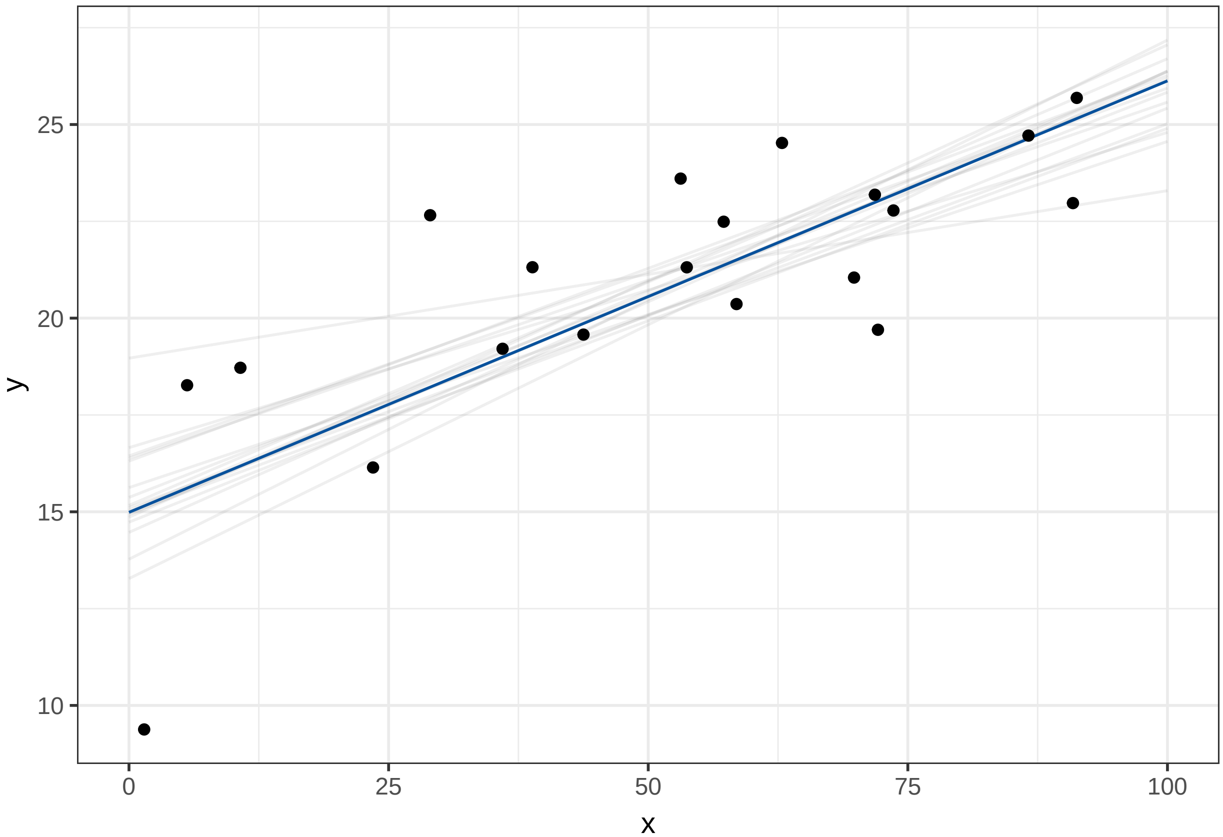

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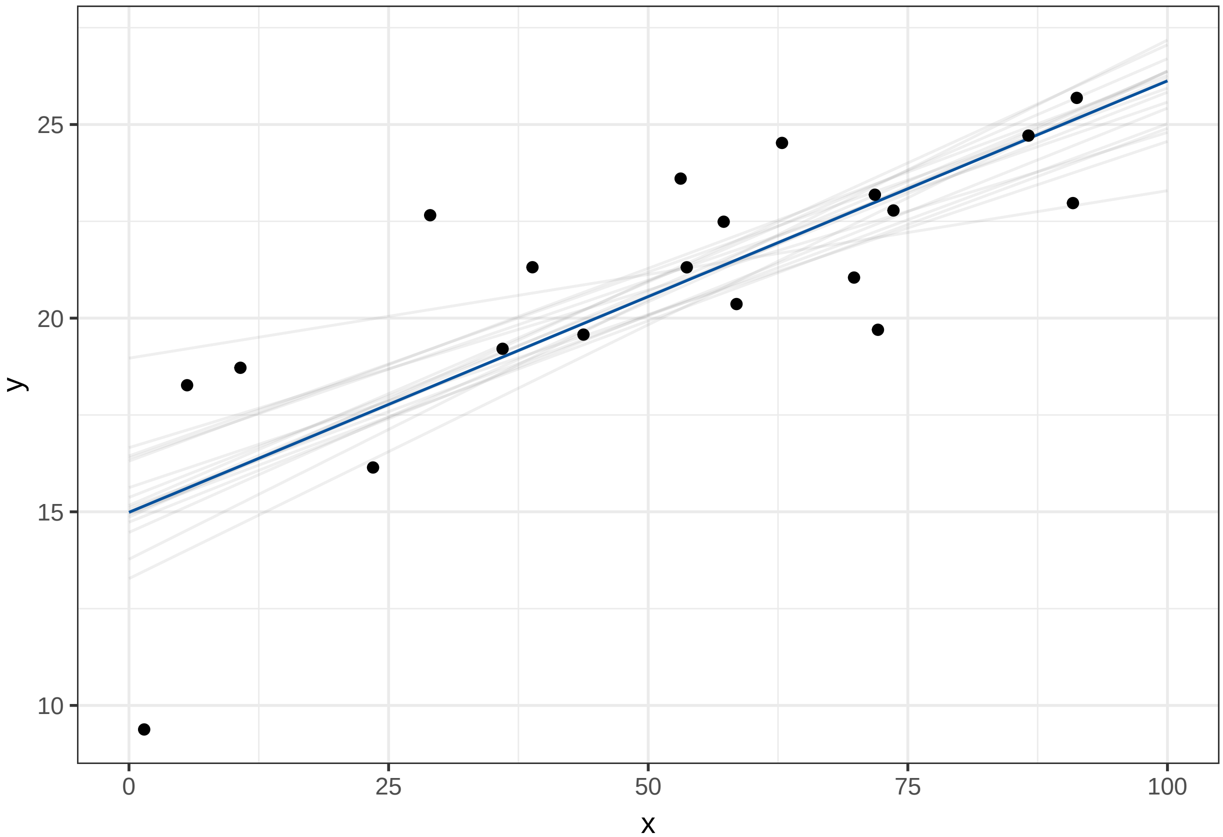
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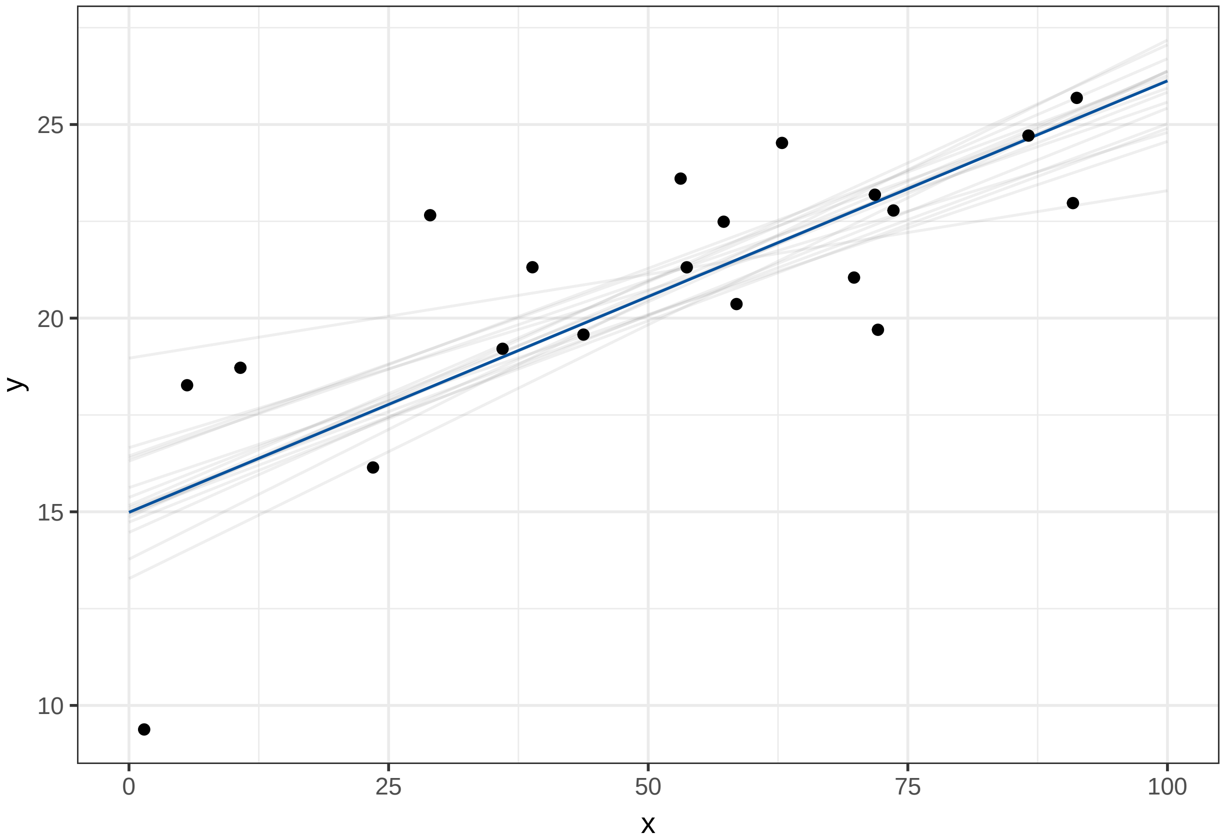

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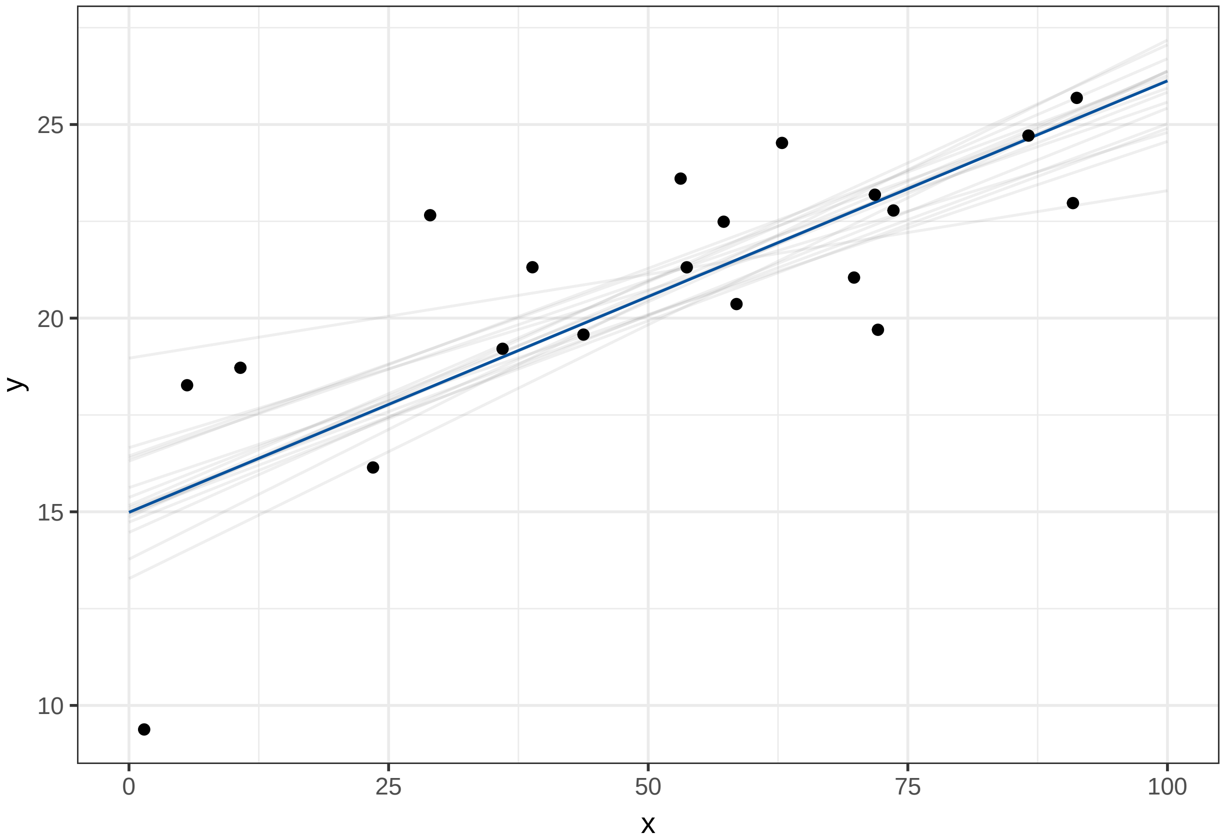

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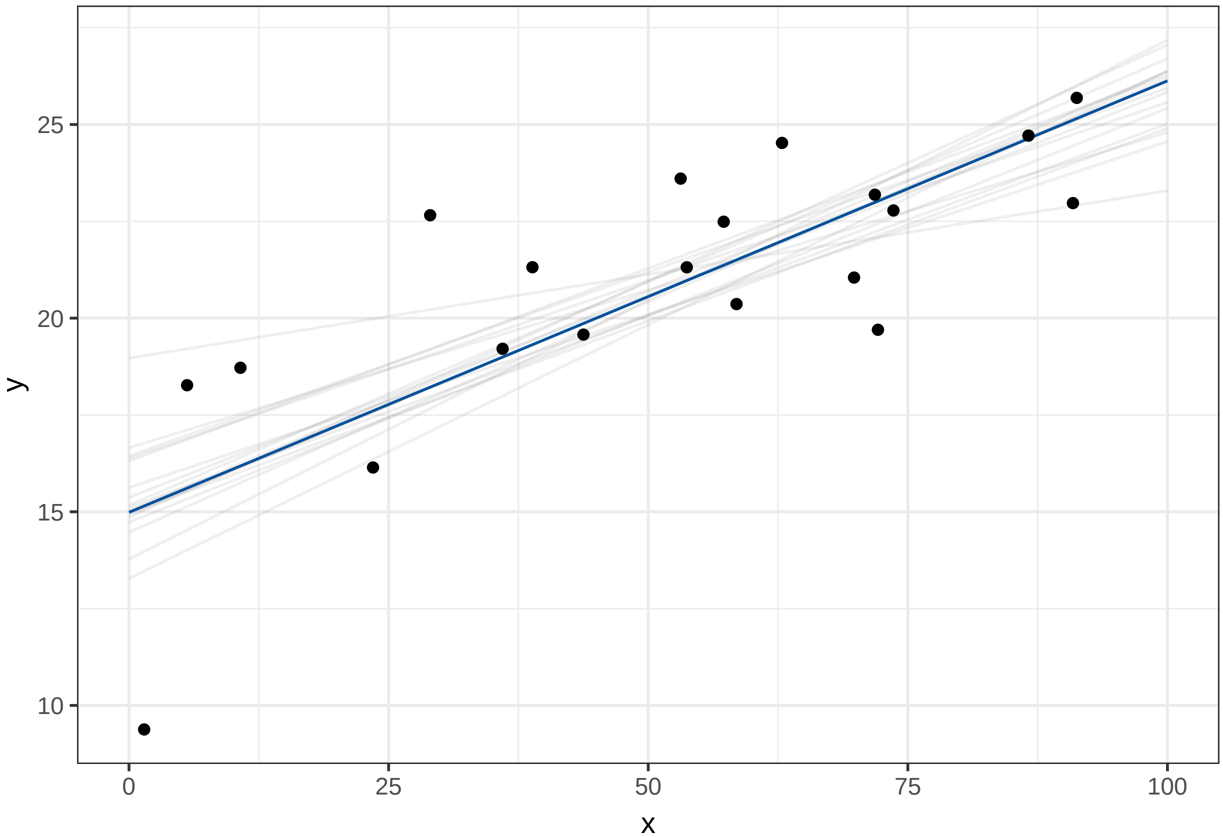
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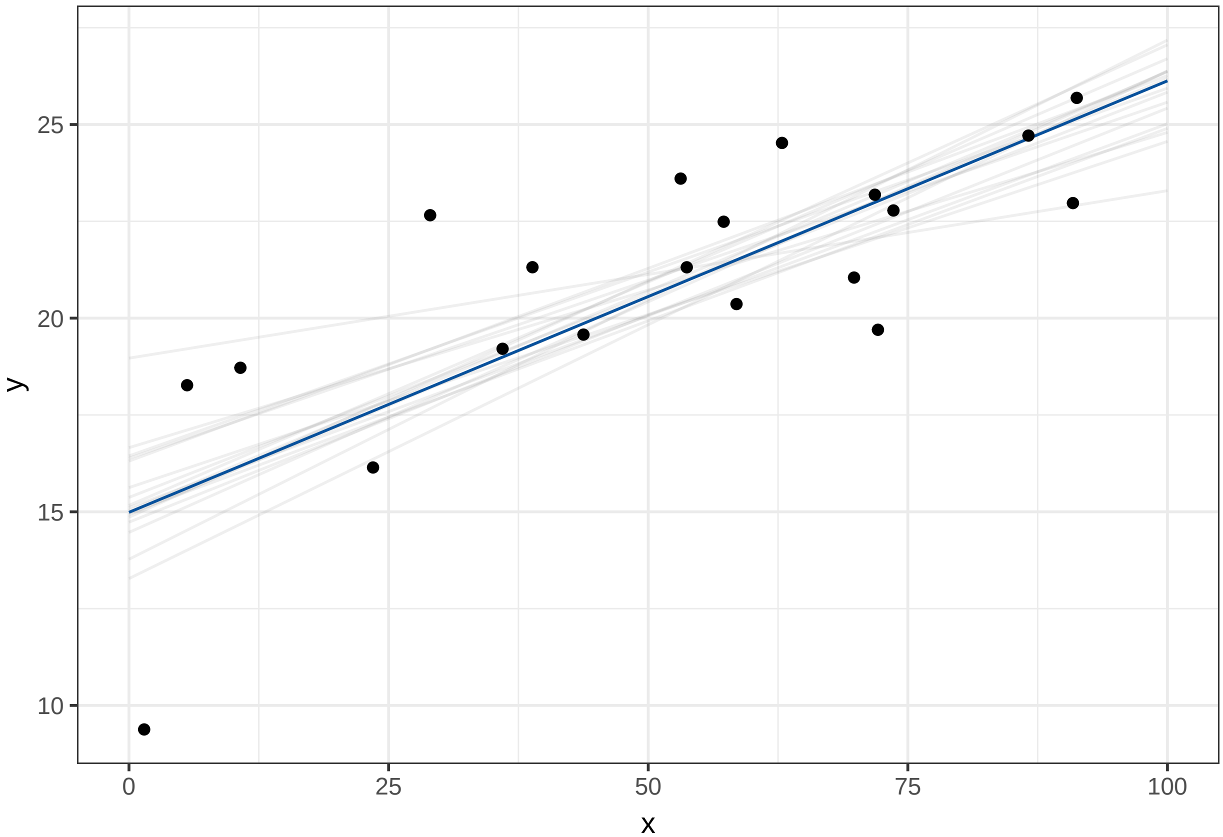
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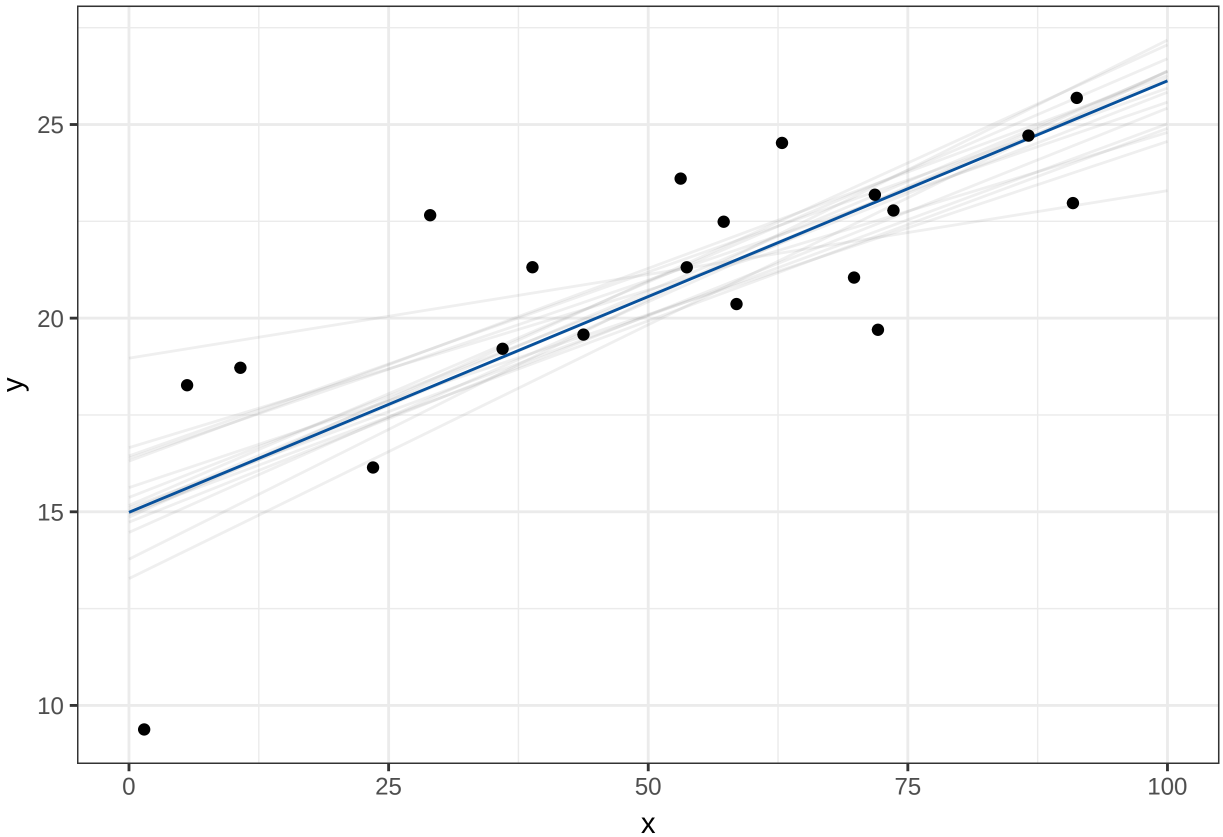

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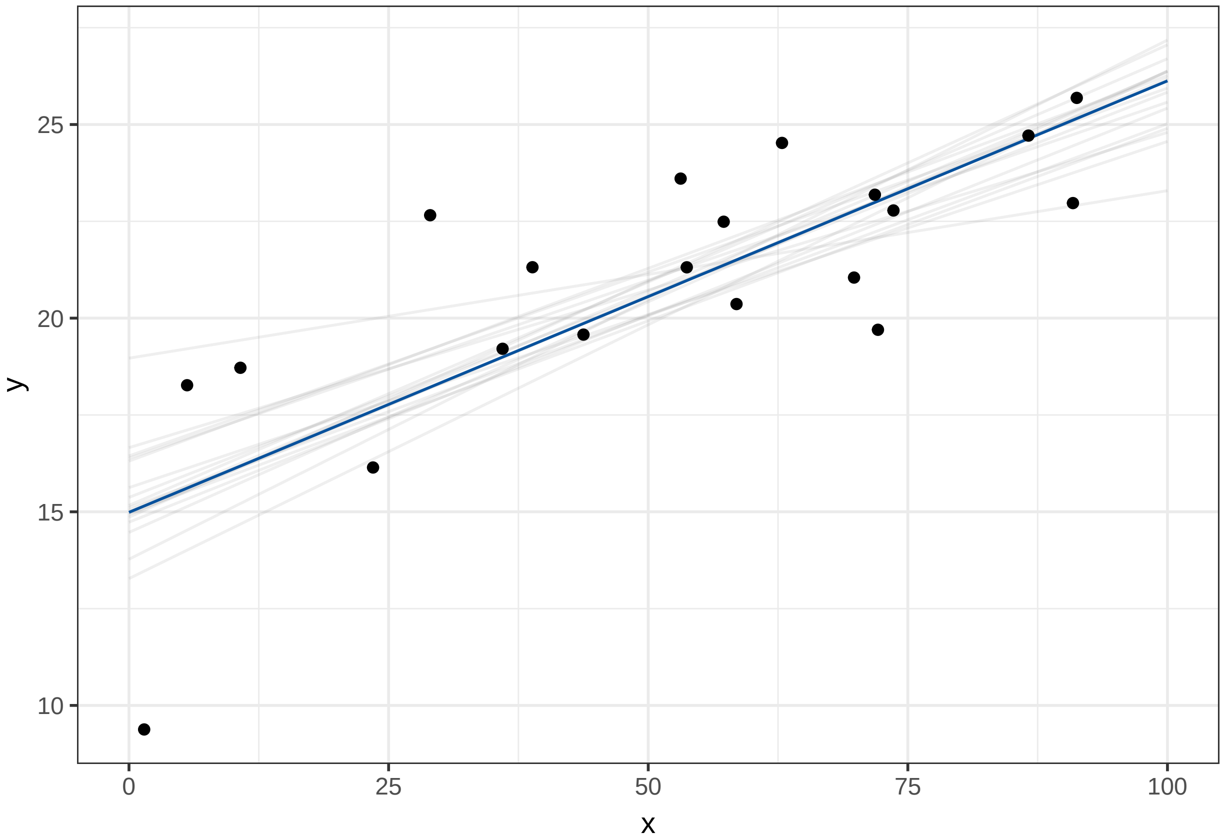

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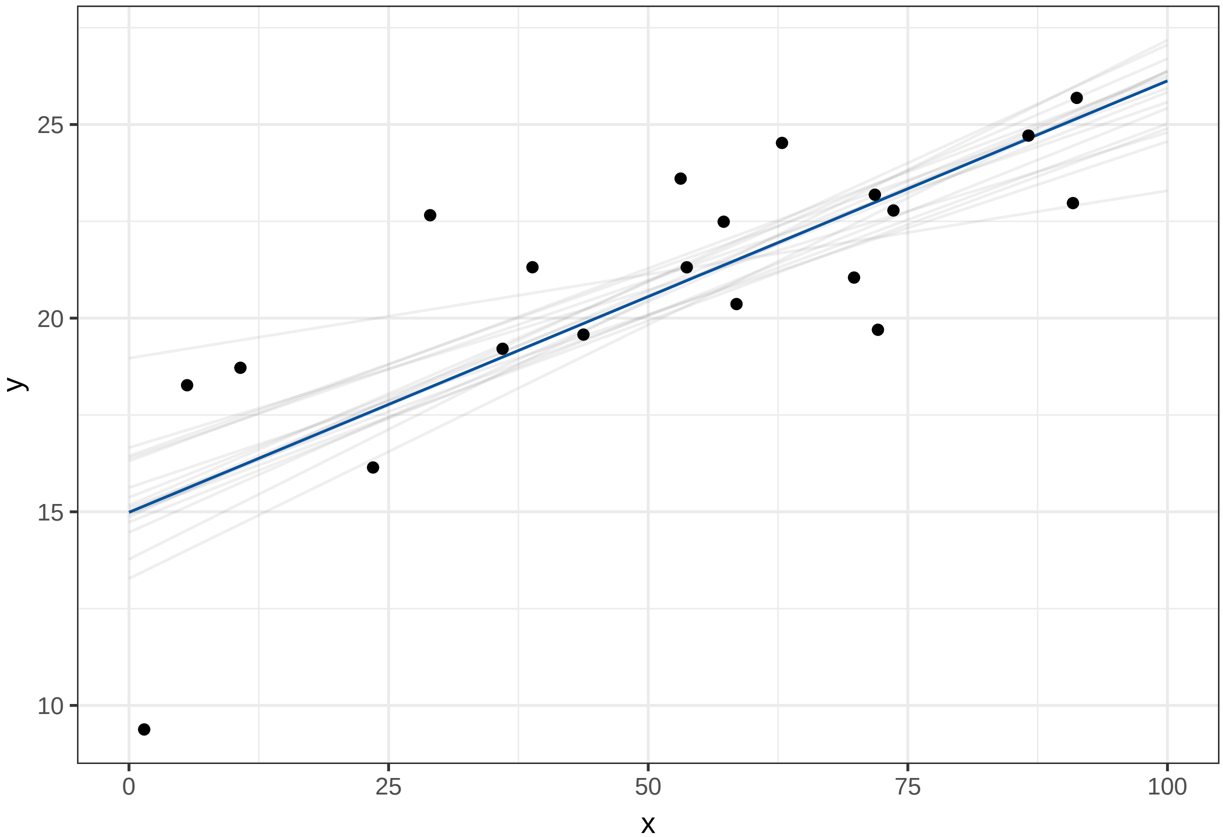

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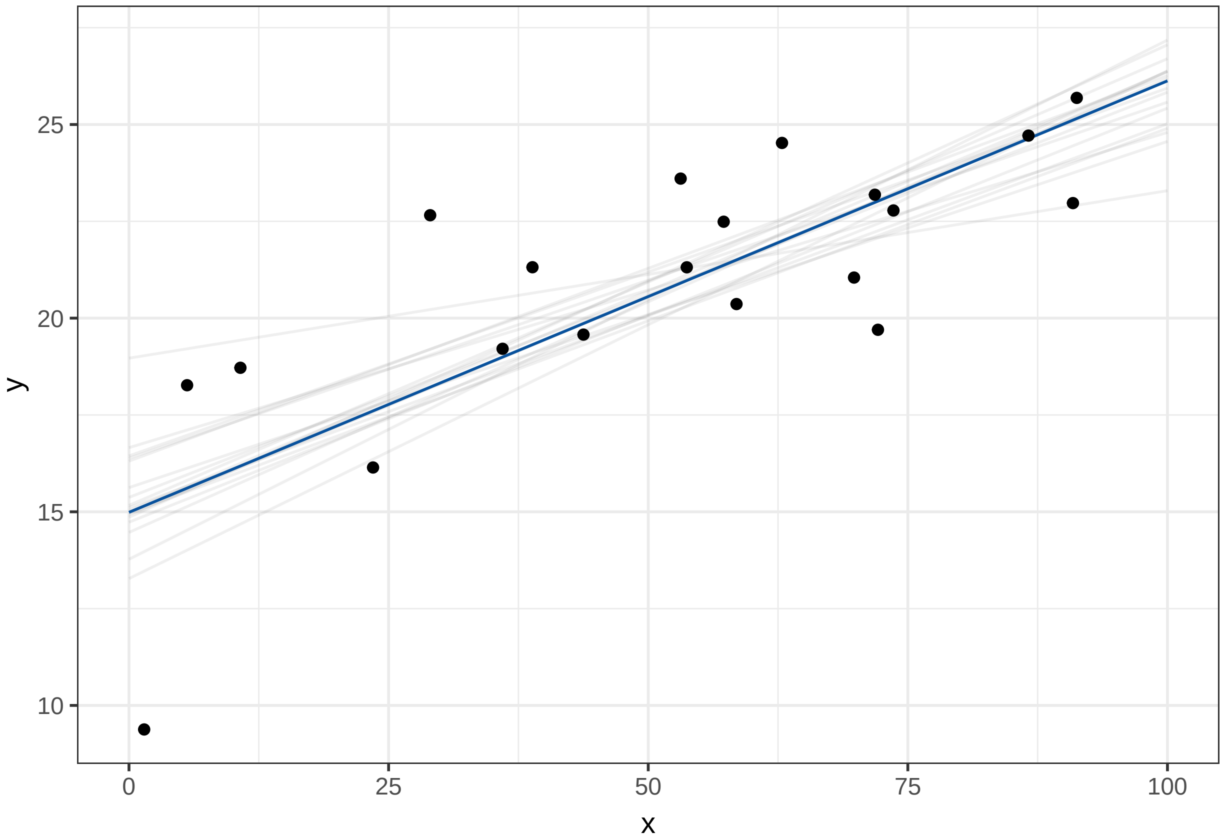

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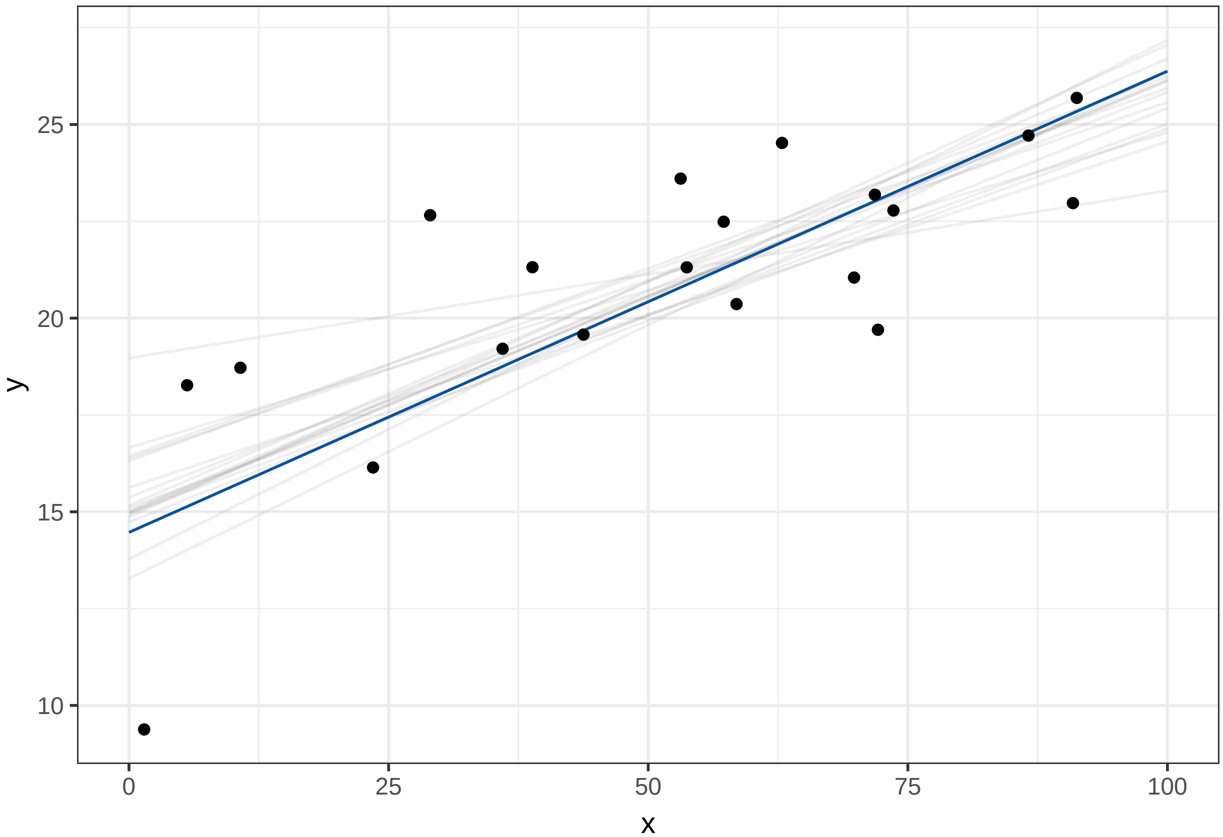

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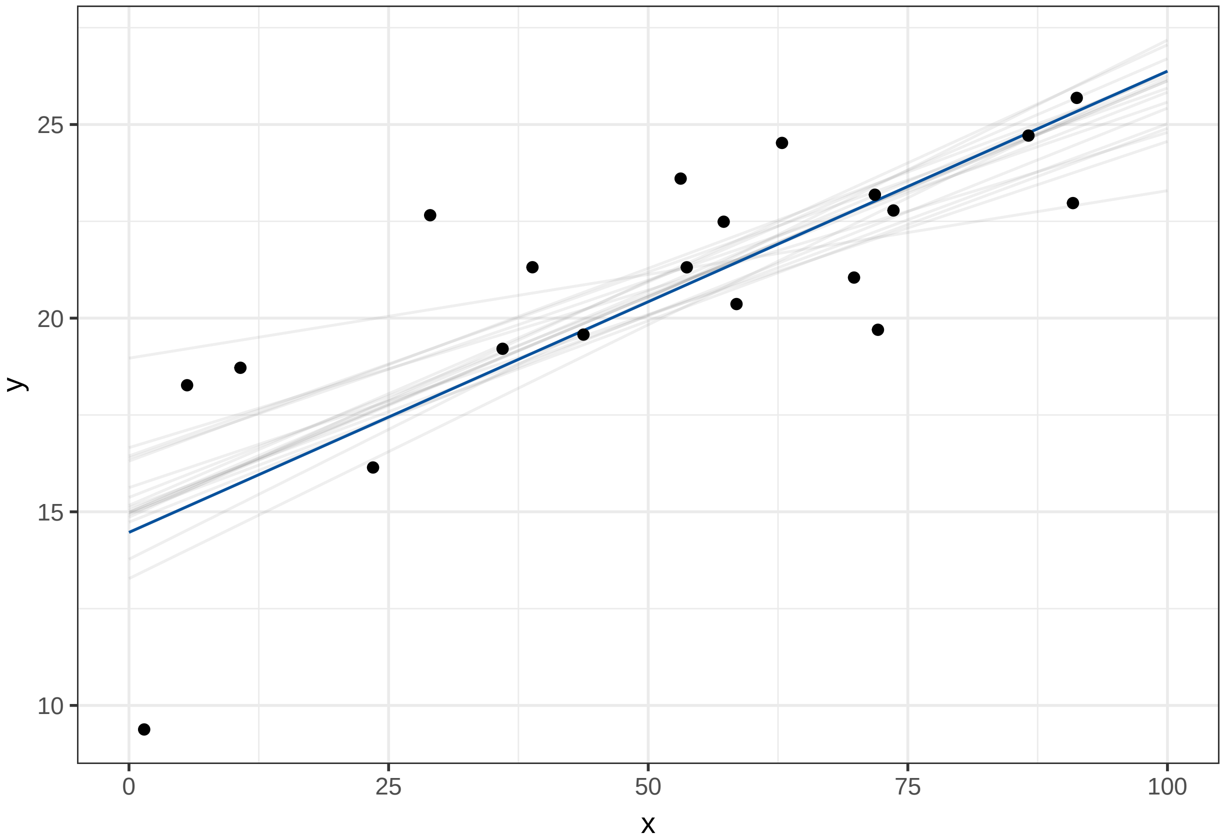

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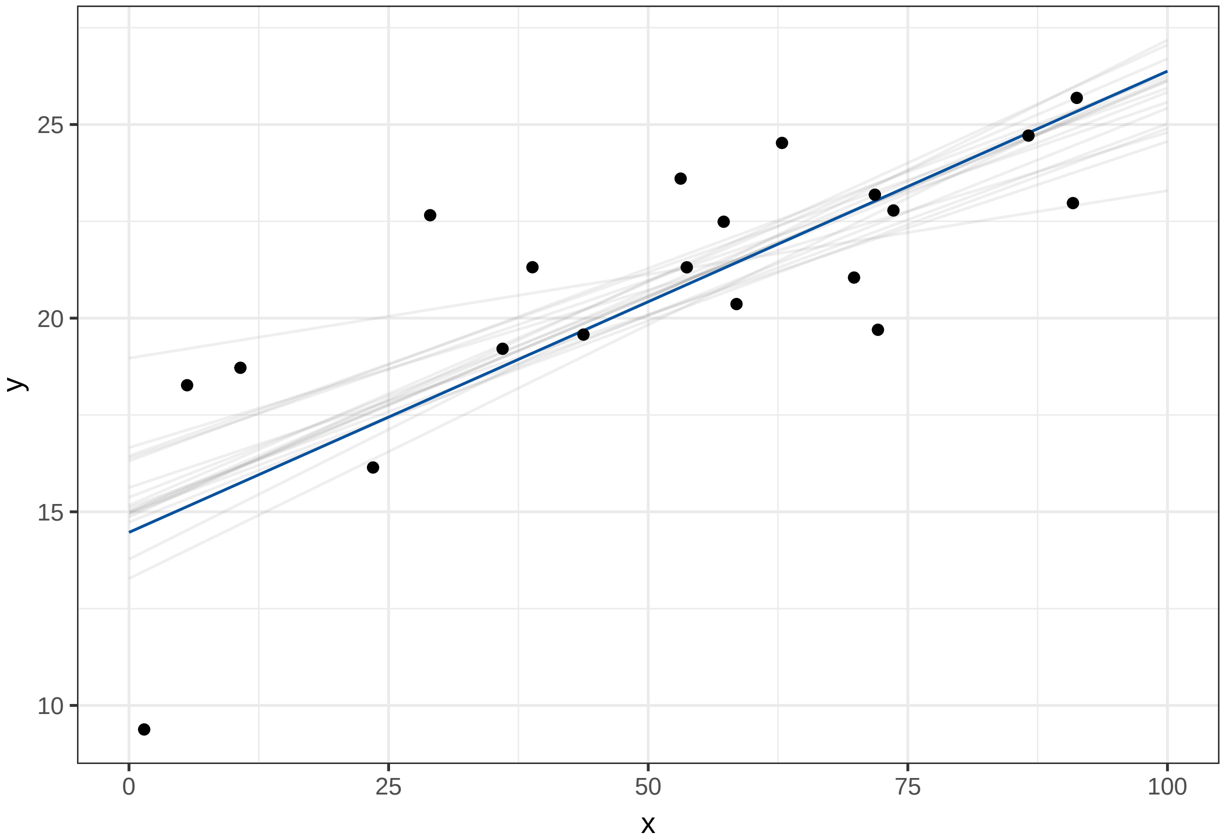

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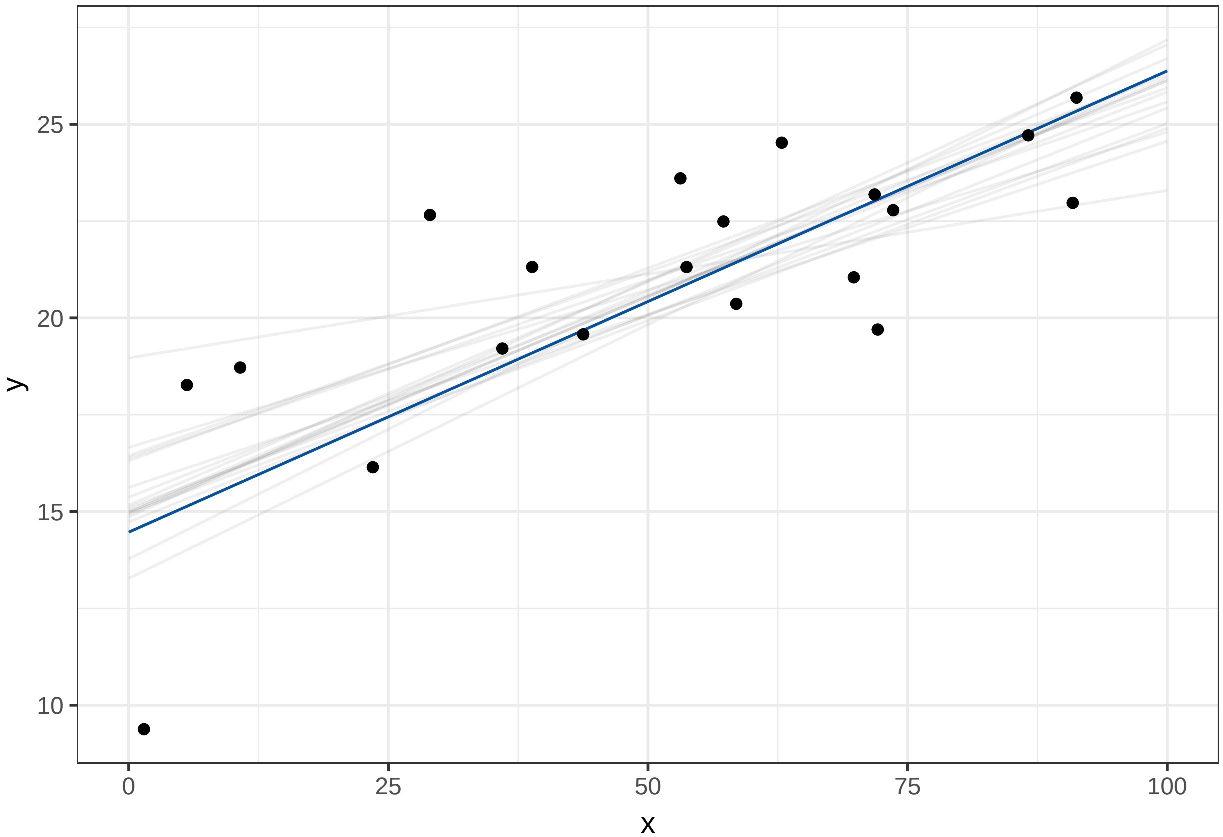
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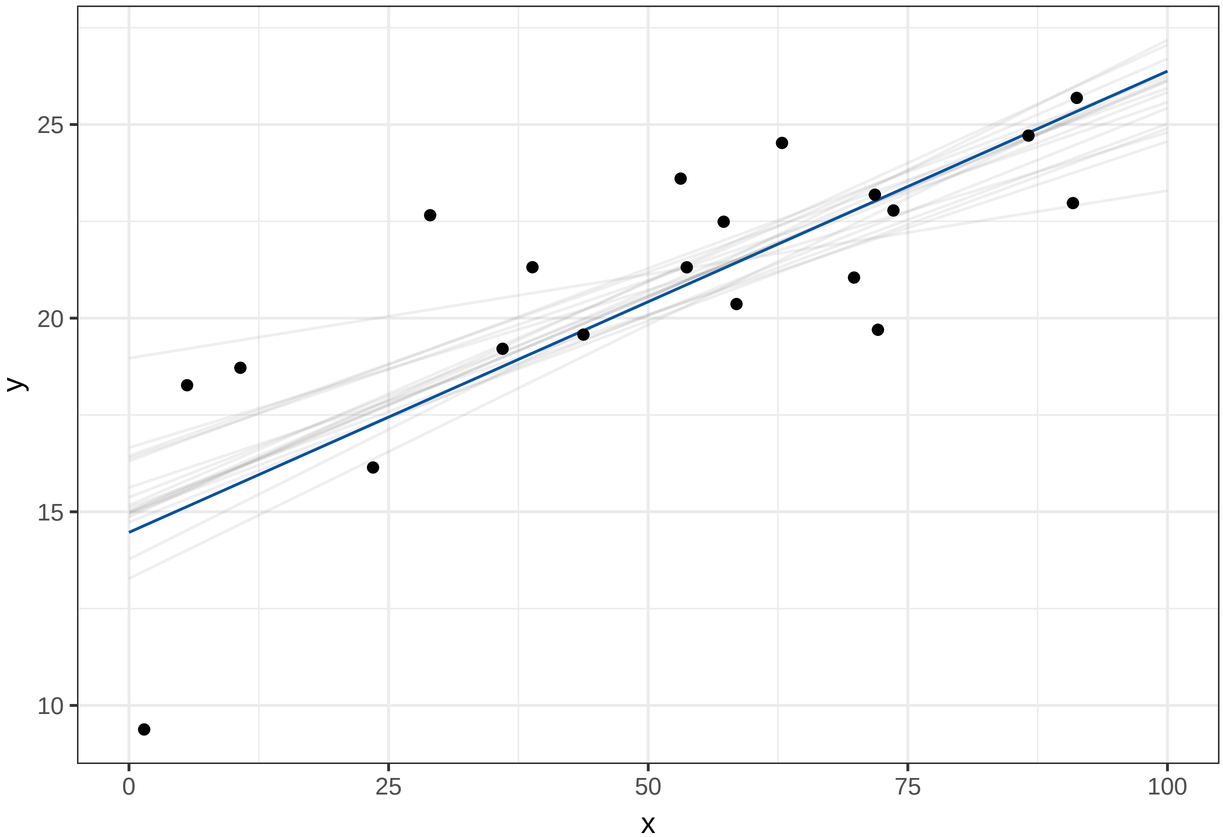

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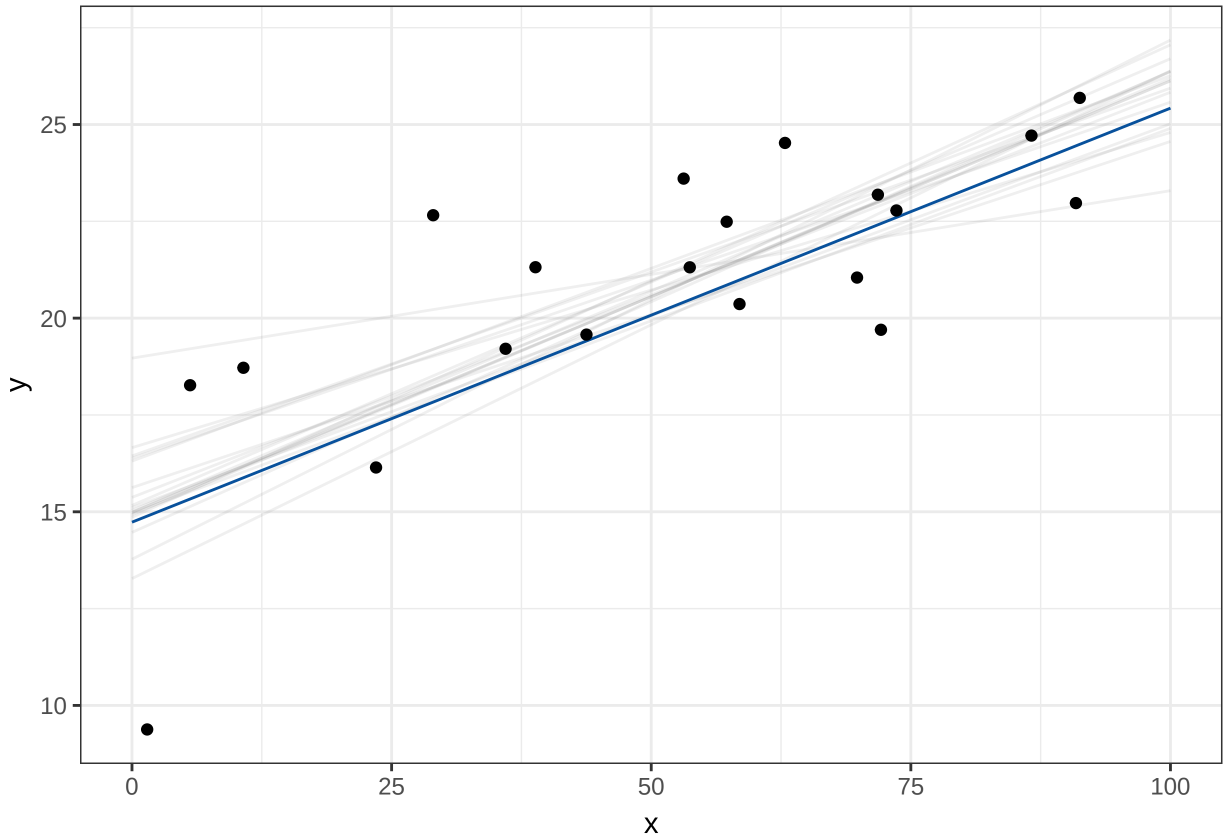
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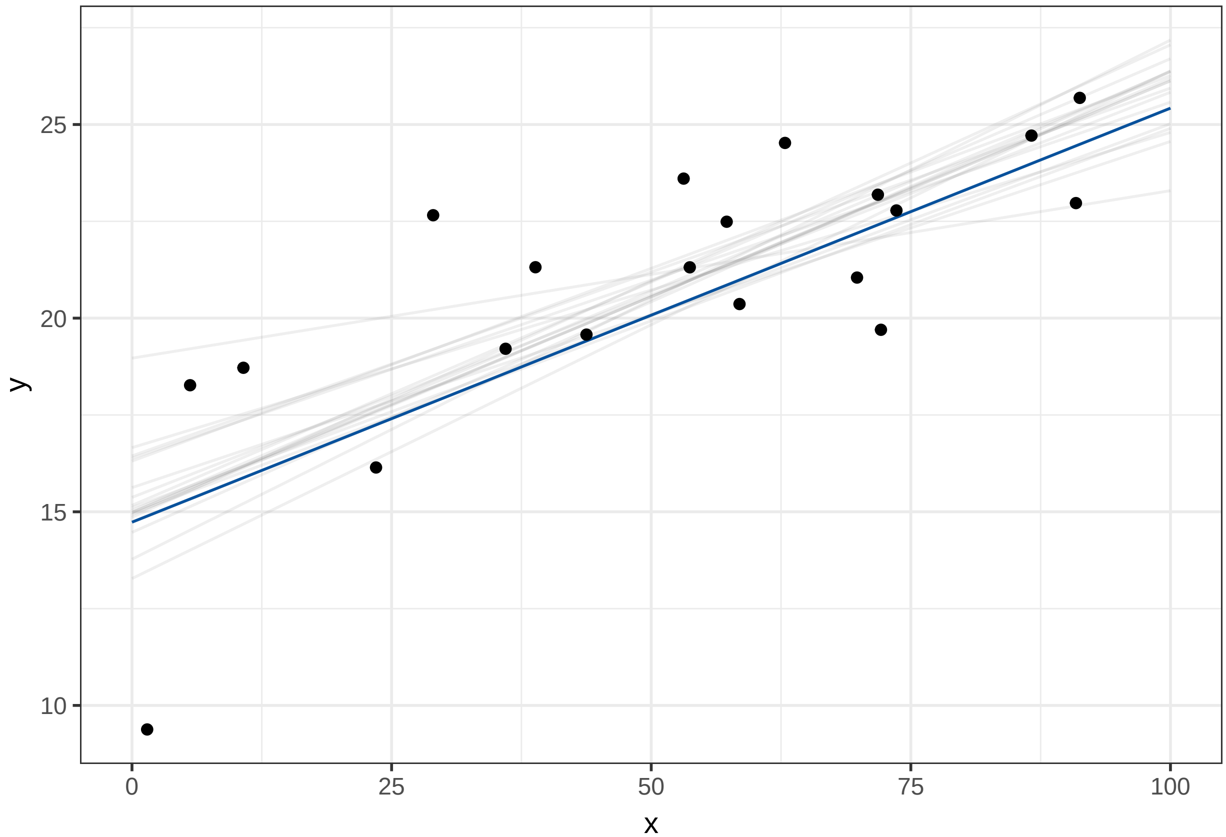
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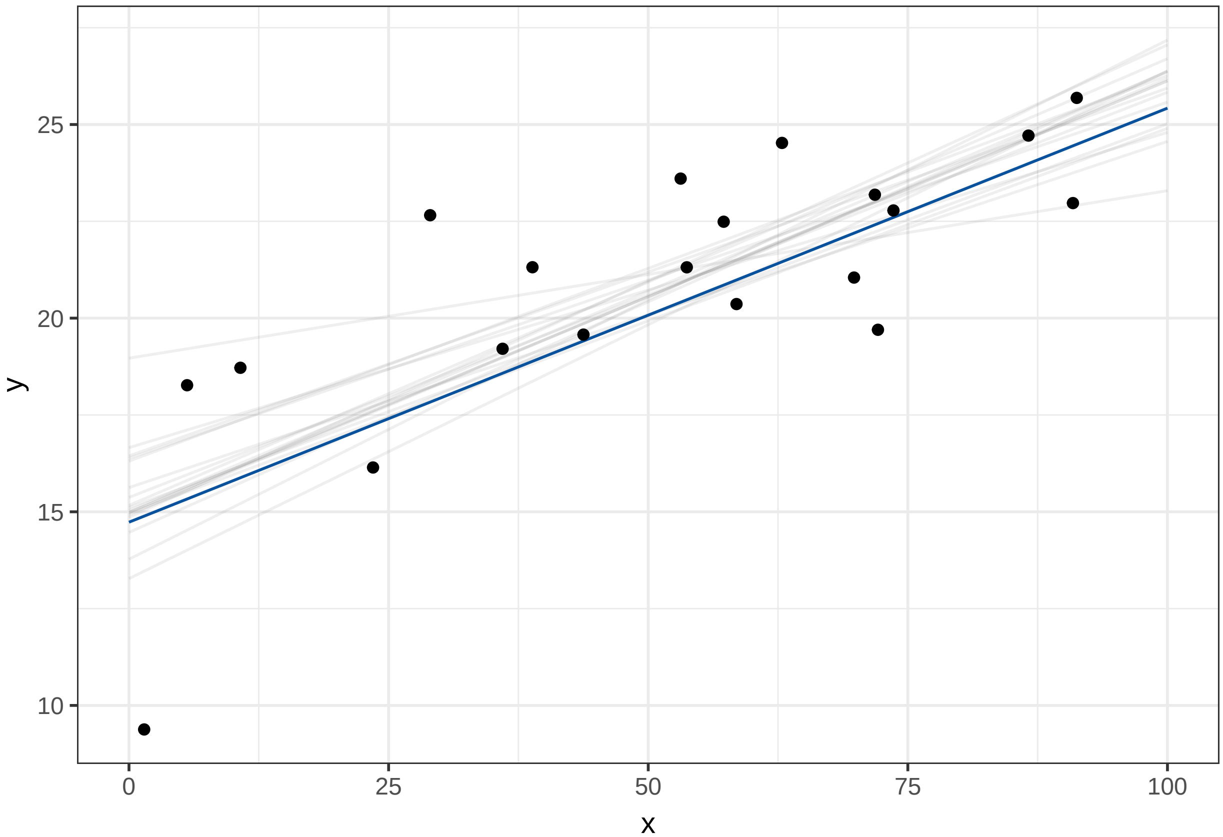

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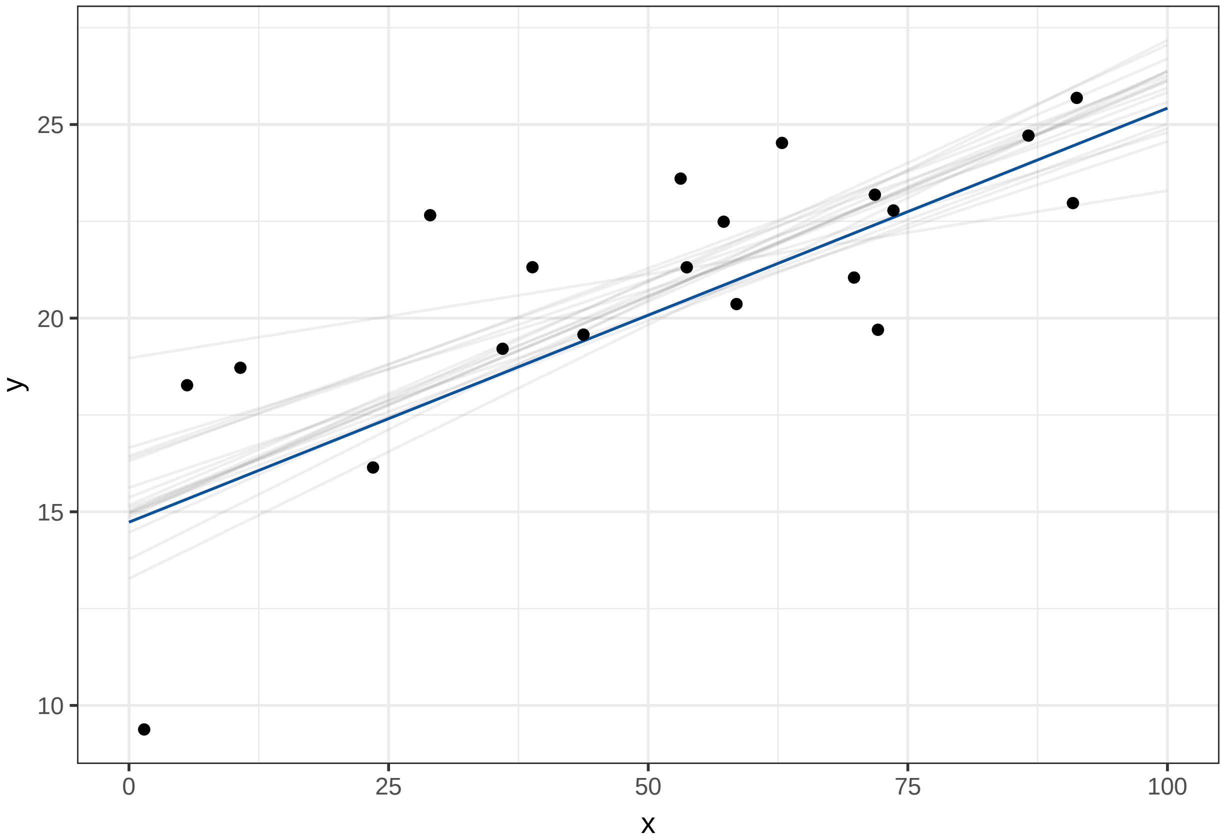

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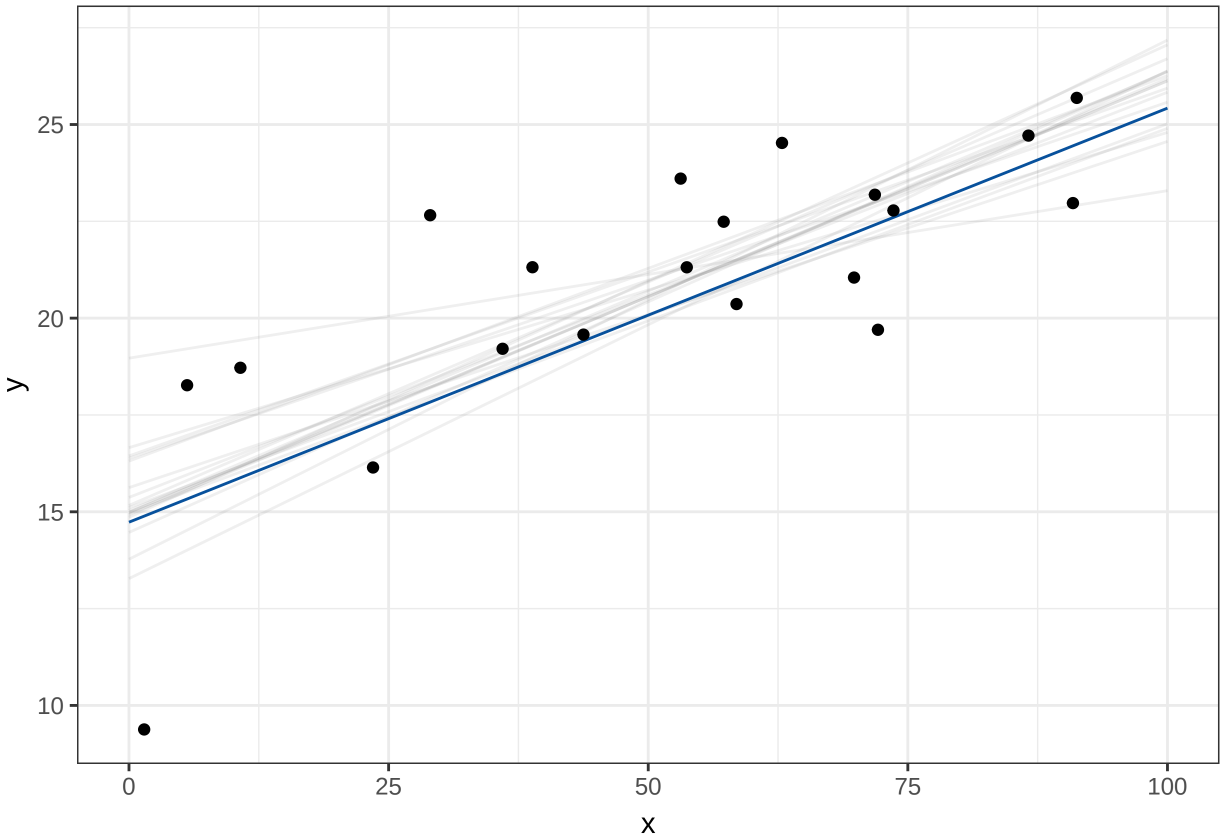

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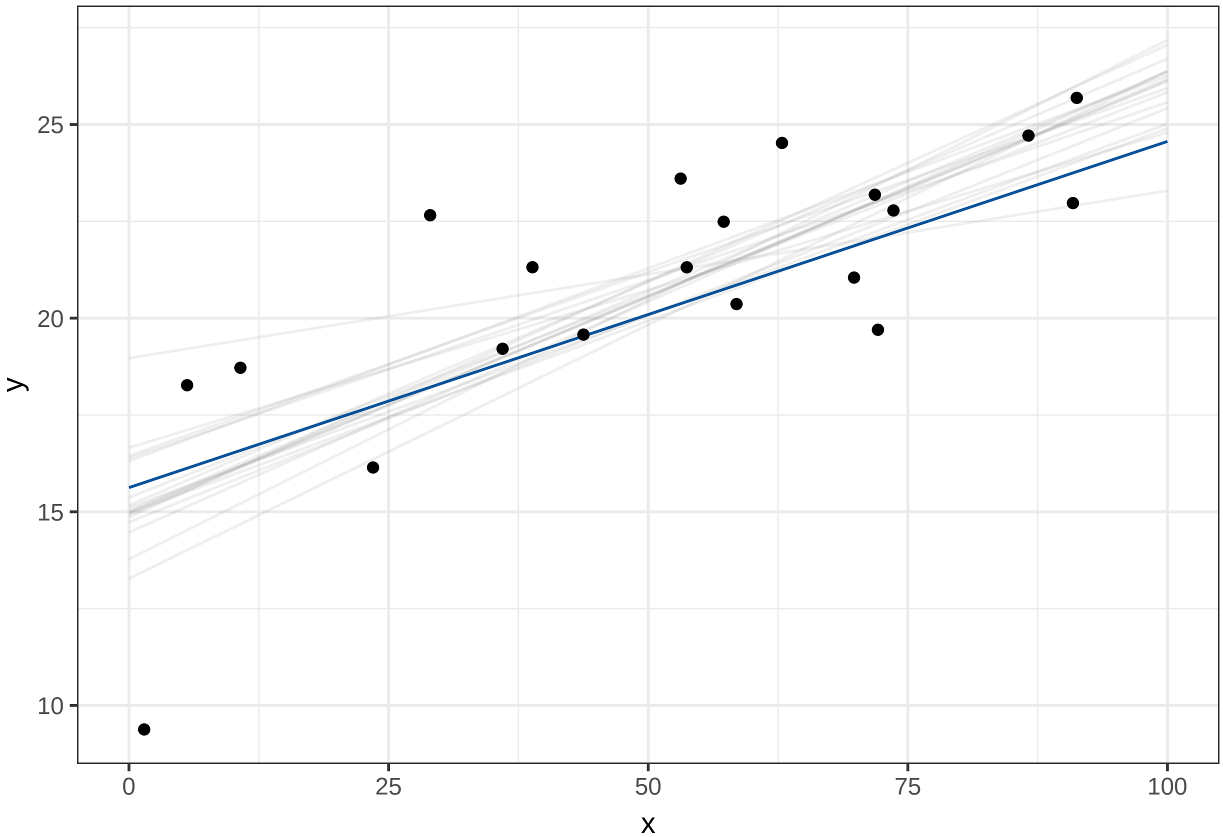

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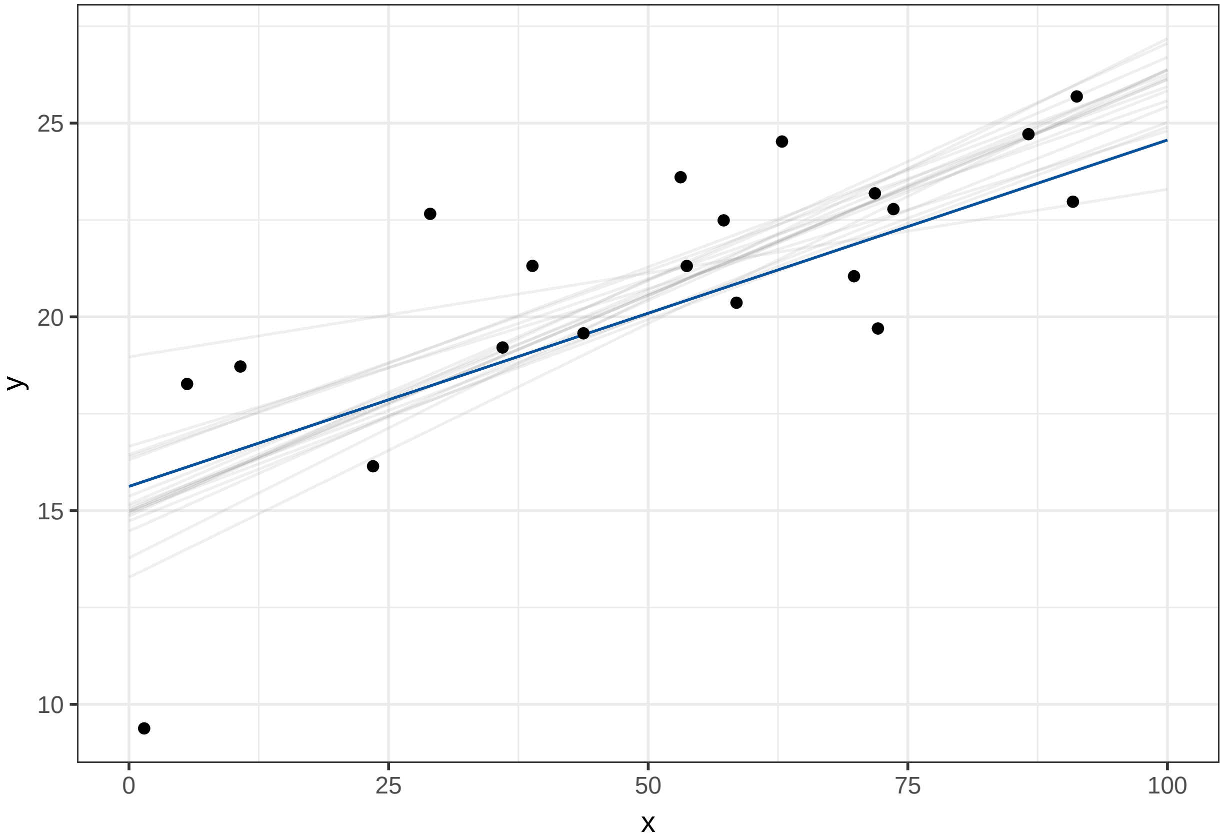

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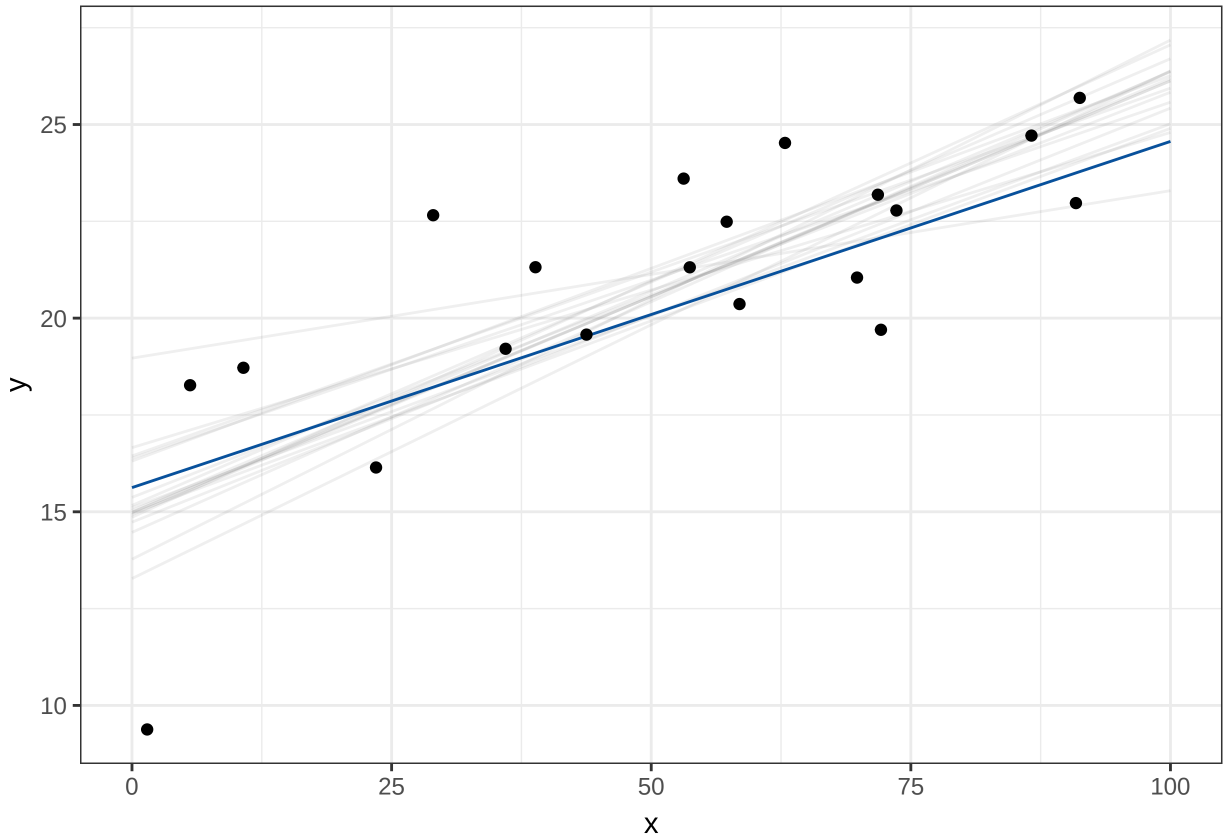

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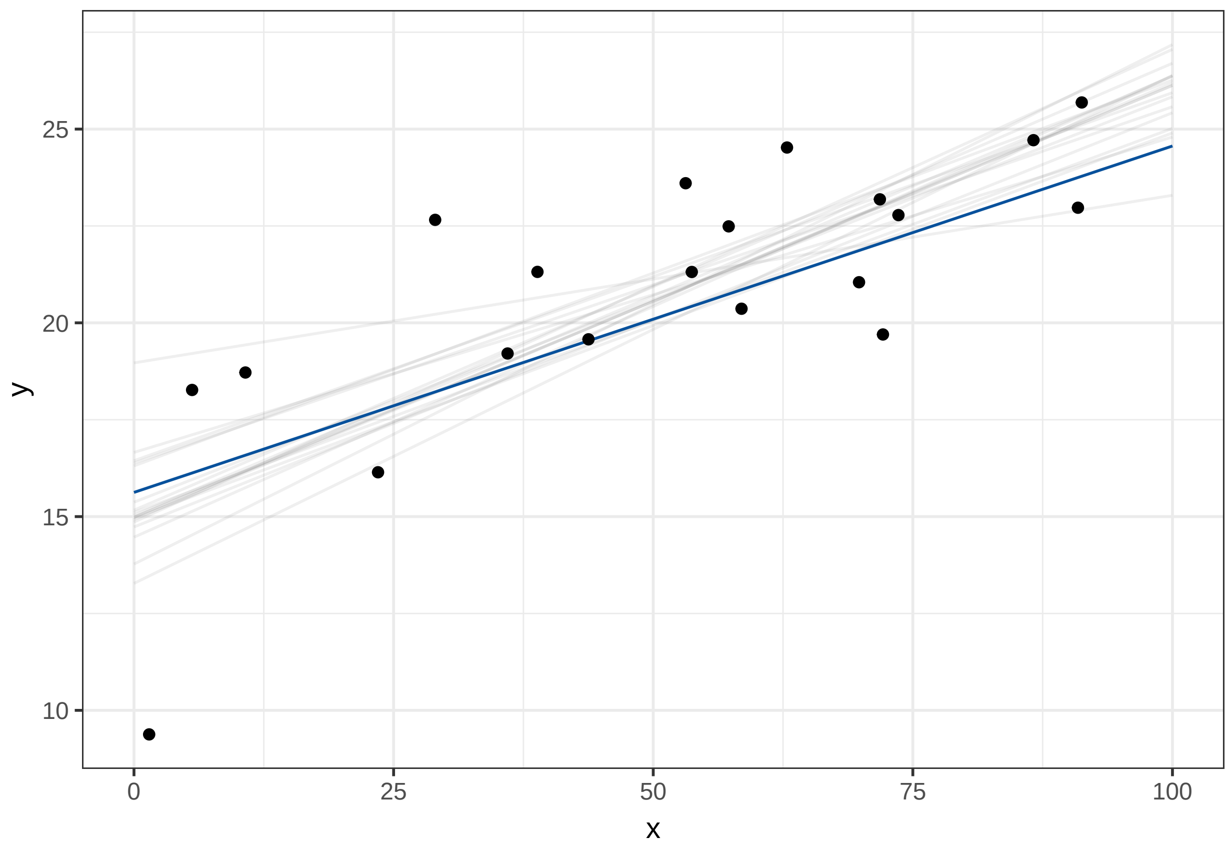
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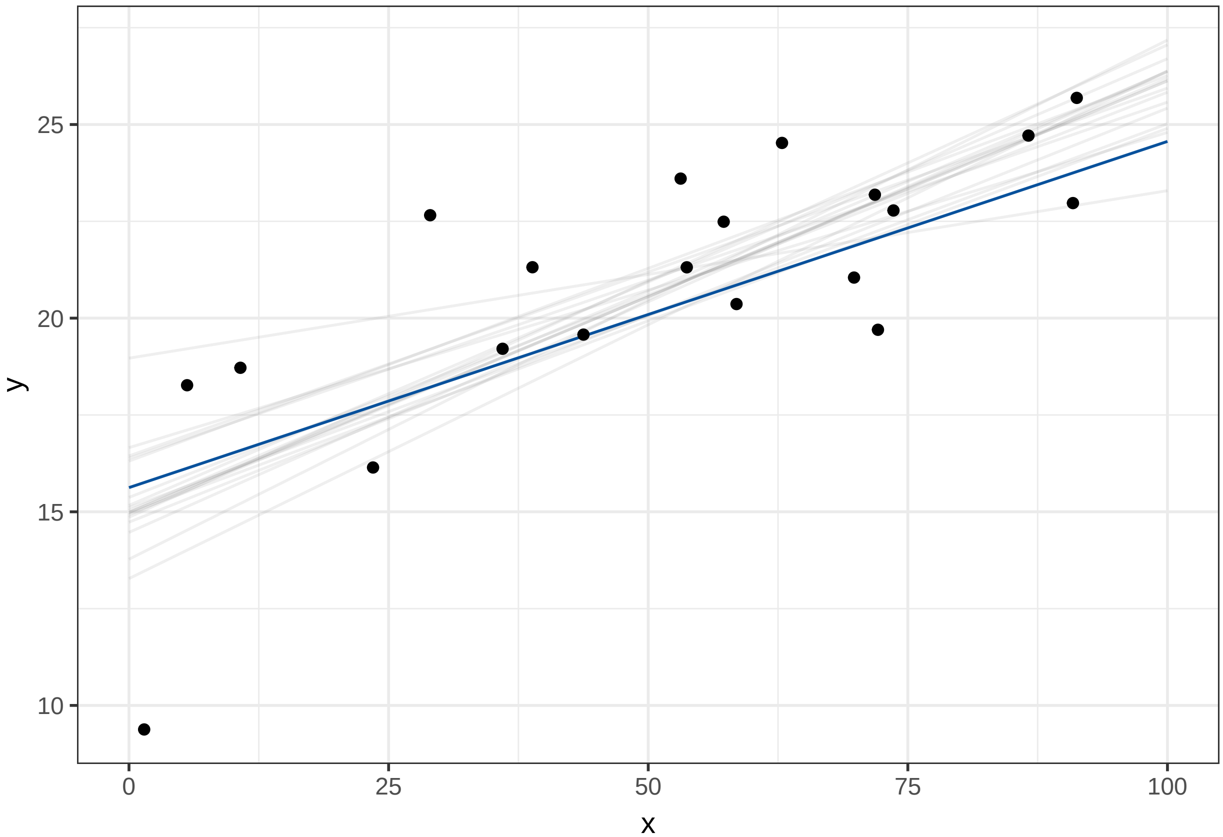
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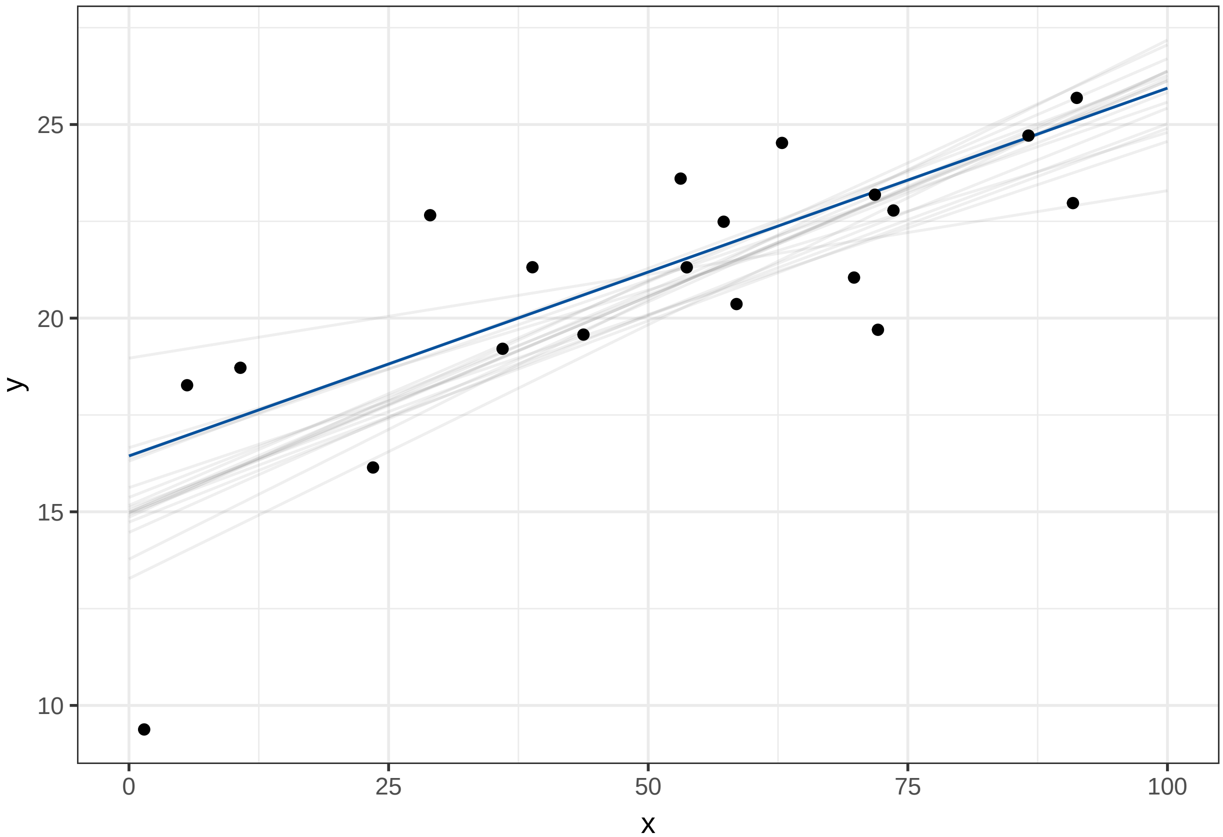

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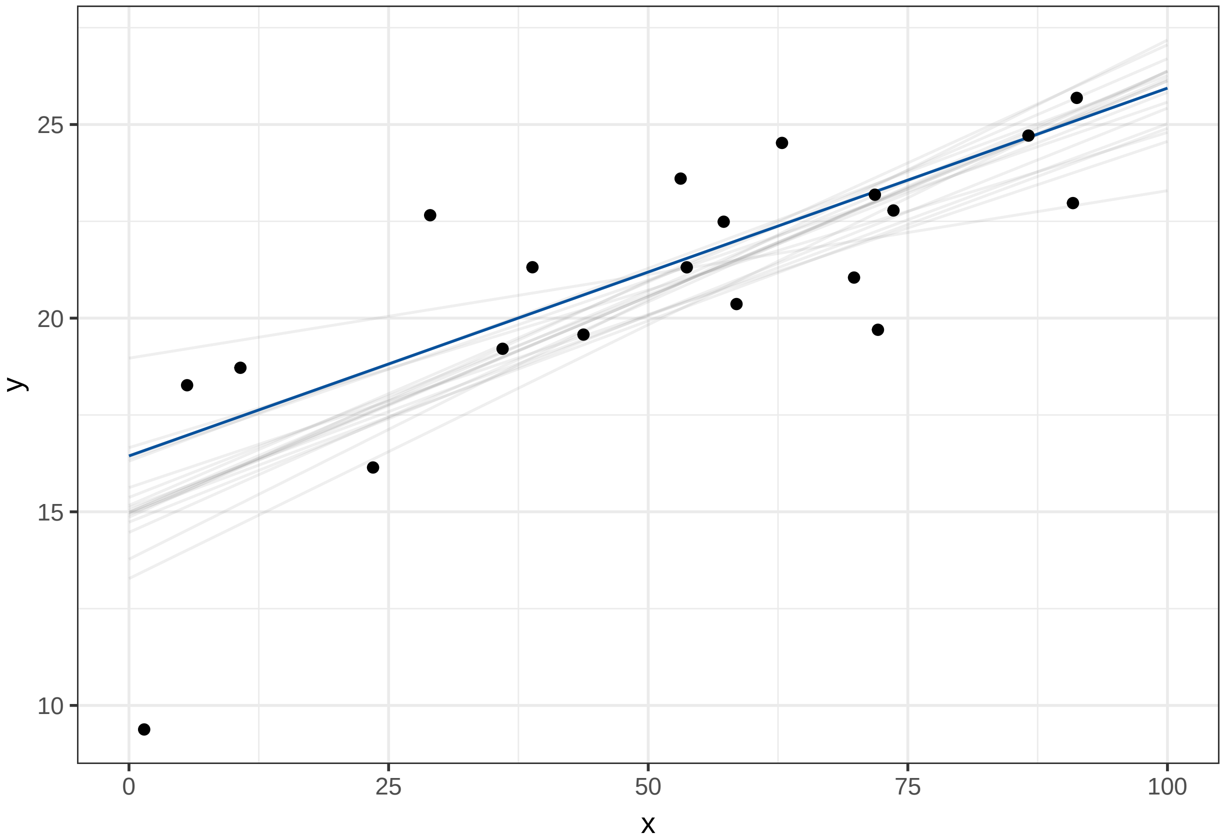

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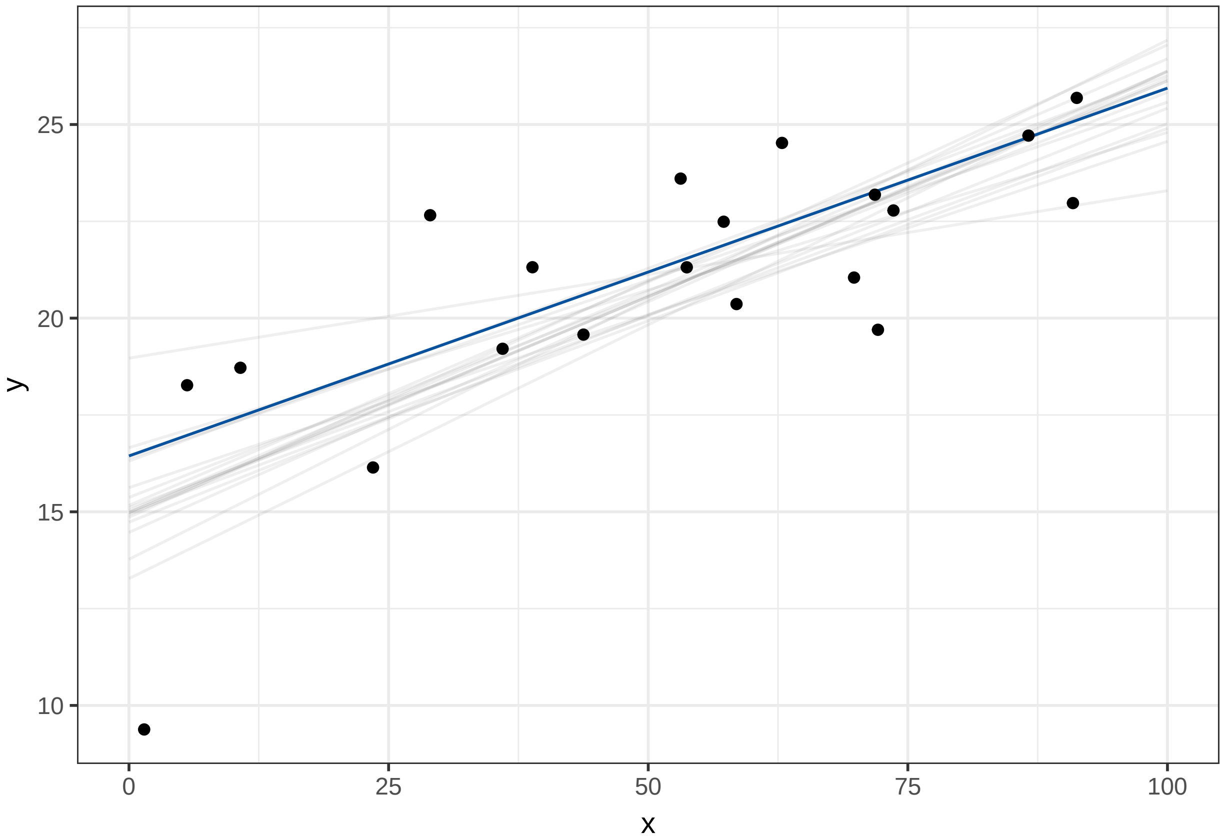

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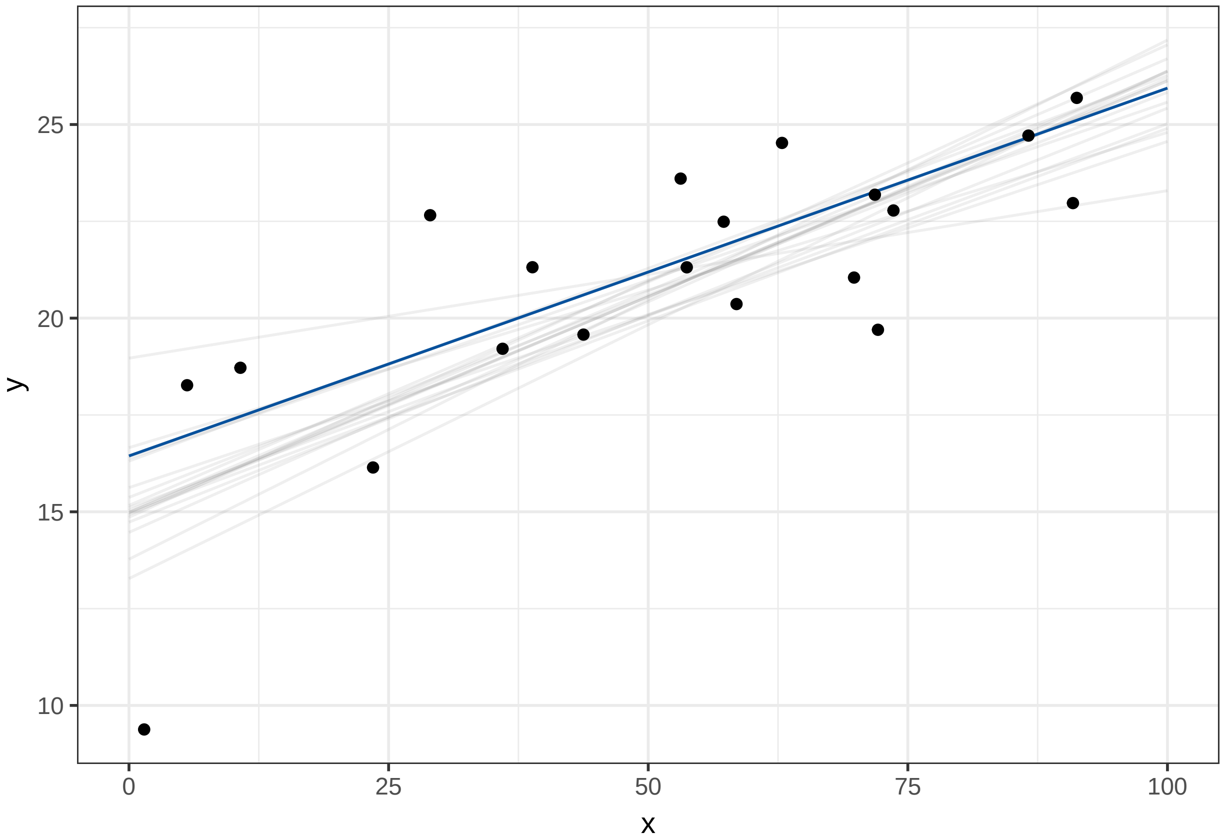

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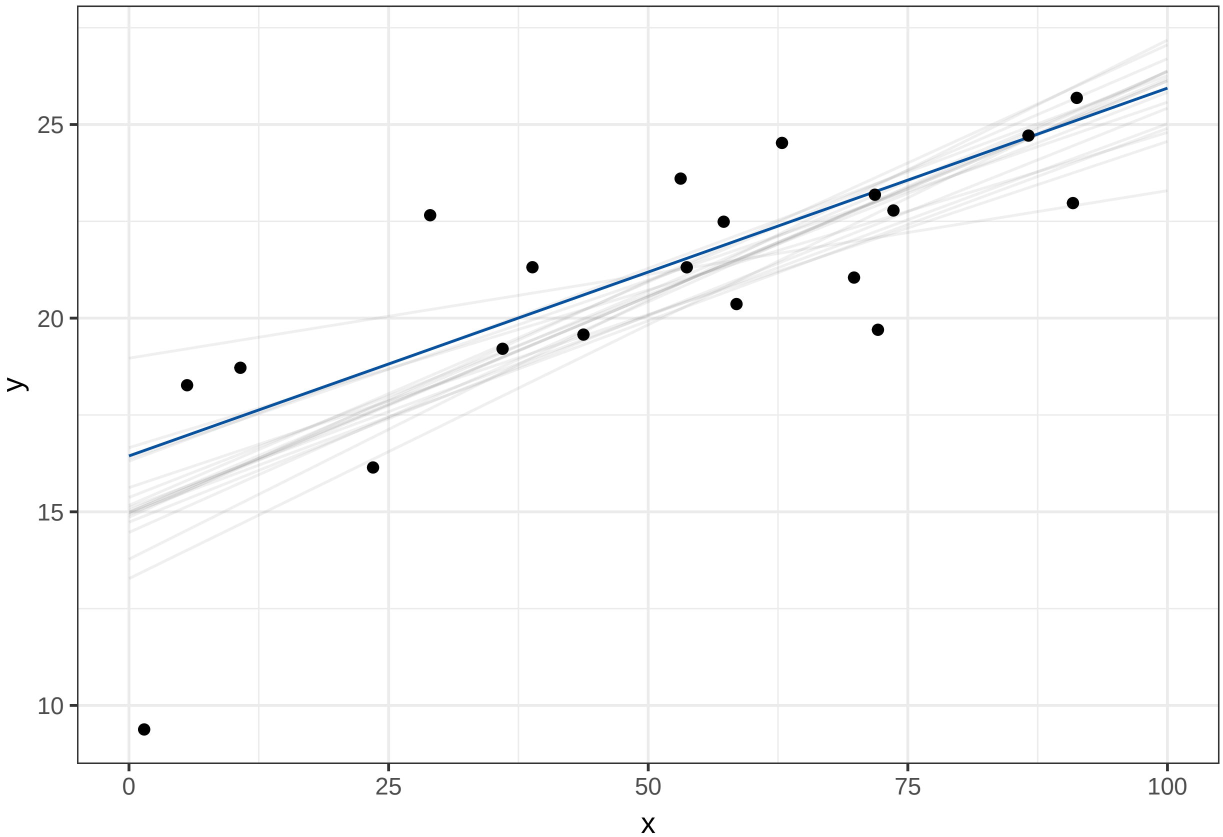

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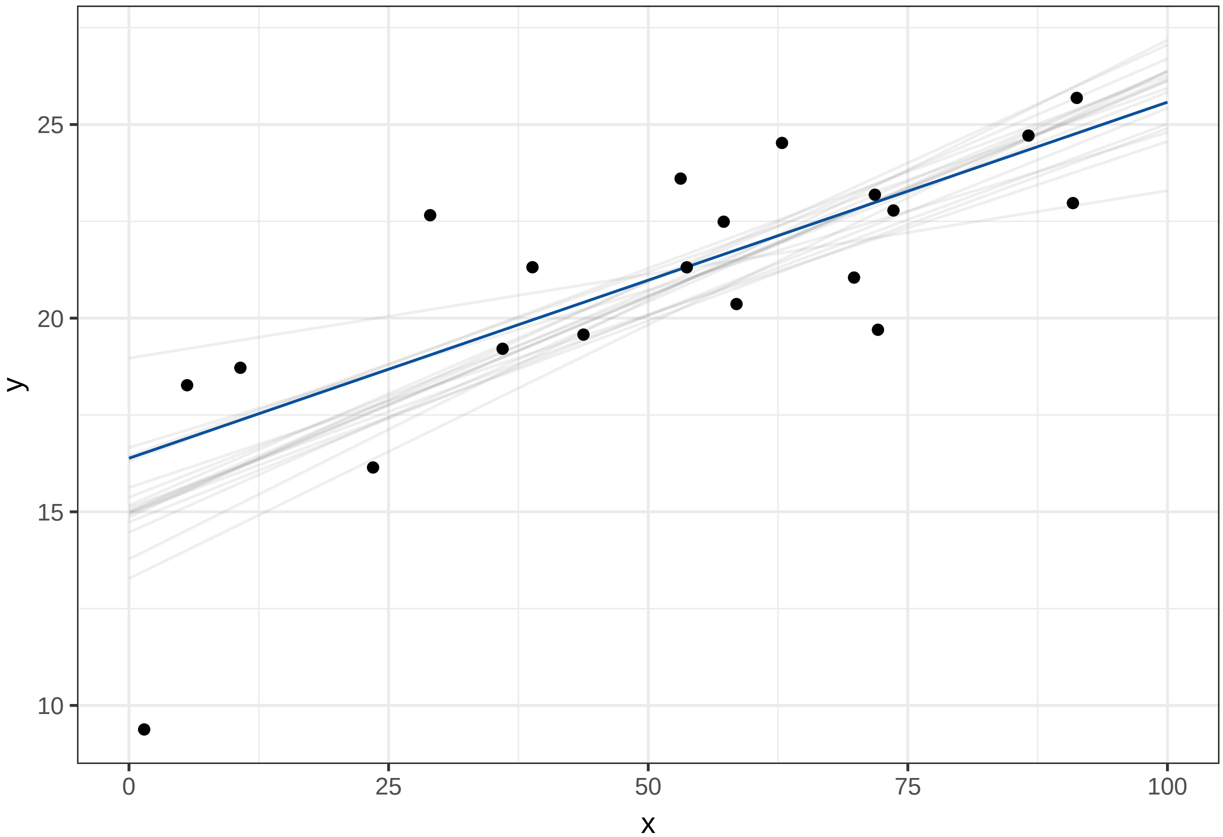

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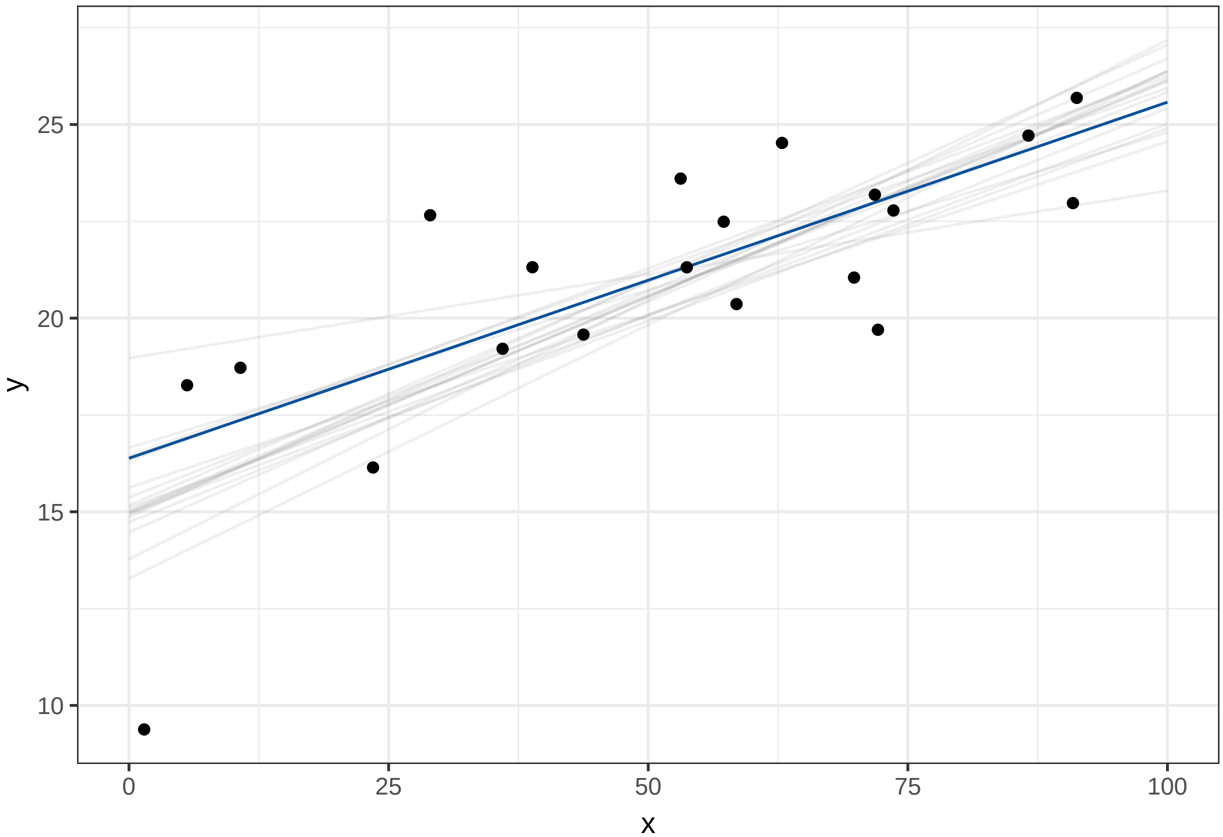

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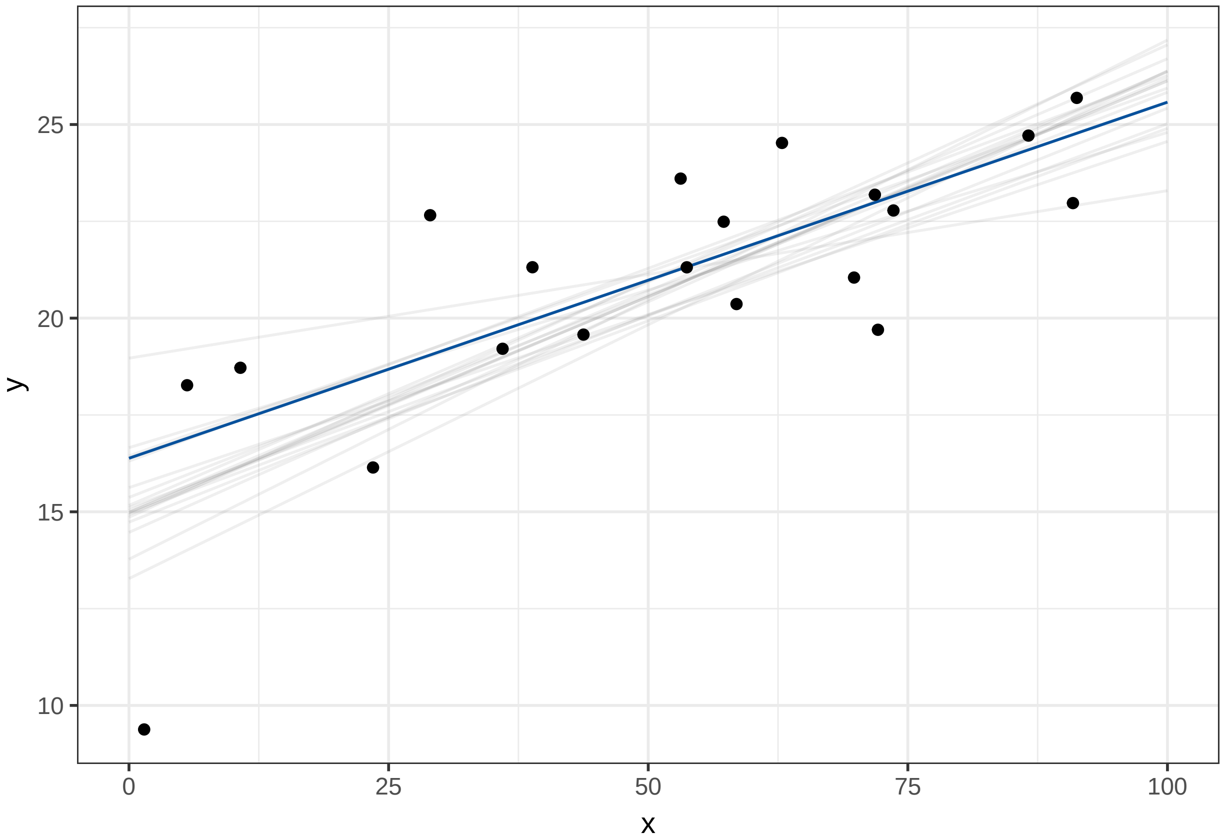

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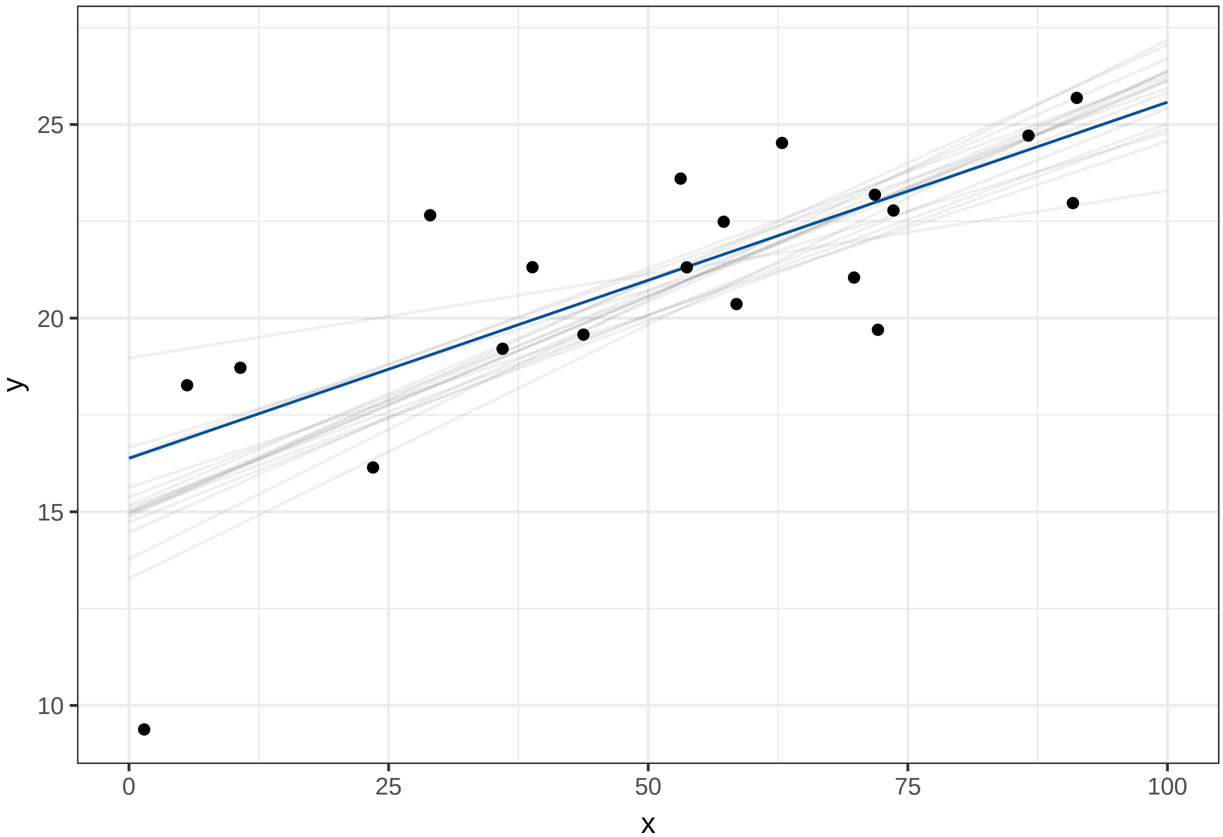

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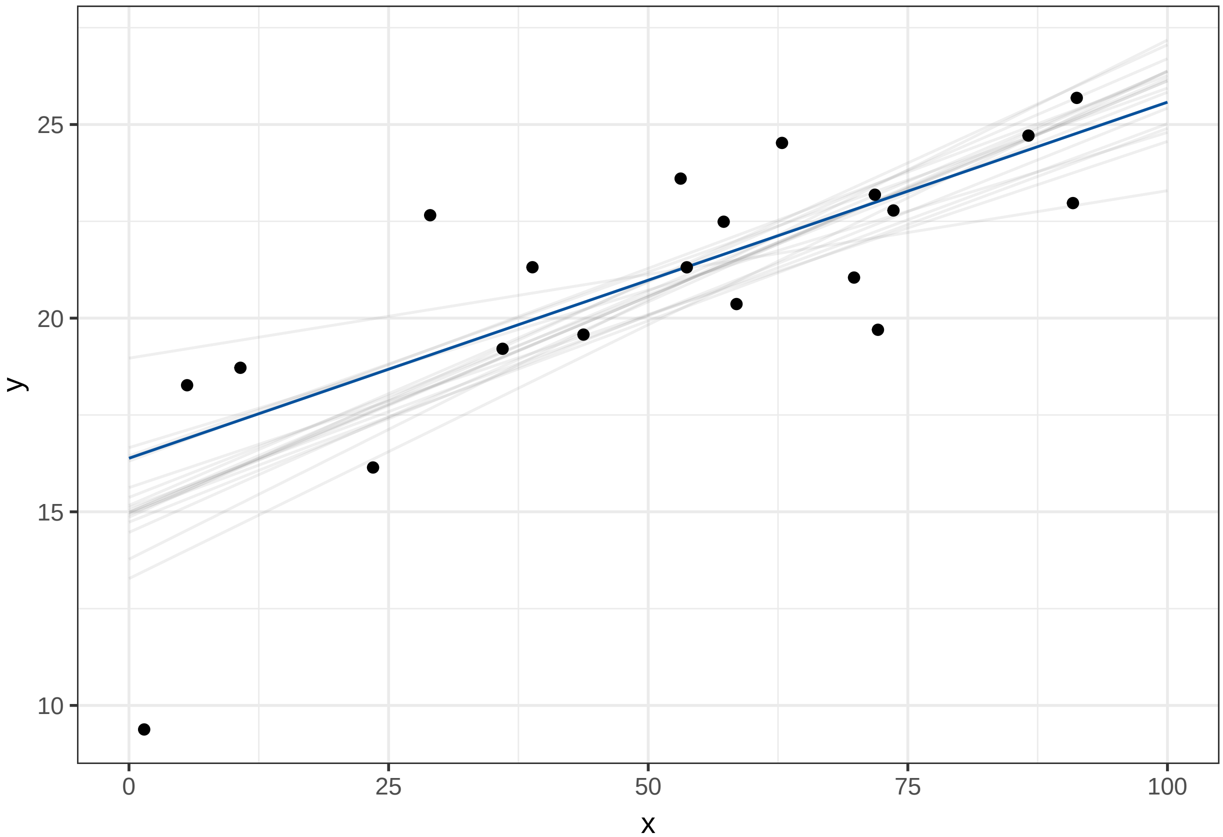

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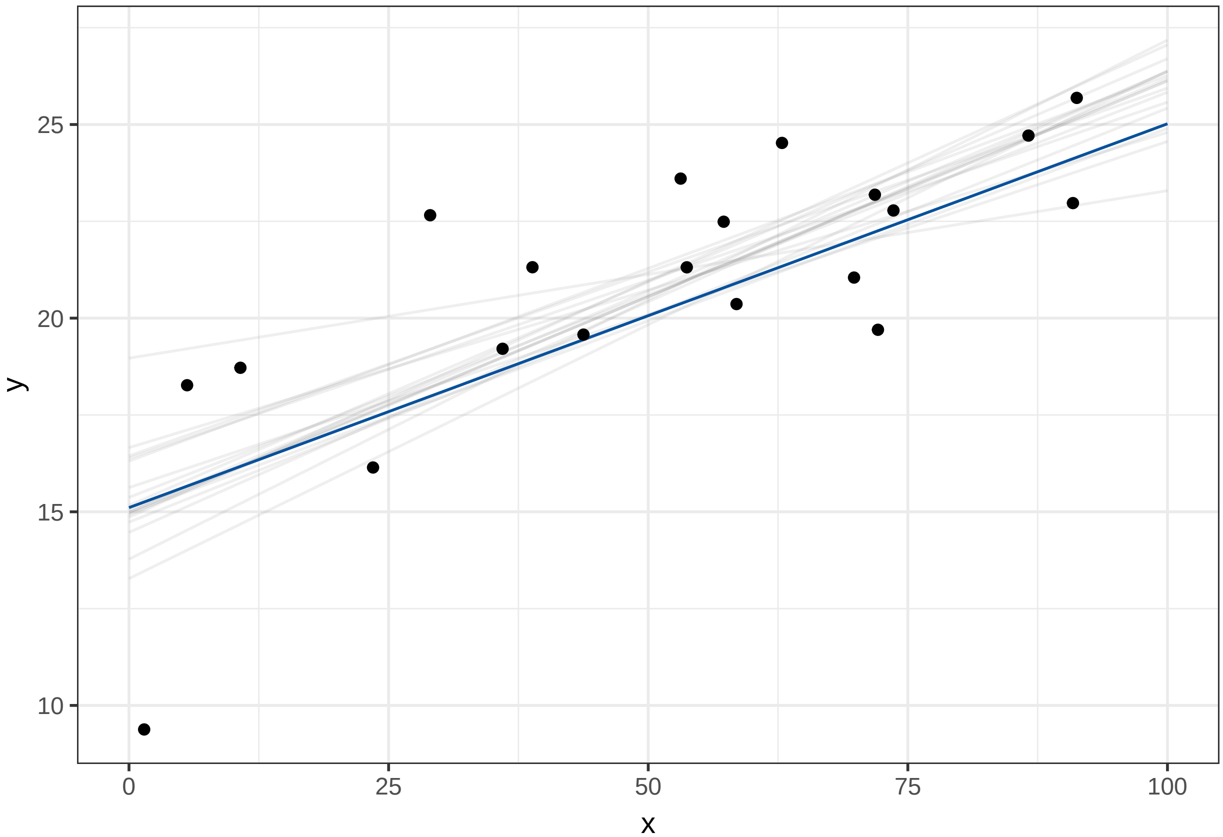

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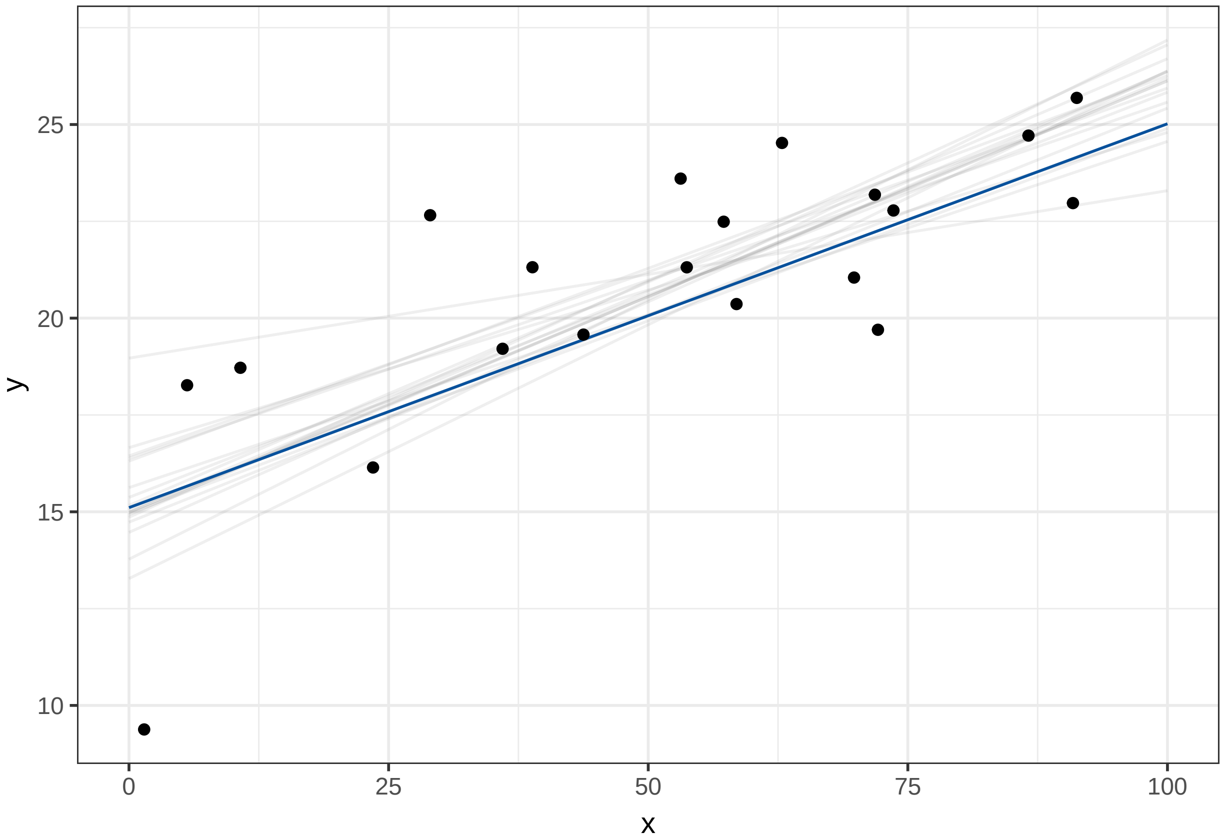

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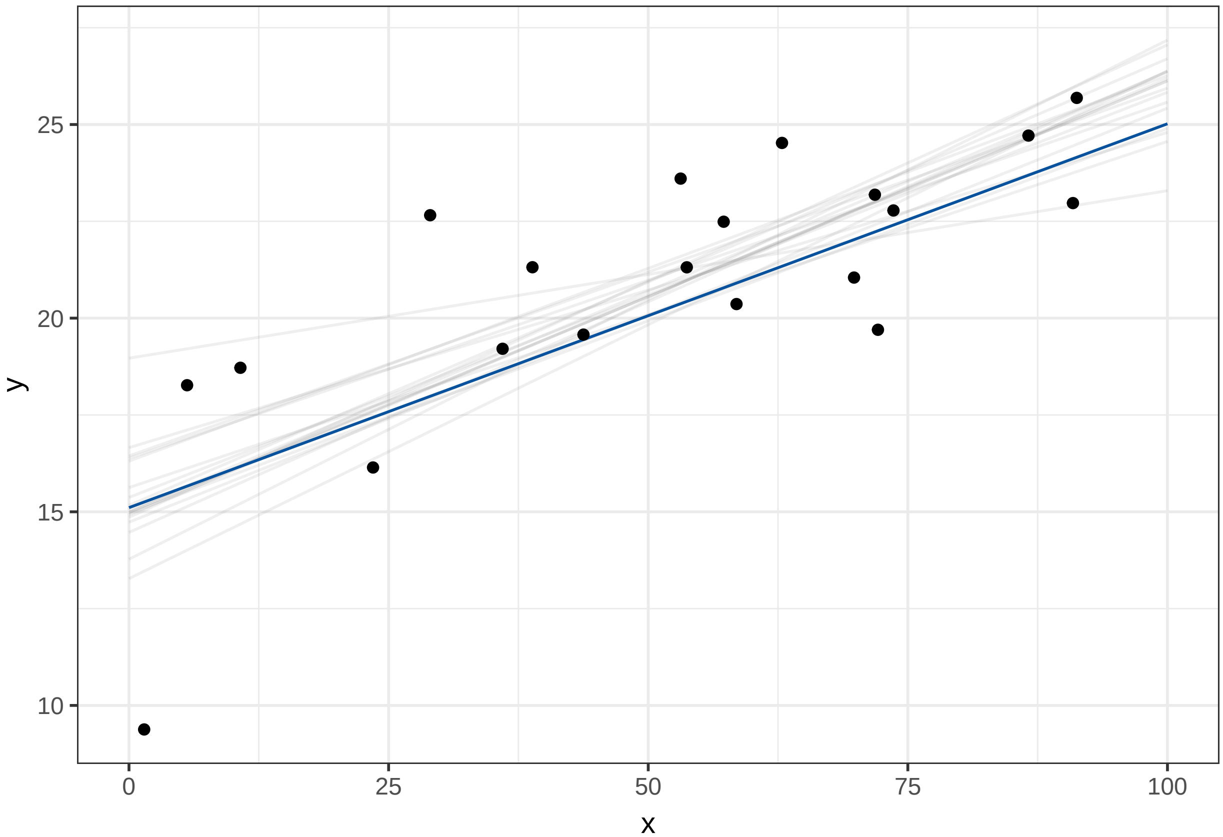

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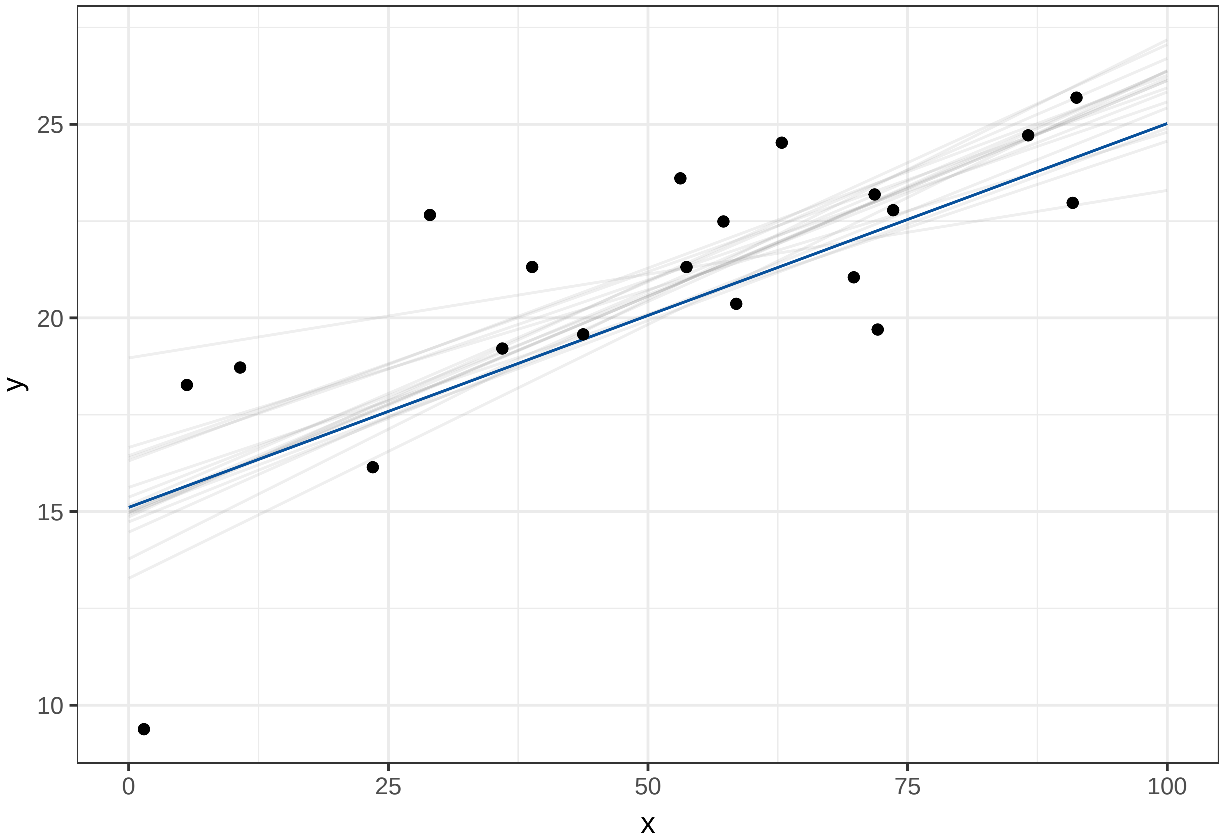
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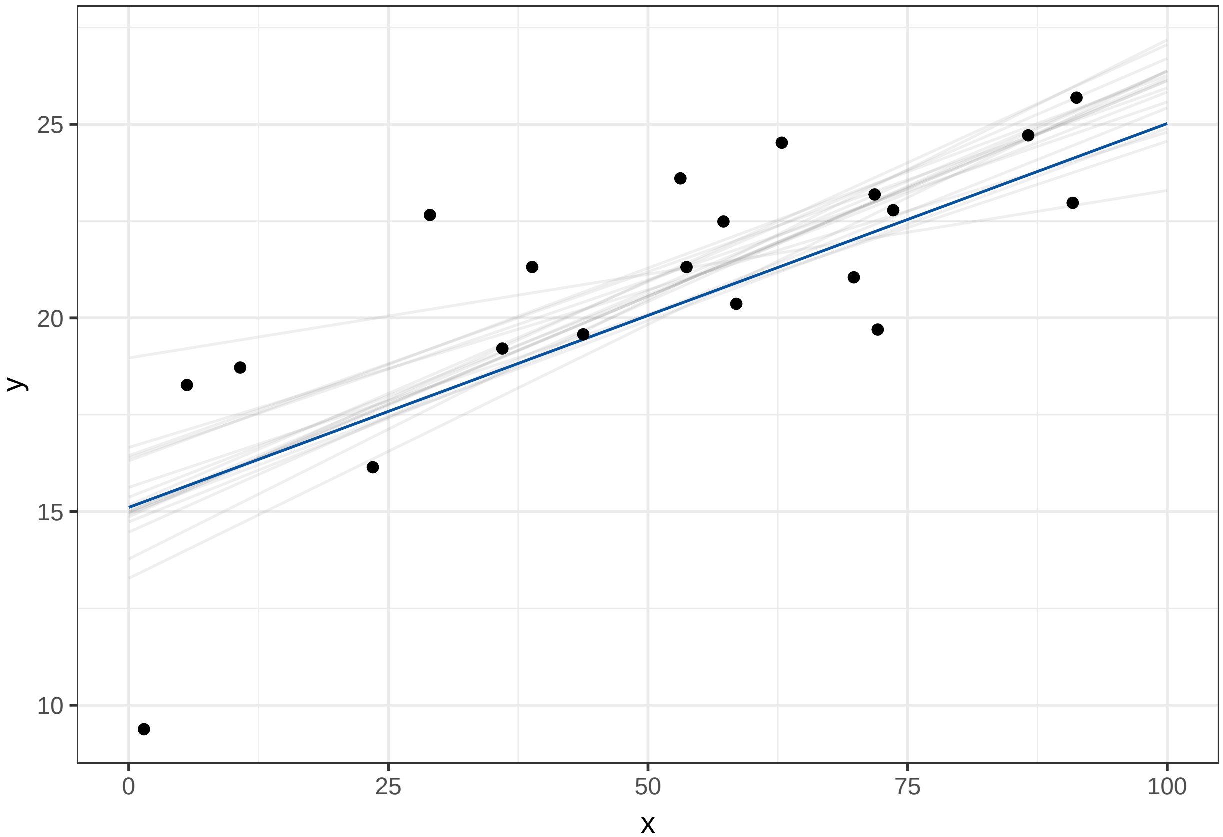
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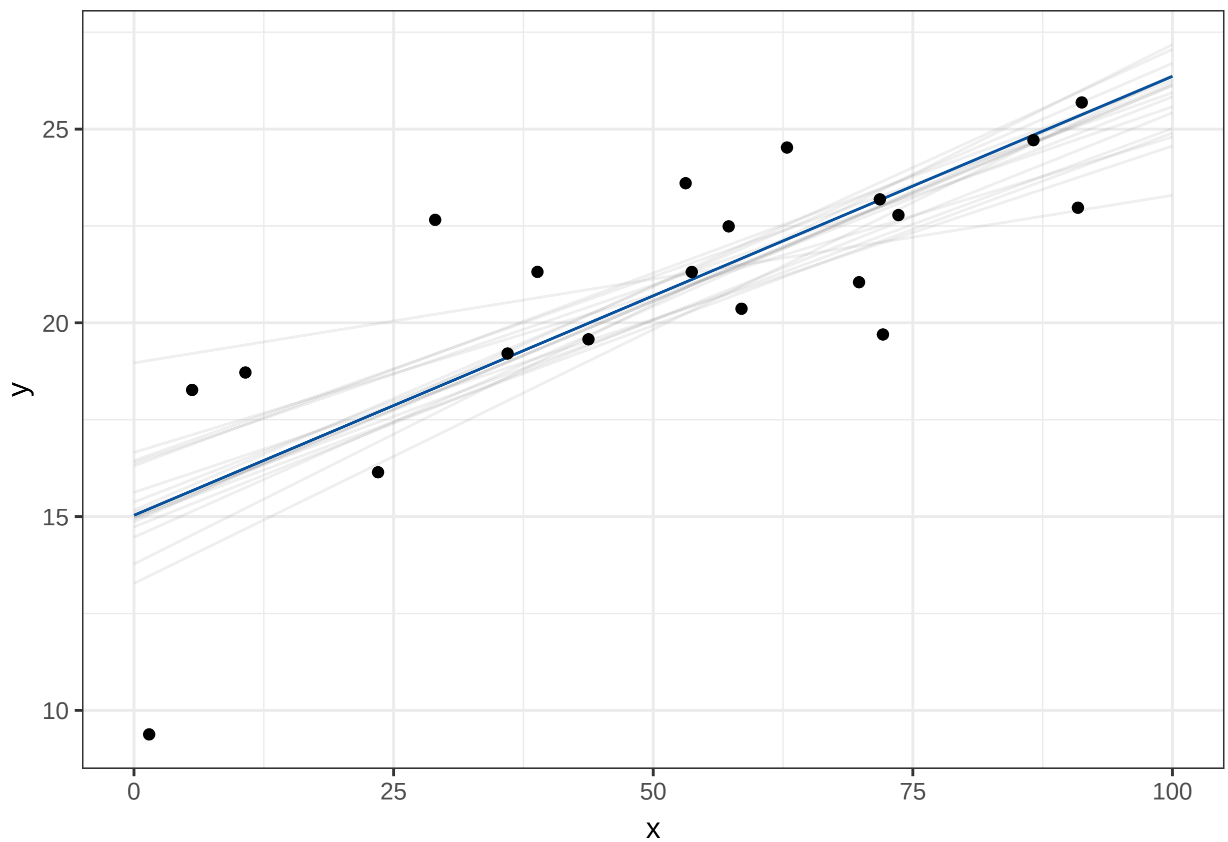
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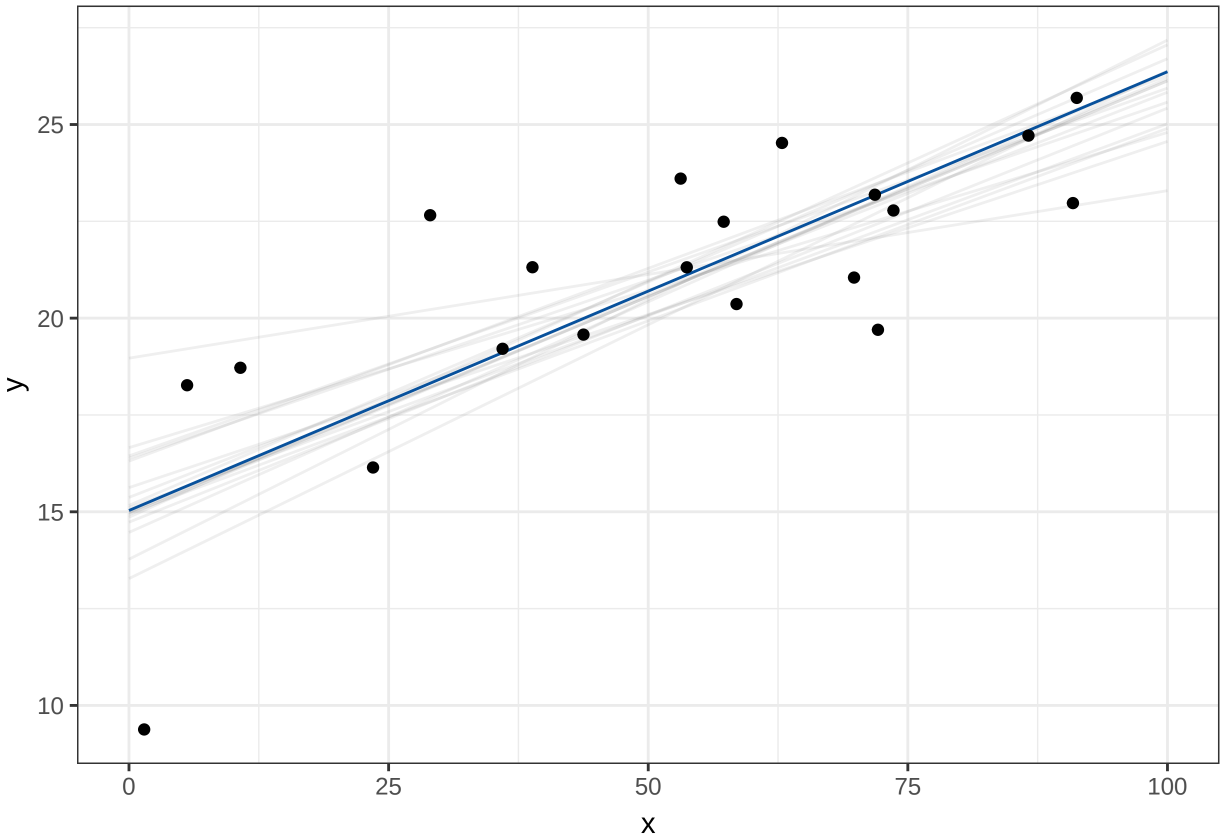
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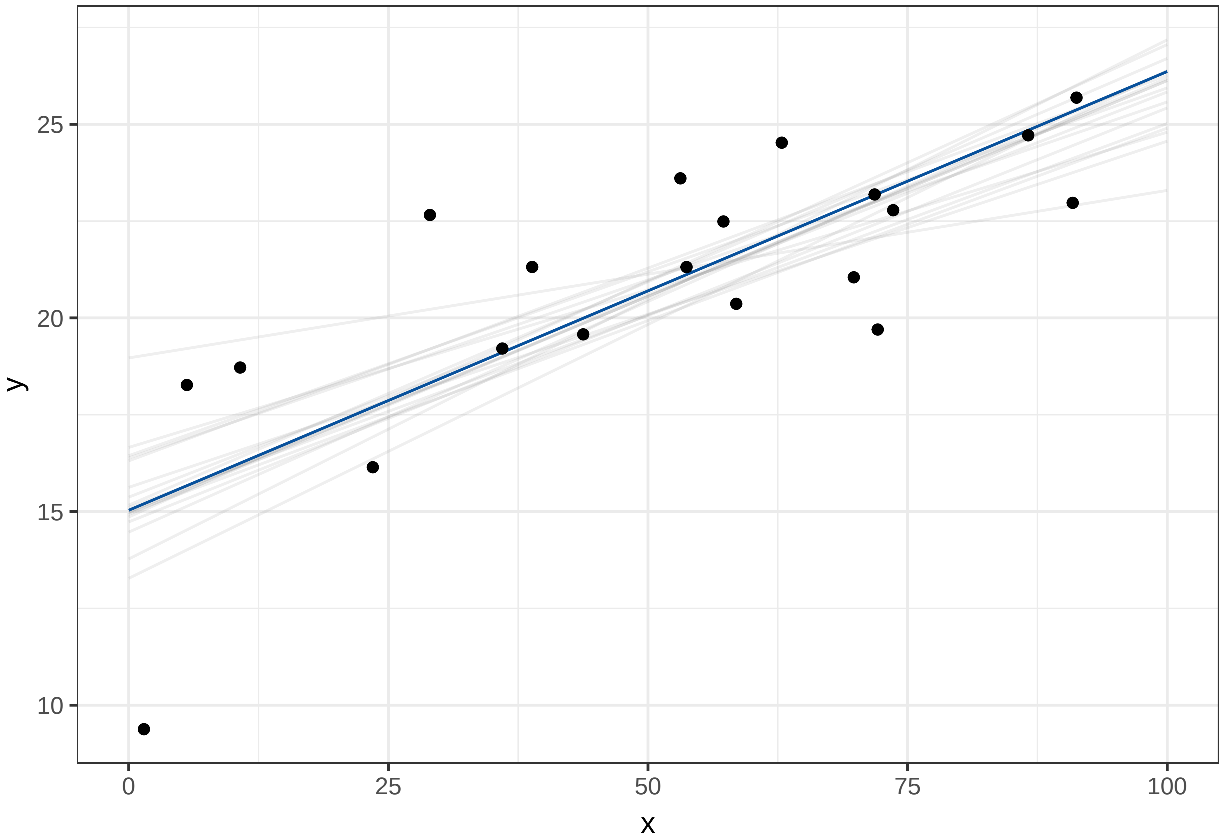
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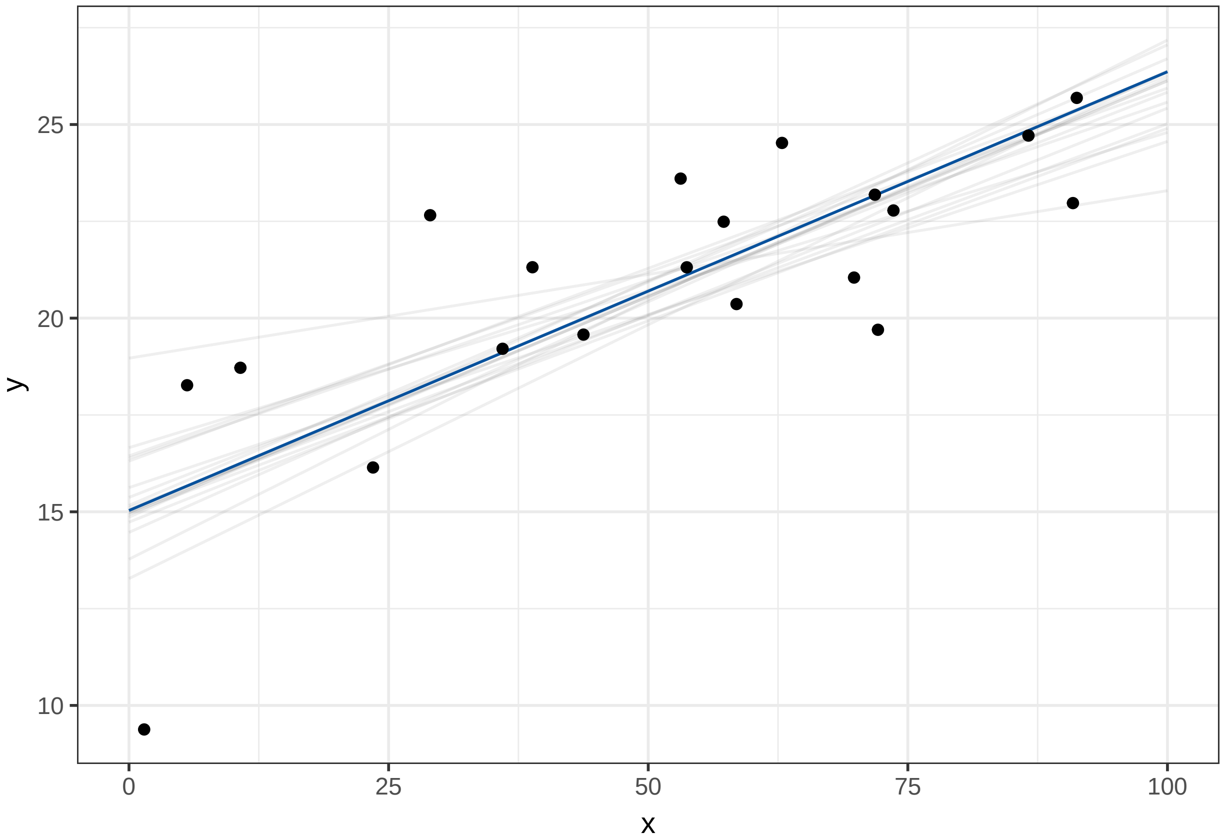

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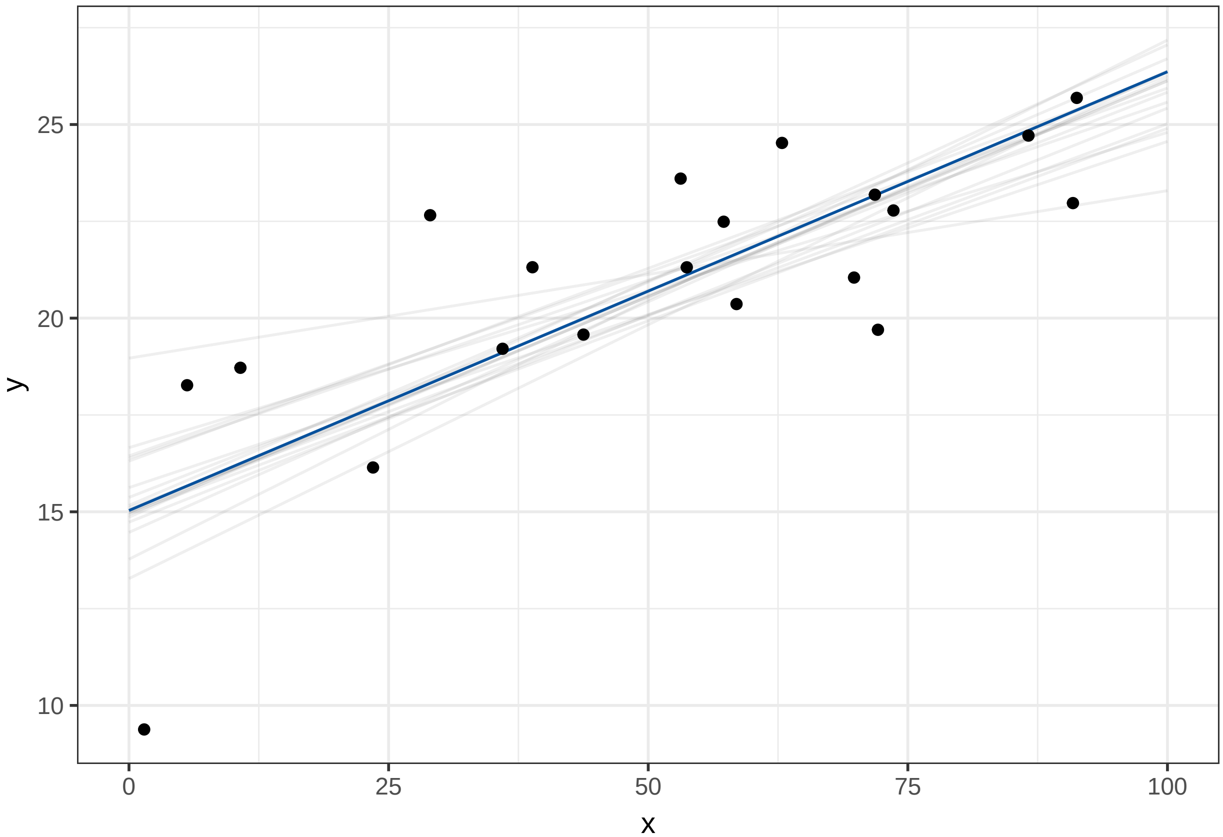
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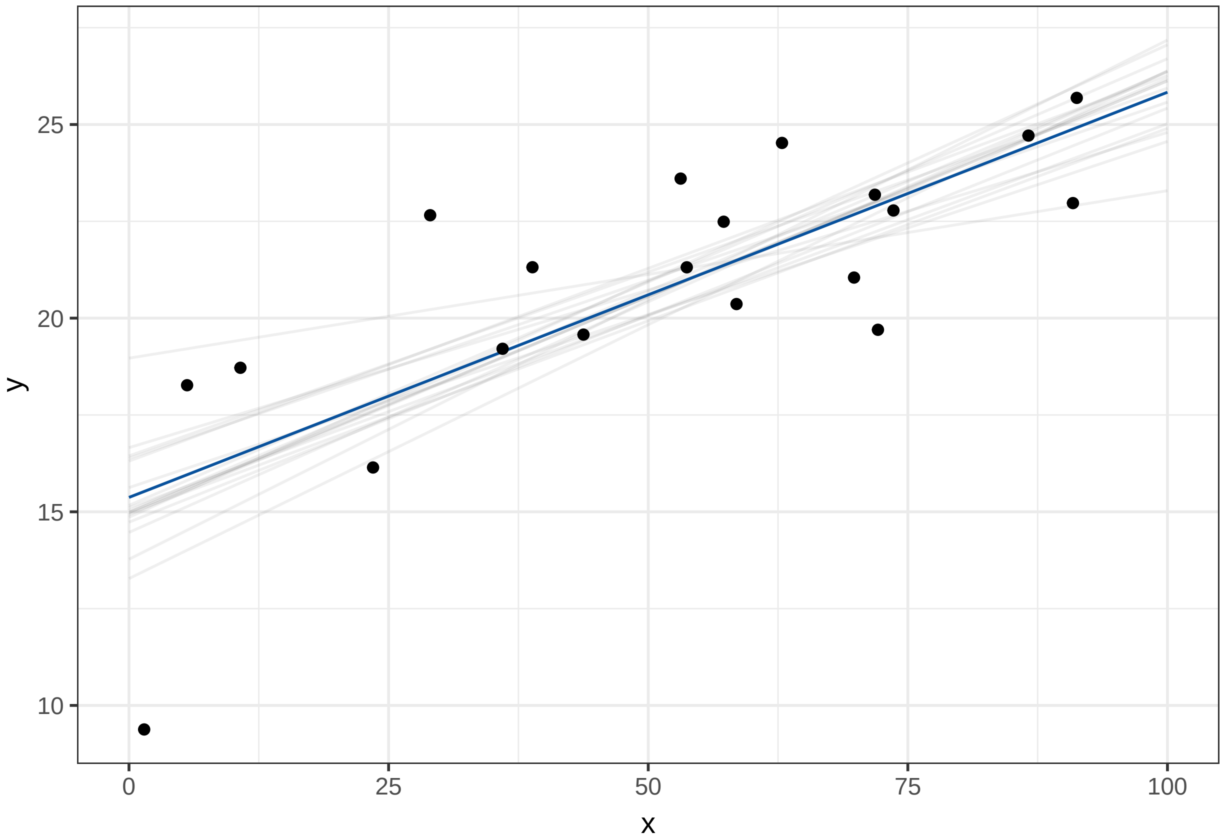

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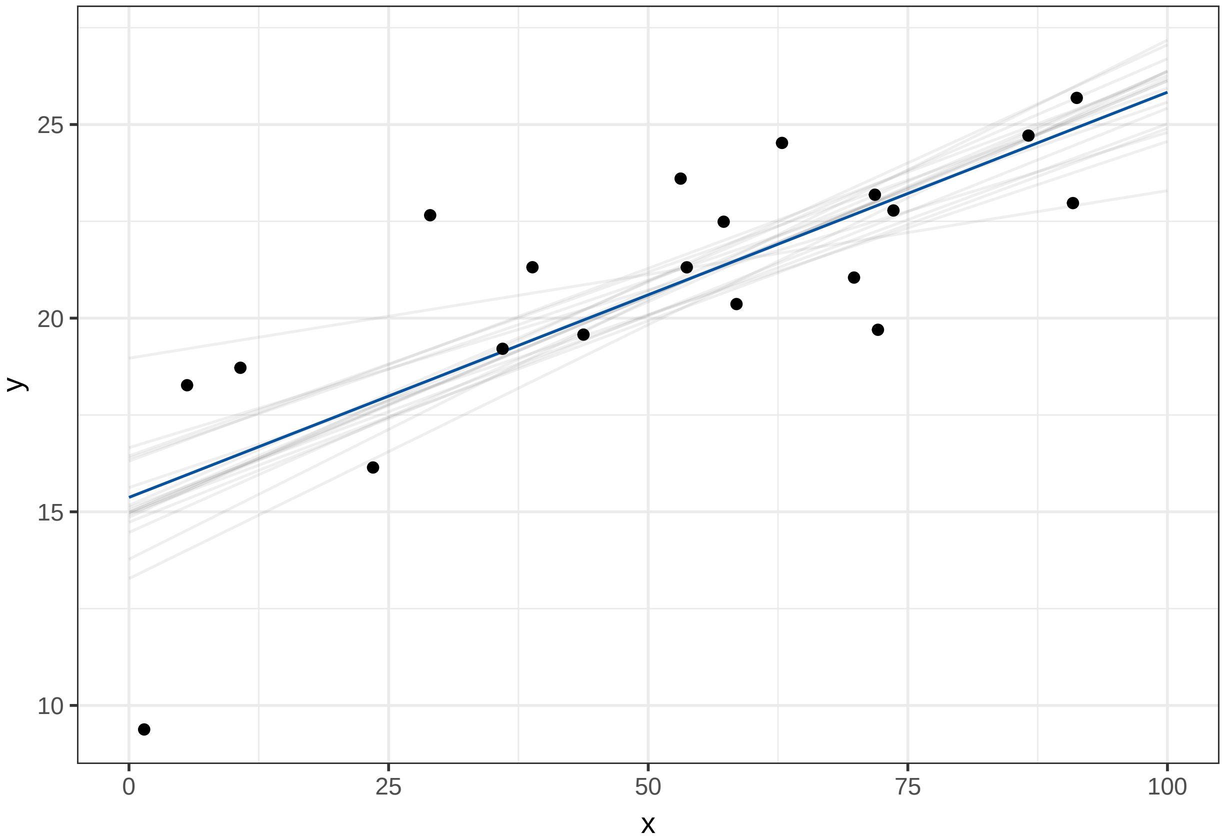

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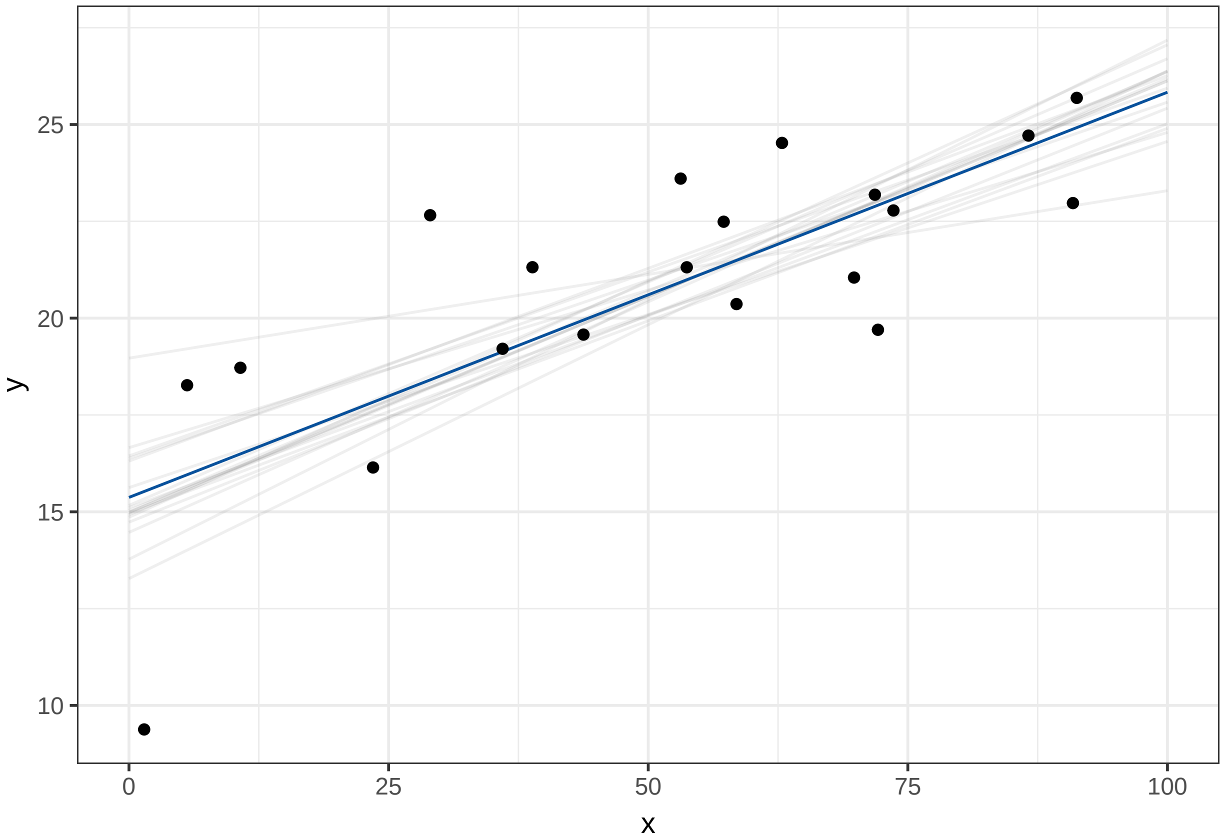

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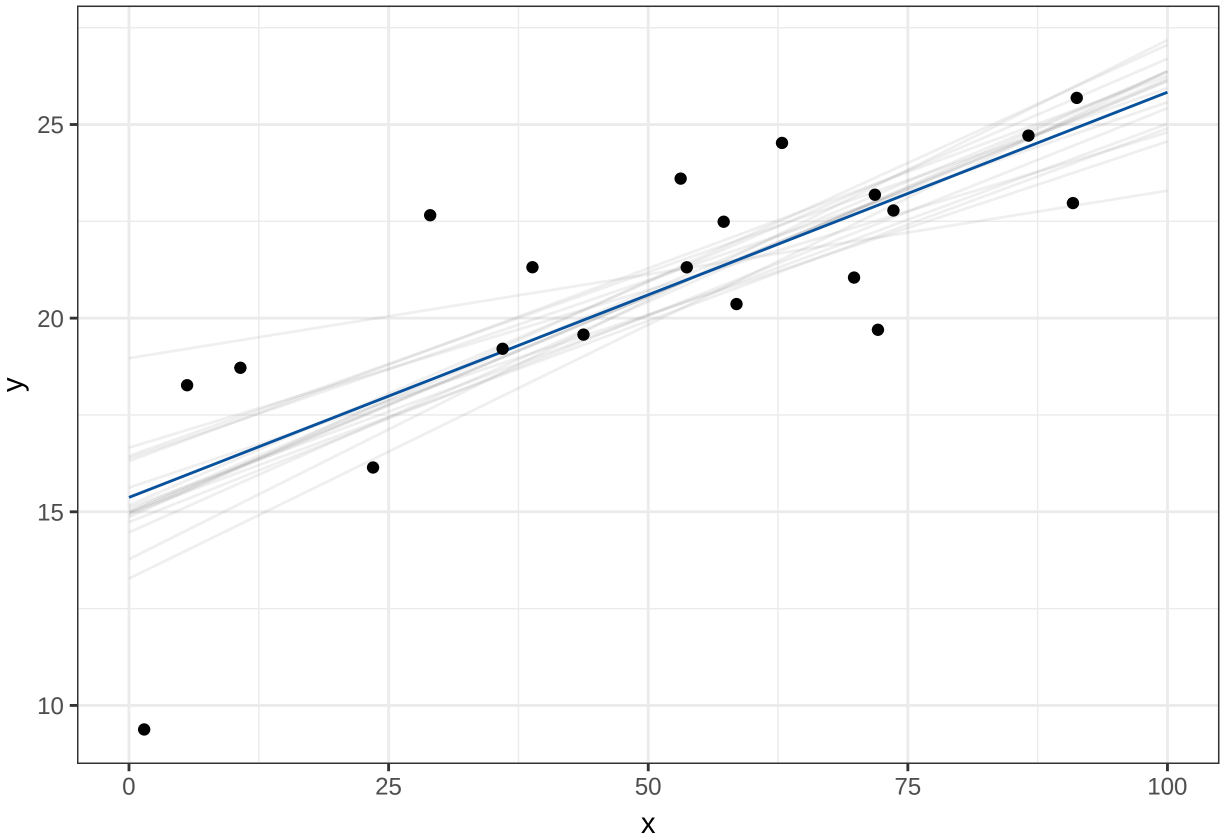

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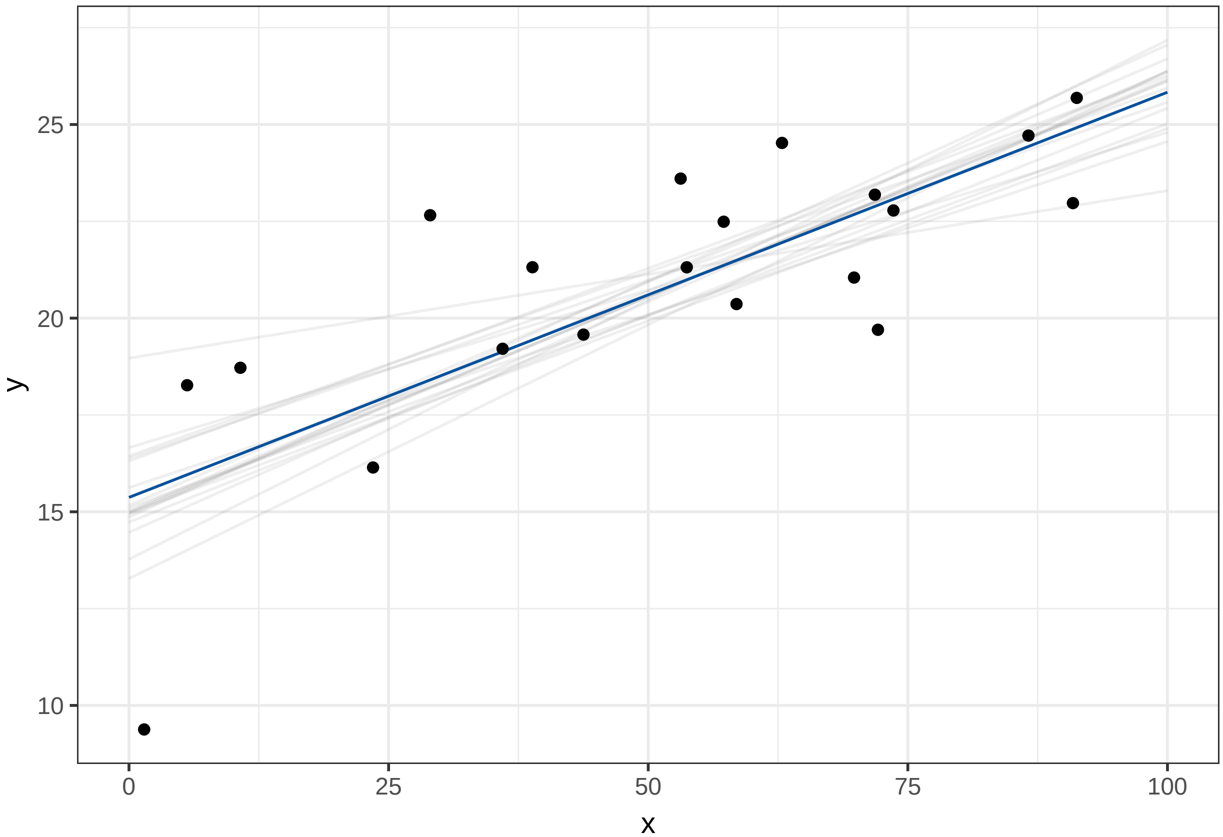

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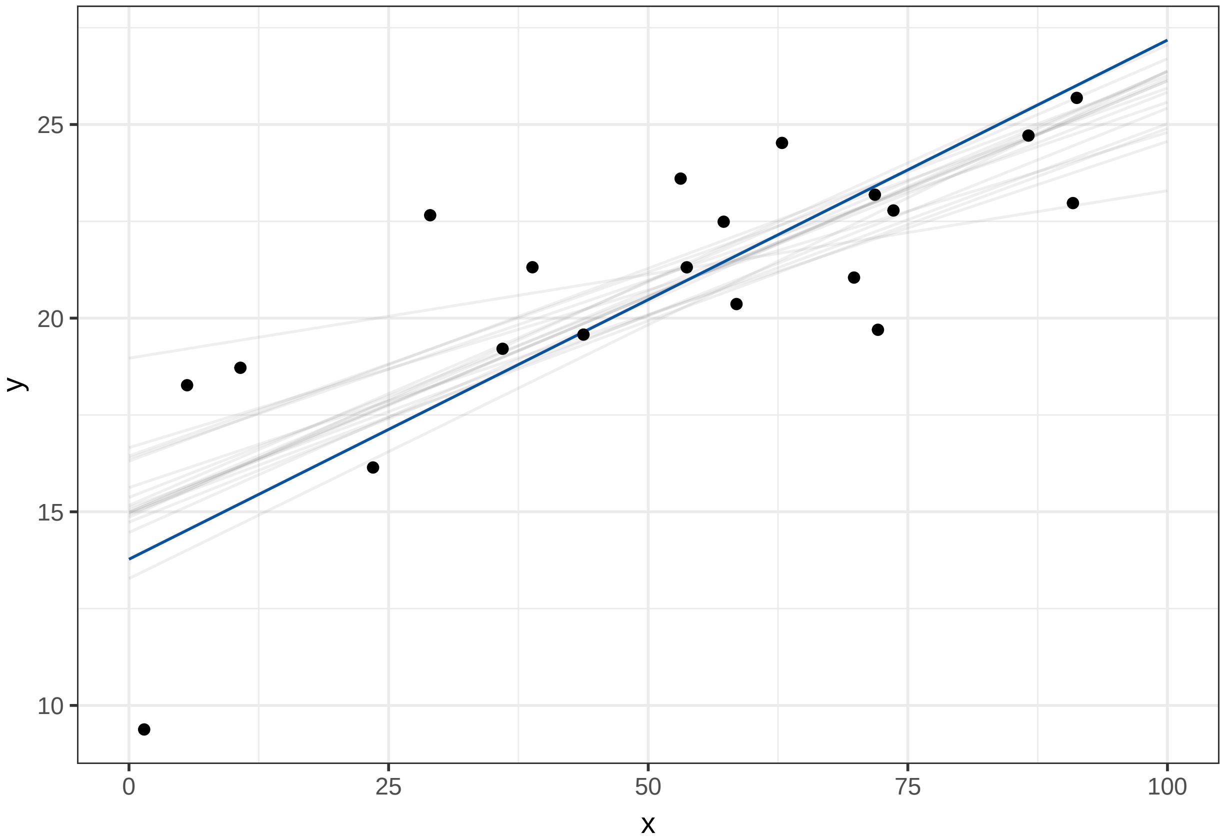

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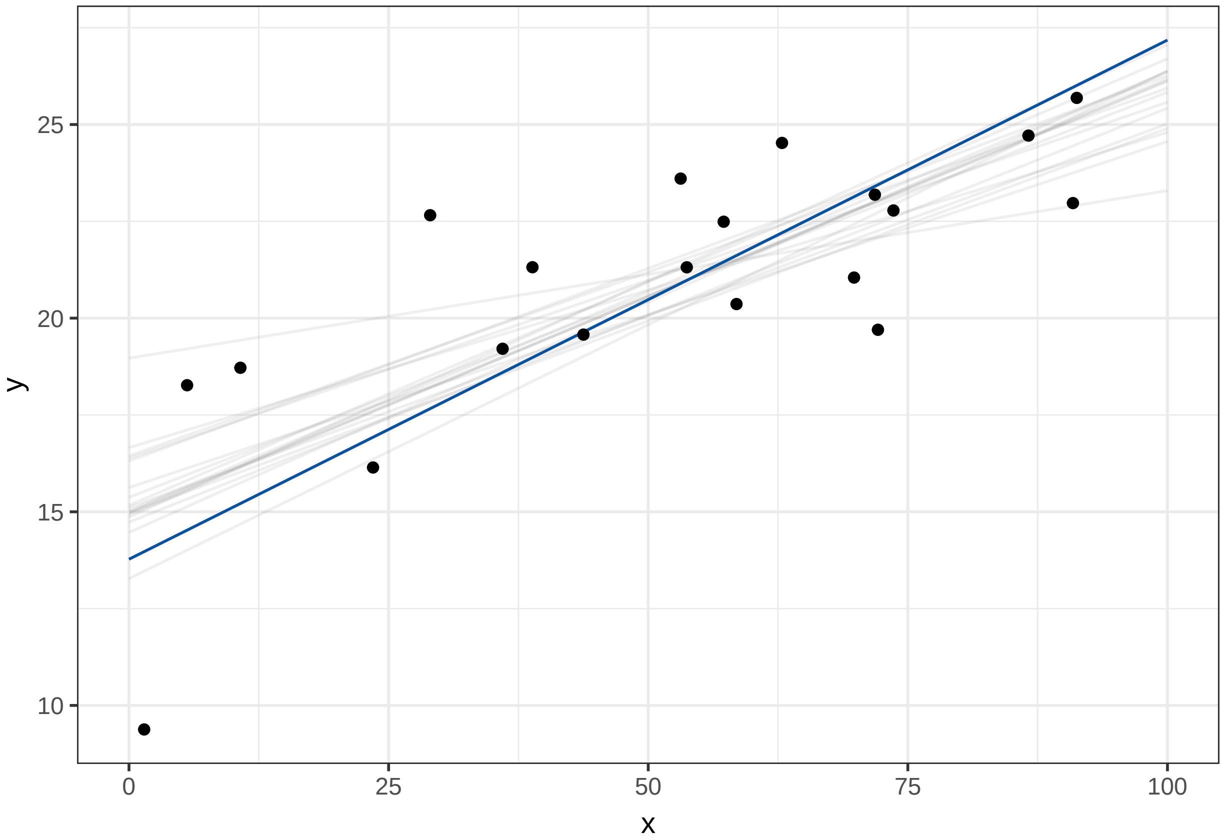
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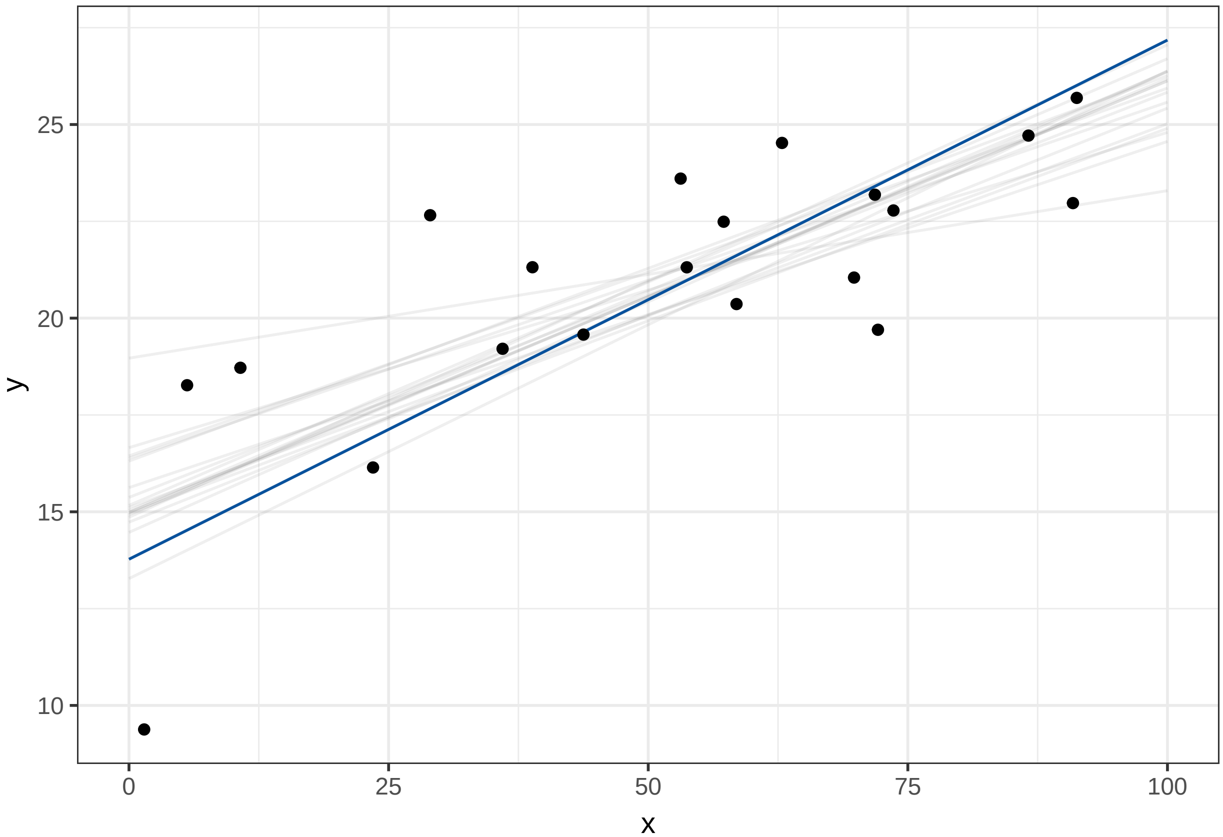

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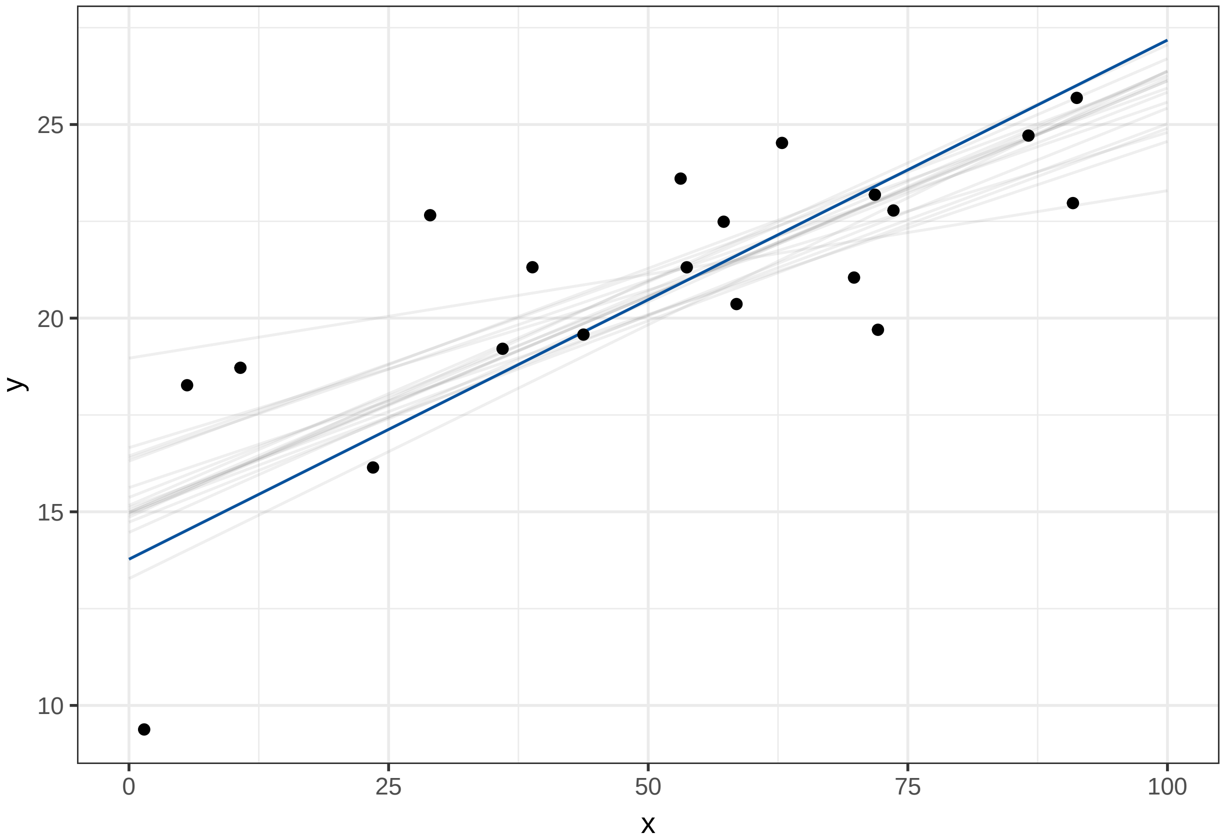

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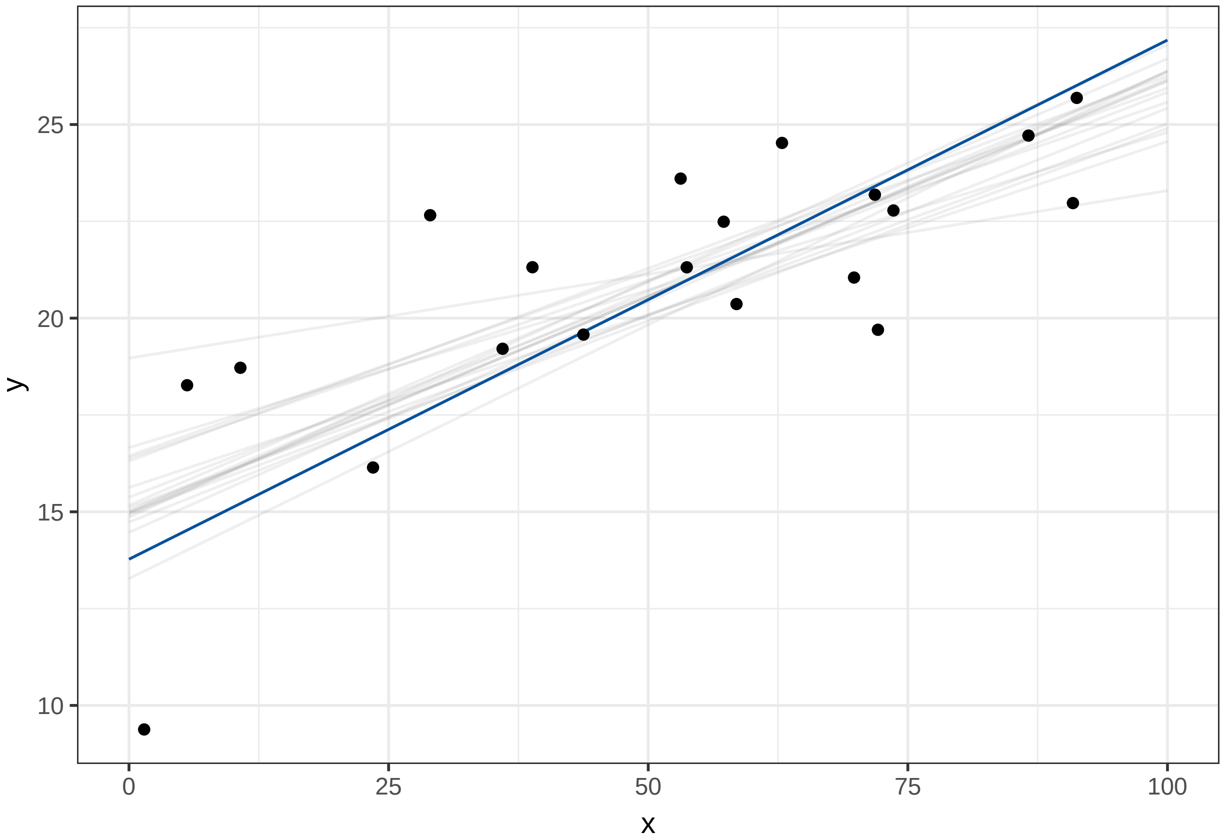

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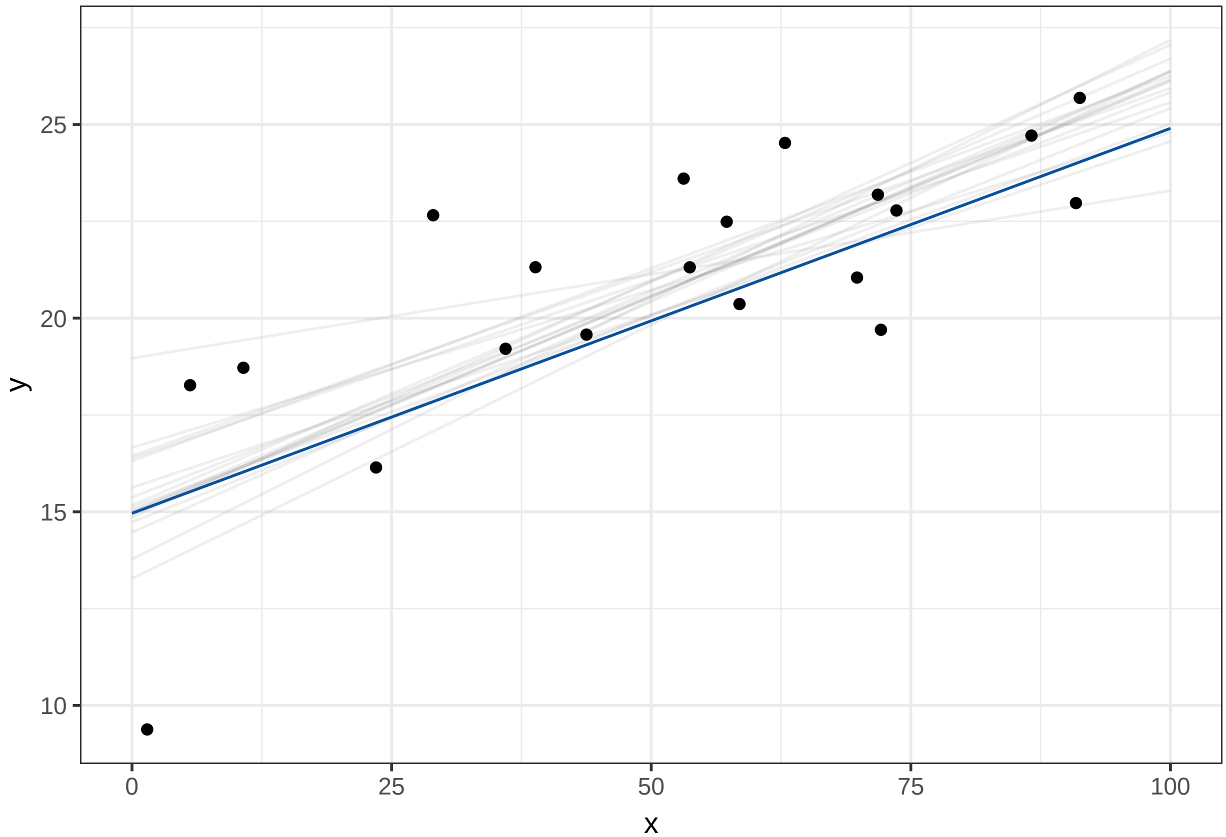

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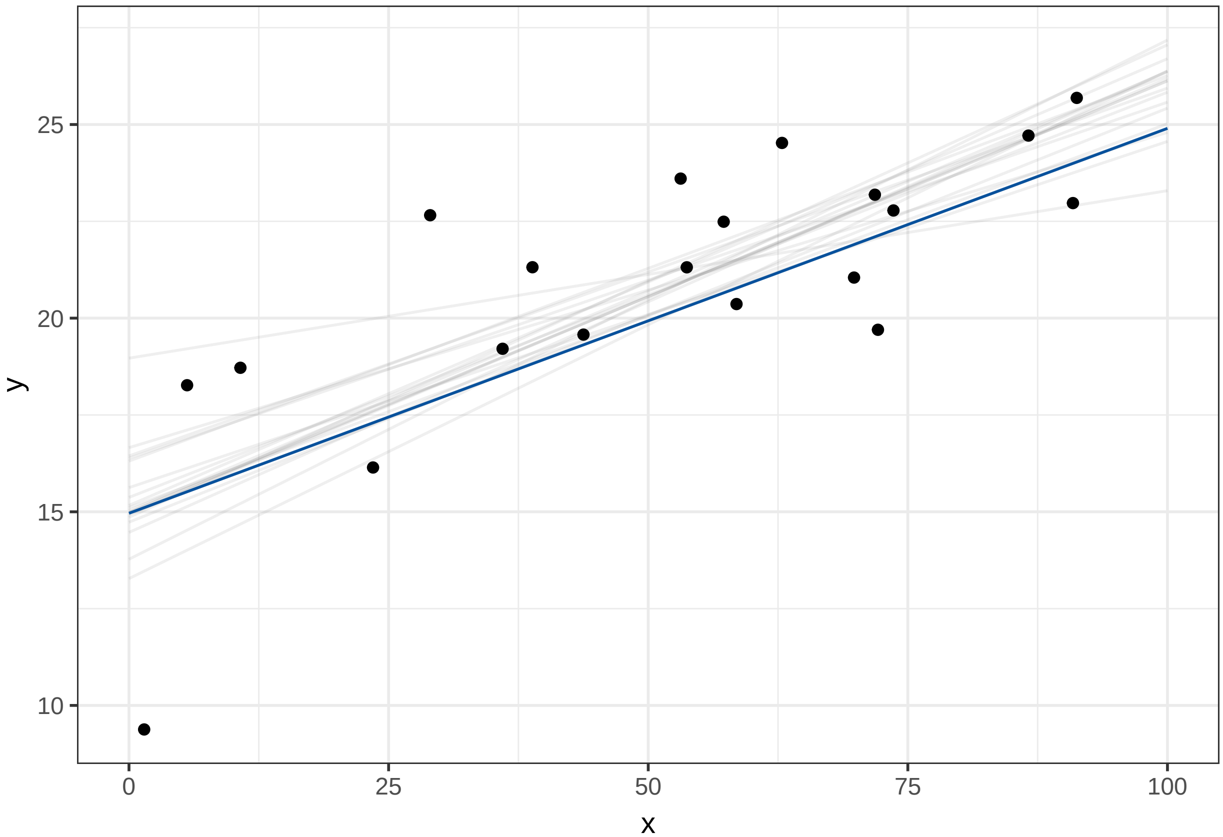

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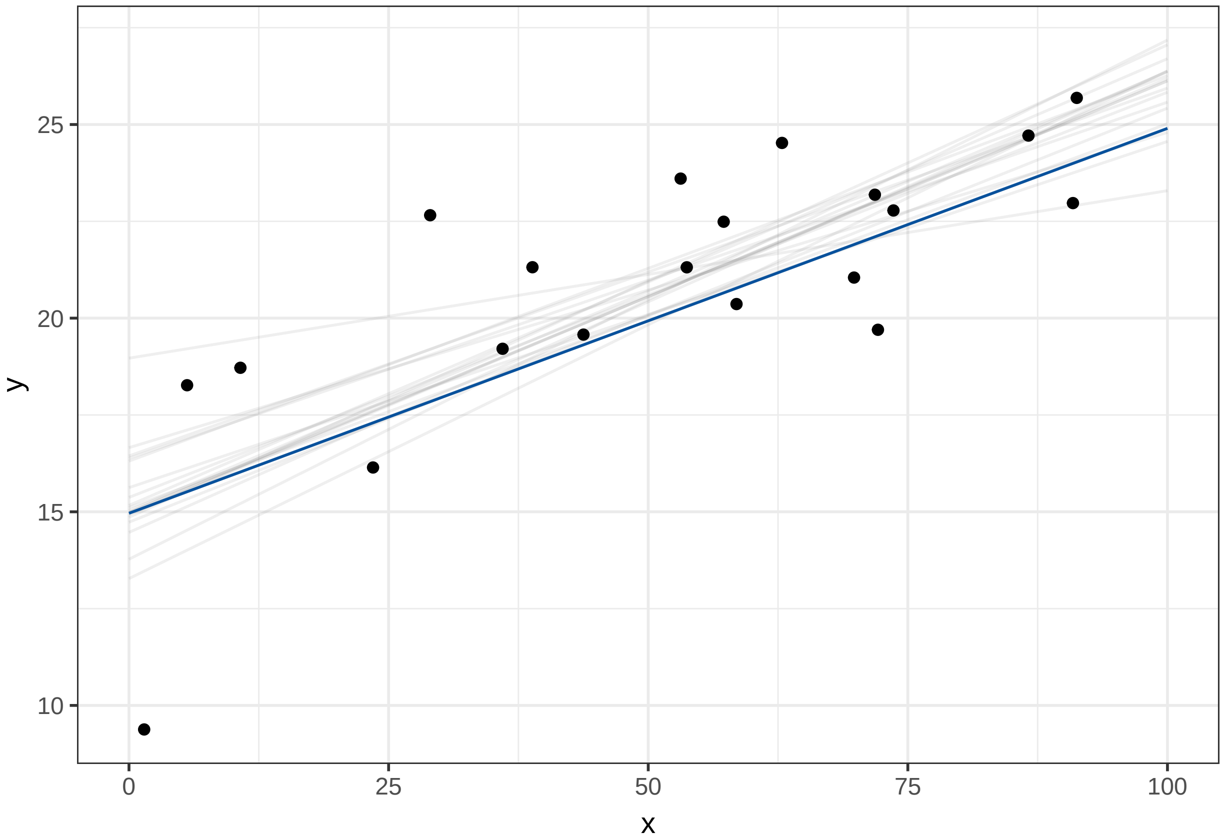

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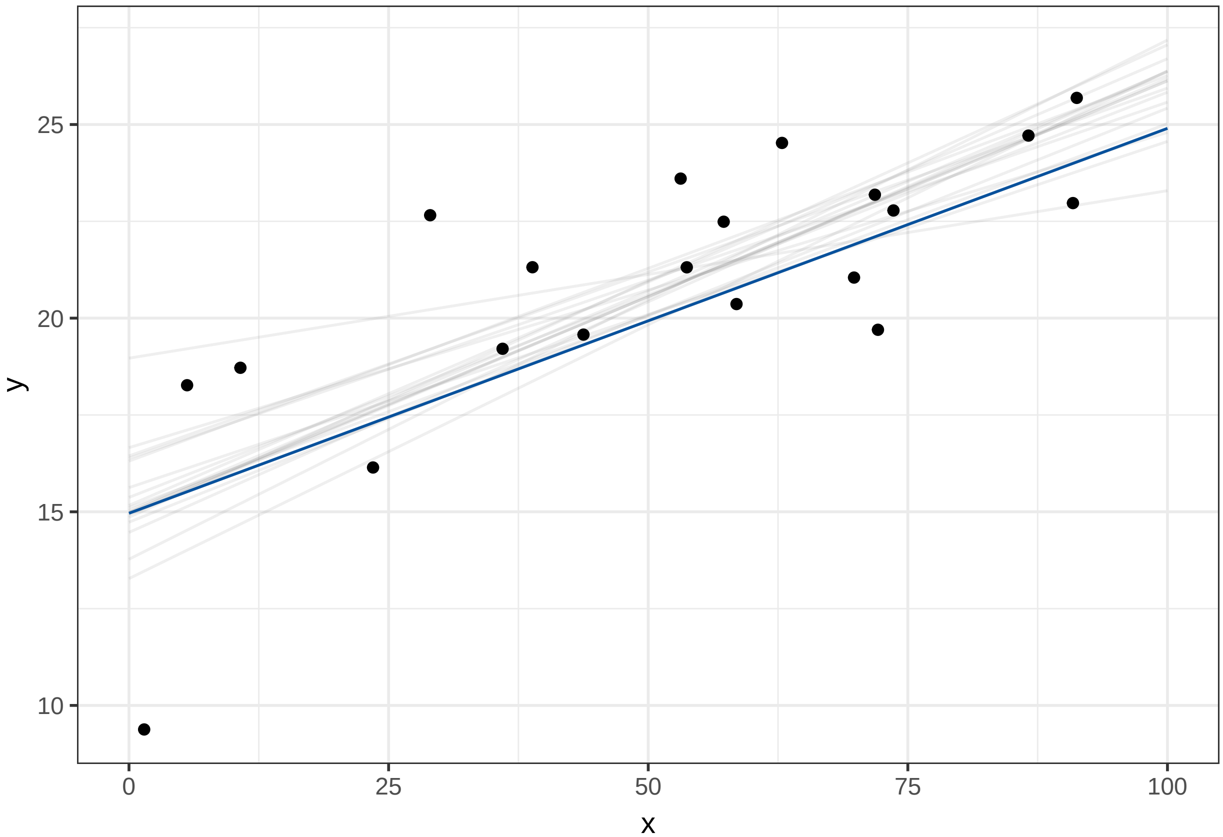

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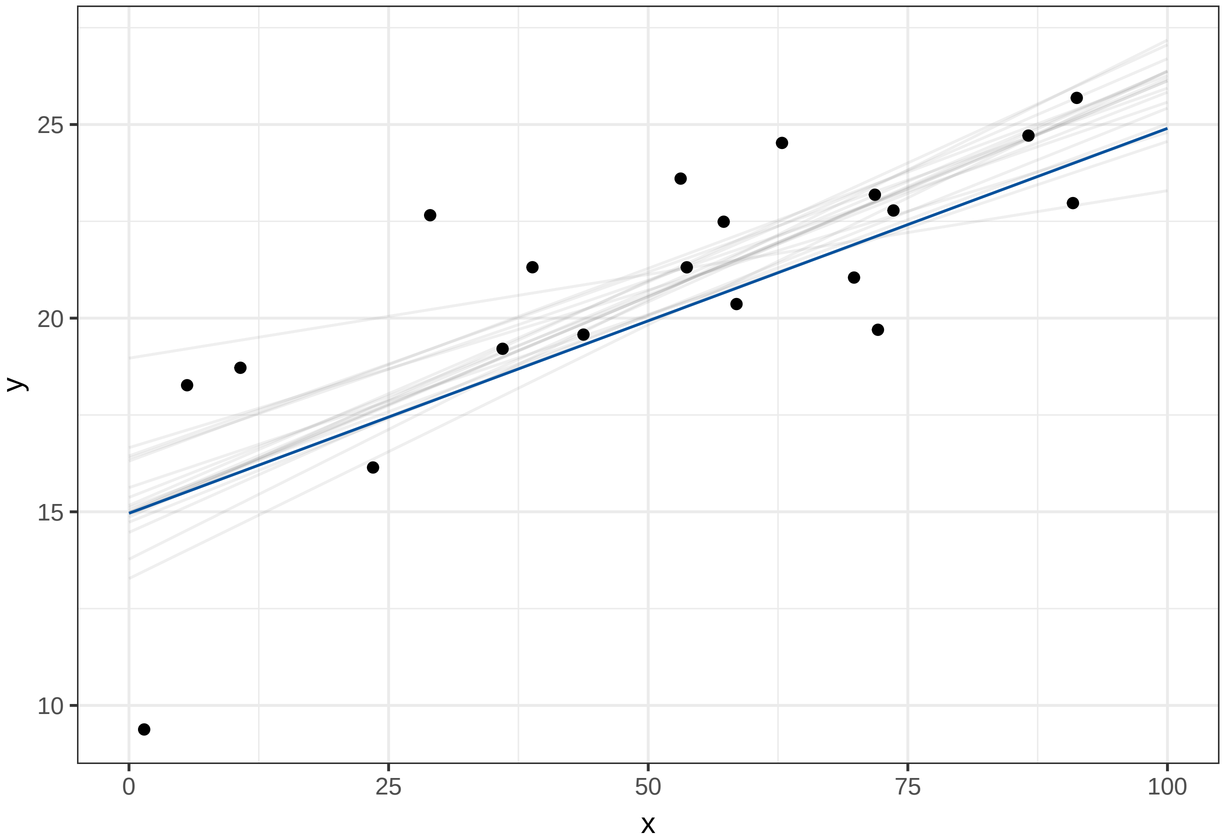

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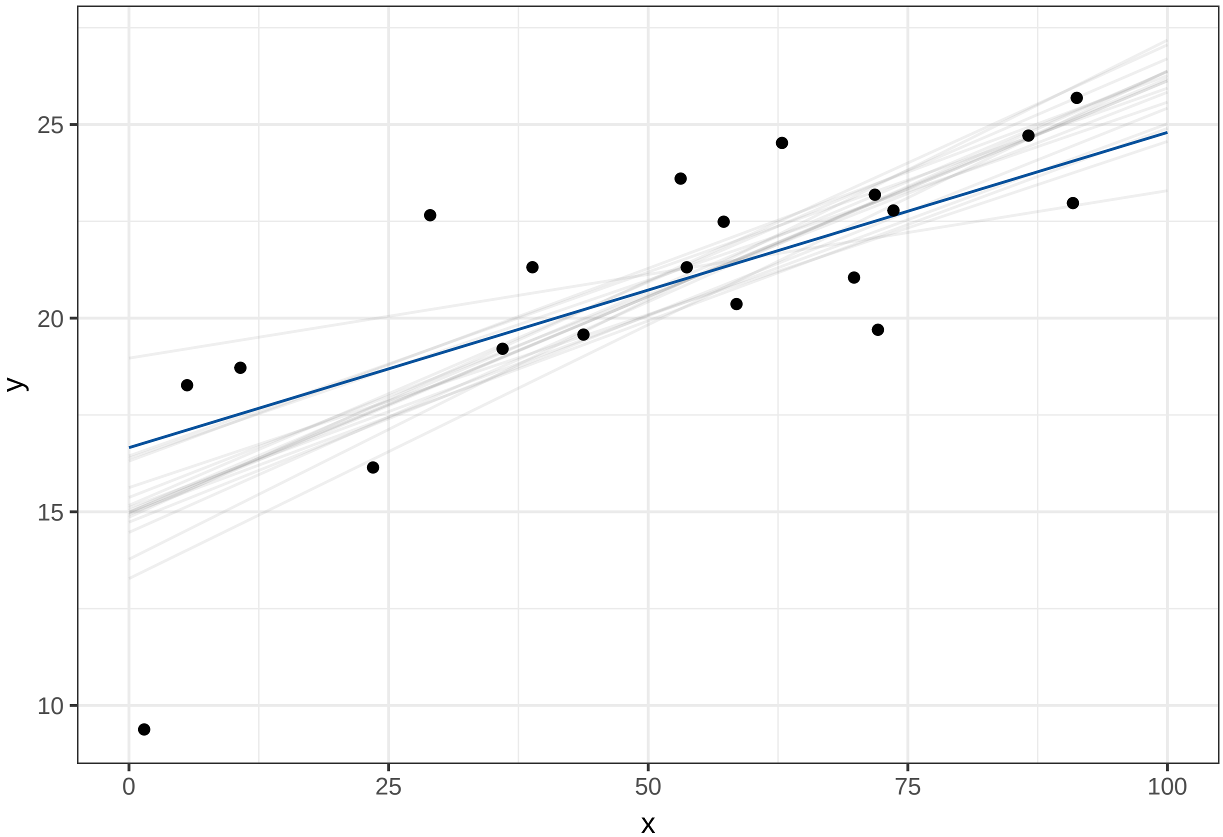
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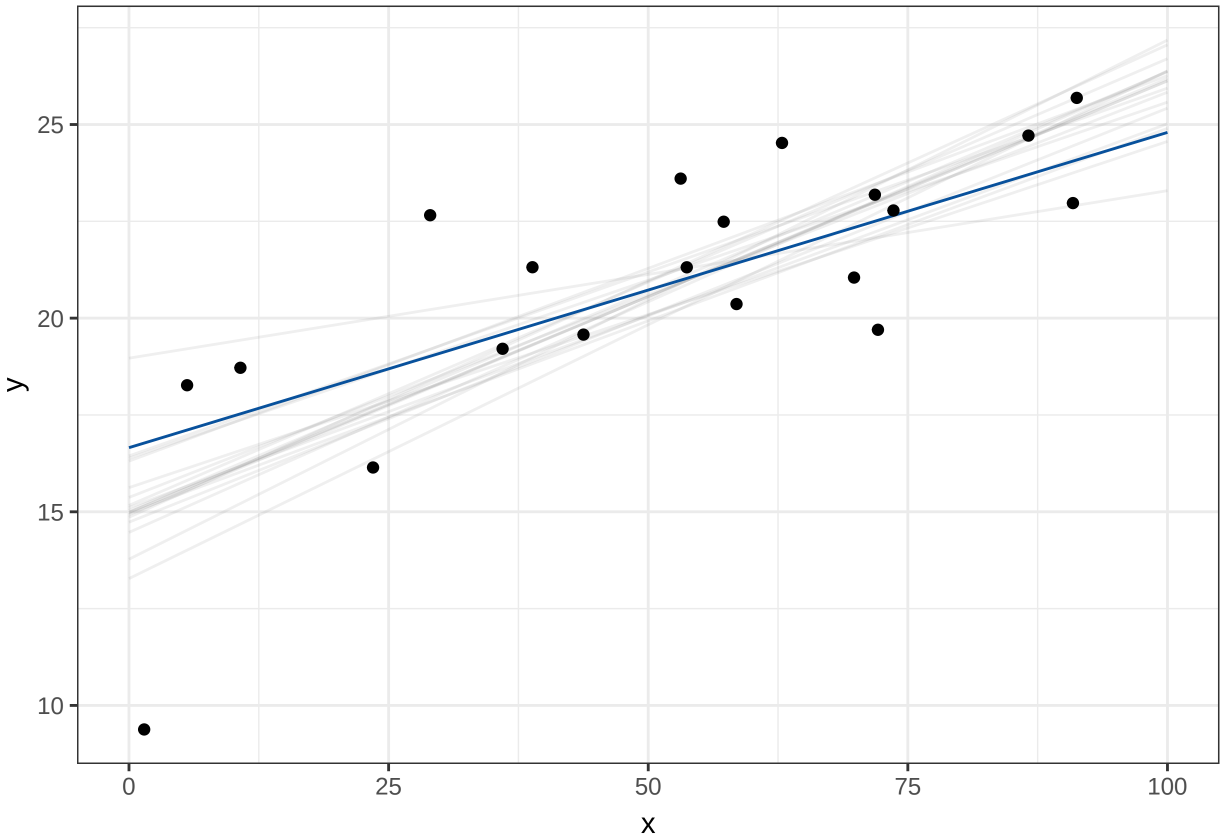
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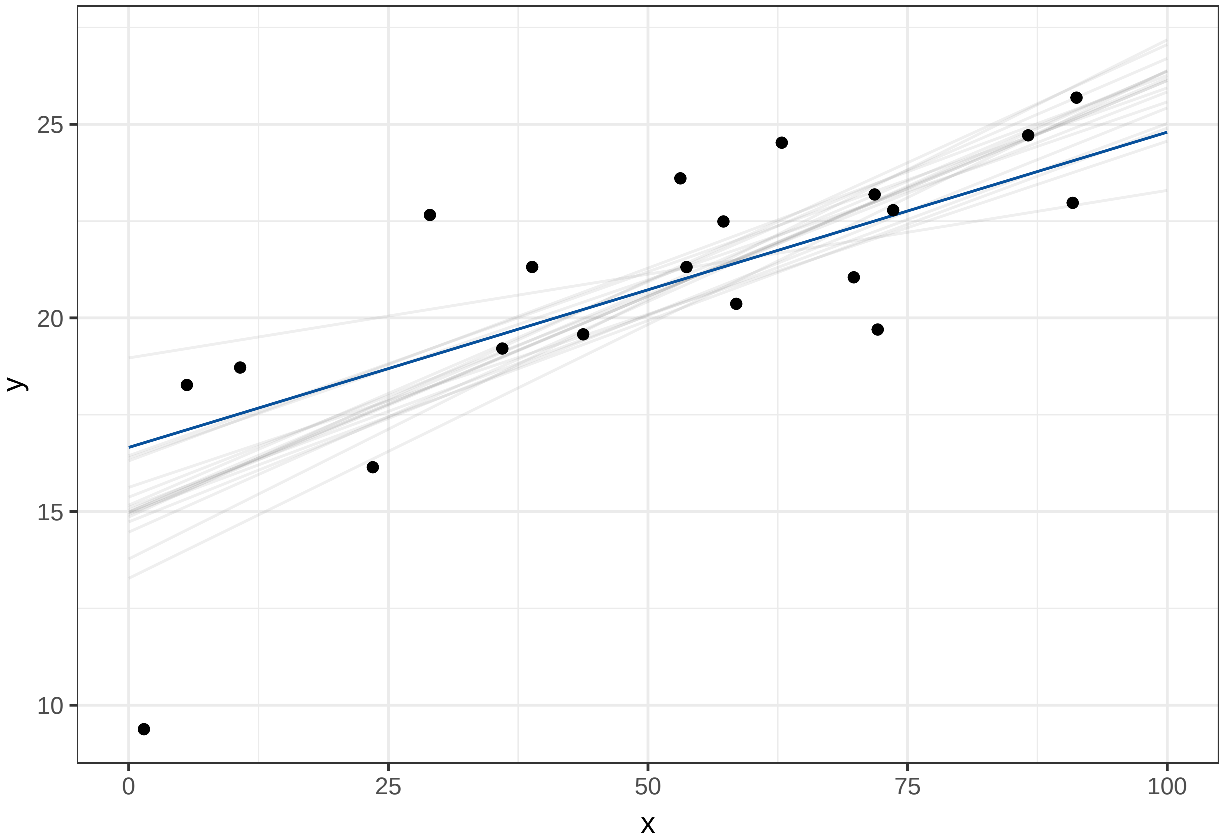

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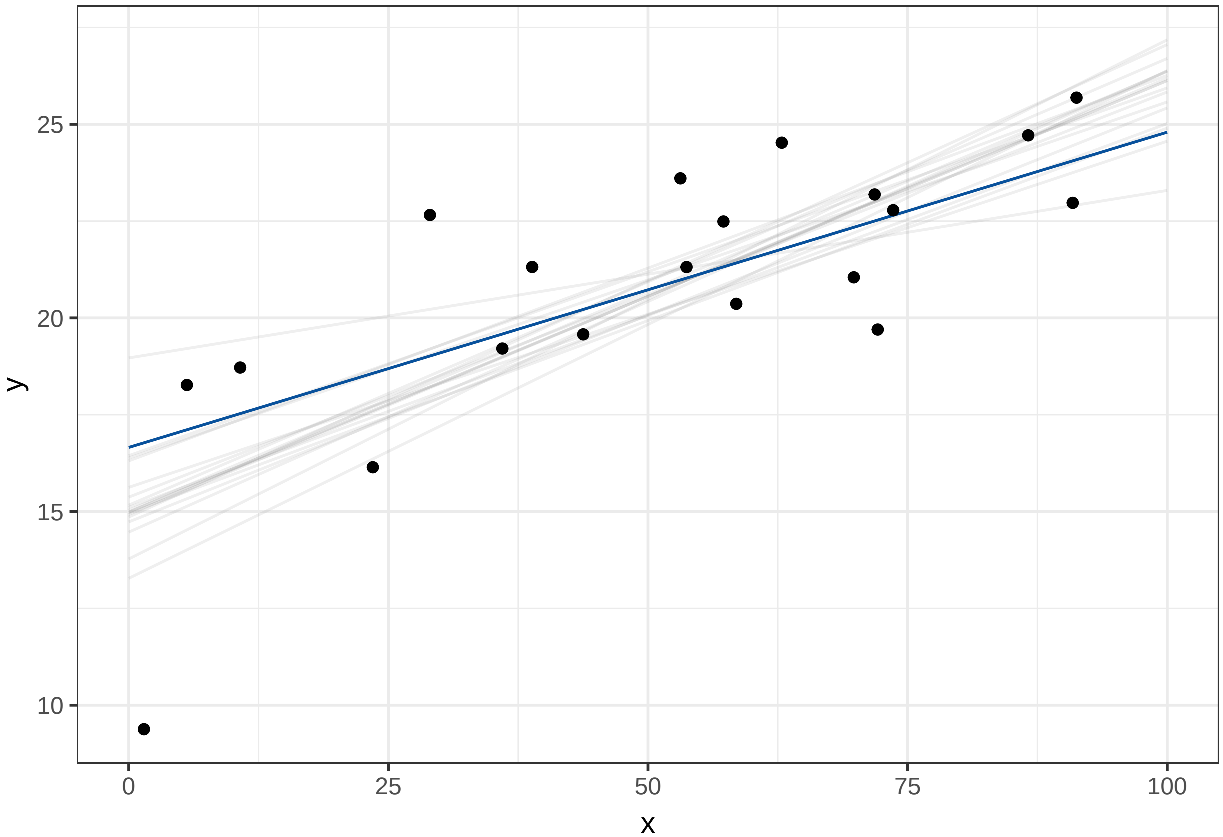

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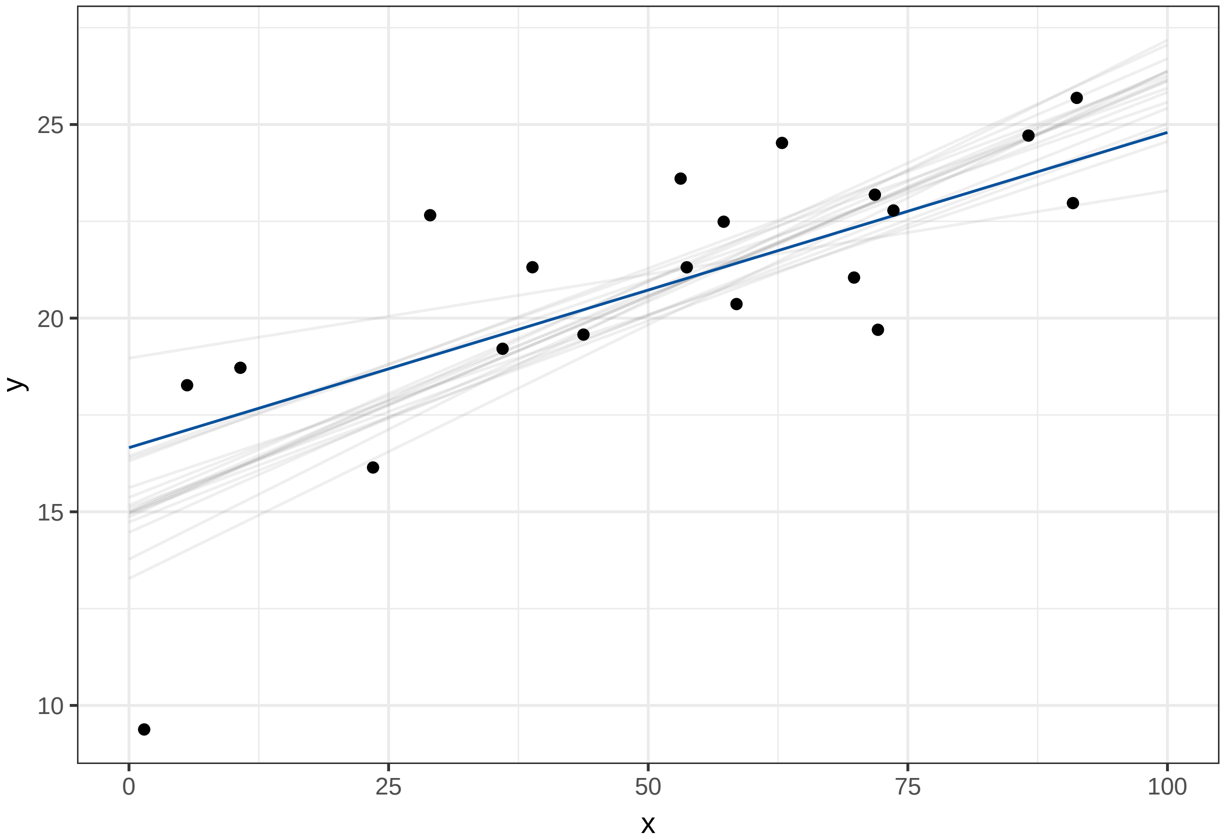

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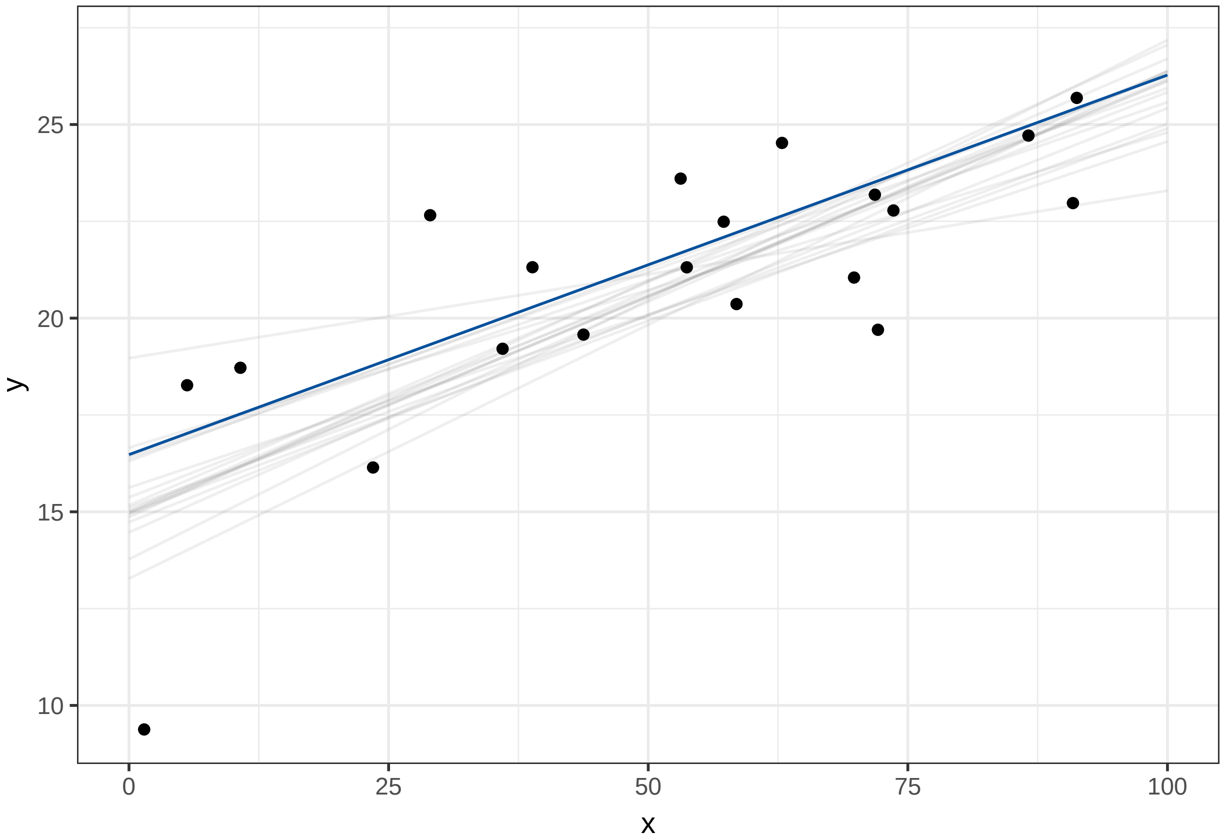

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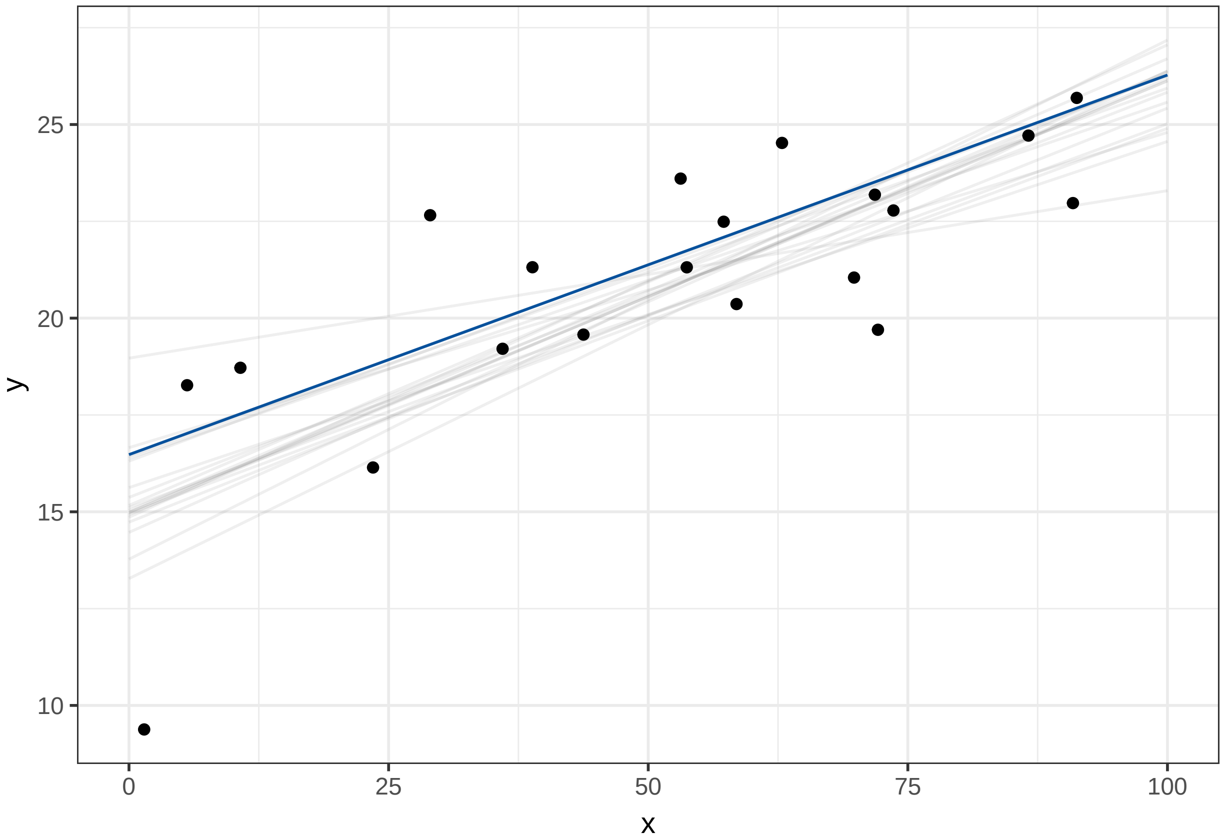

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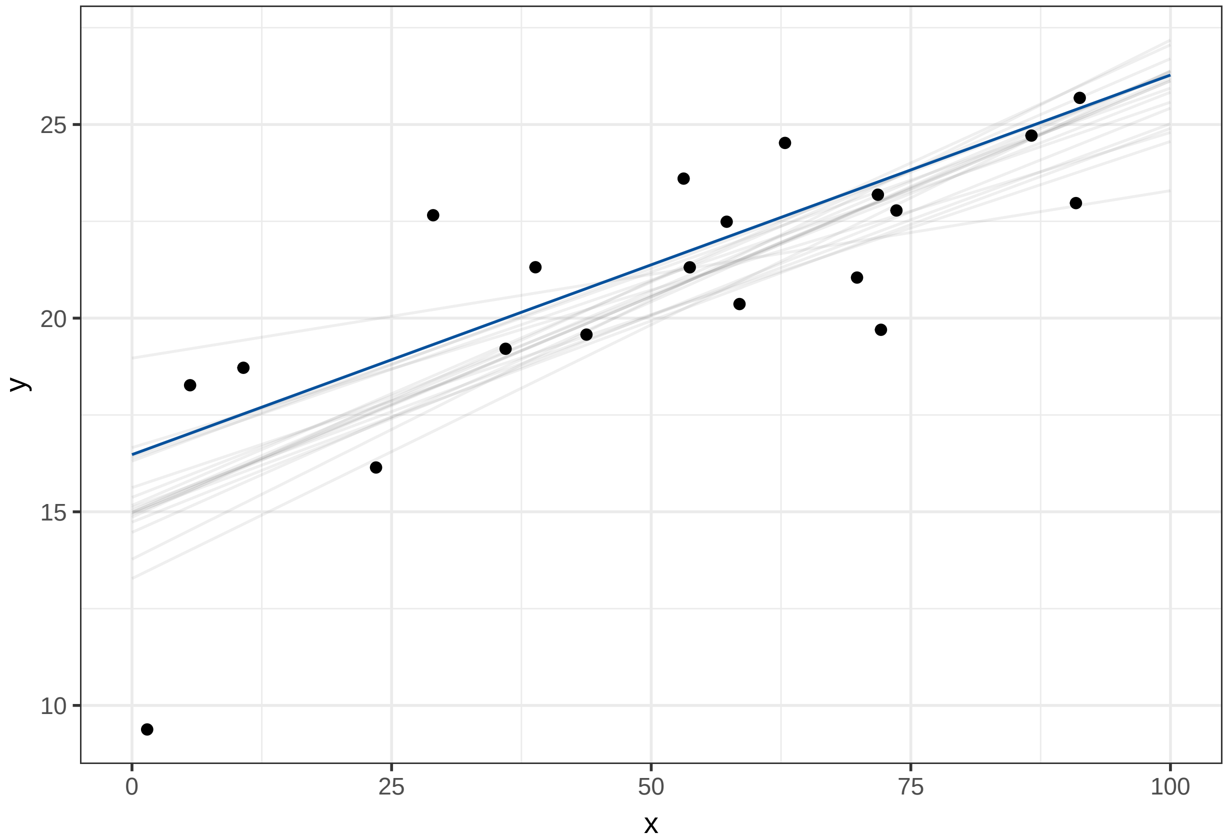

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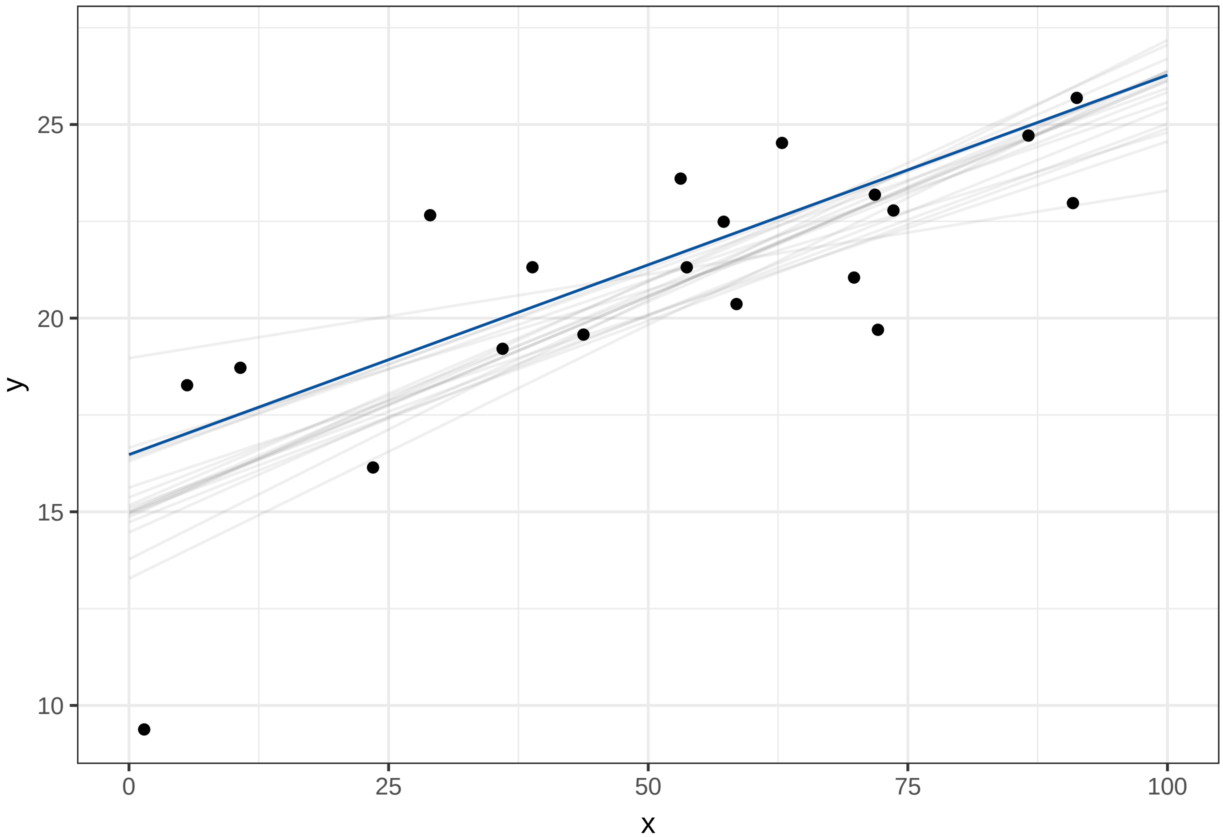


Monte Carlo simulation to generate model predictions given uncertainty quantified by Bayesian inference

Monte Carlo simulation can be used to evaluate the combined impact of parameter uncertainty on a prediction from the model.

Let us say we are interested in the value of y when x = 60.

Different ways to perform Monte Carlo simulation based on an MCMC sample from the posterior distribution of a Bayesian model

(1) summarise on the marginal distributions (and fit distributions to it) and sample from these to run the MC simulation

(2) plug in the MCMC sample into the MC simulation directly (useful to consider dependencies between parameters)

(3) generate the quantity of interest inside the MCMC sampling

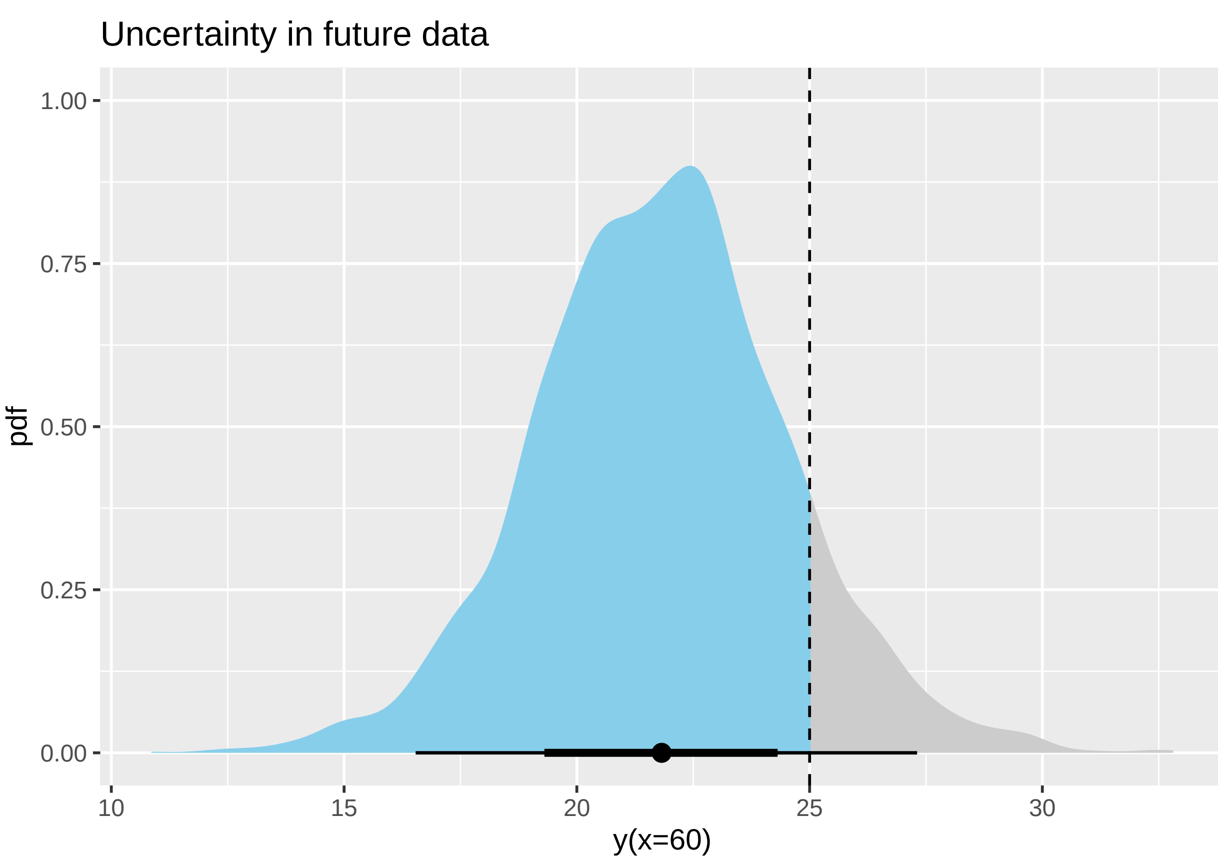
Illustrate uncertainty in future data using the predictive distribution

We want to characterise uncertainty in a potential future observation of y, which includes how data may vary around the model and uncertainty about the model.

```r
## derive quantity of interest from the posterior sample
a <- mcmc_sample[,"a"]
b <- mcmc_sample[,"b"]
sigma <- mcmc_sample[,"sigma"]
x <- 60
y_mc <- unlist(lapply(1:nrow(mcmc_sample),function(i){
  a[i]+b[i]*(x-50)/50 + rnorm(1,0,sigma[i])}))

df_y <- data.frame(y = y_mc, gr = y<25)

##plot prob density for Y
ggplot(df_y,aes(x = y,fill = stat(x < 25))) +
 stat_halfeye() +
  geom_vline(xintercept = c(25), linetype = "dashed") +
  scale_fill_manual(values = c("gray80", "skyblue")) +
  ylab('pdf') +
  xlab('y(x=60)') +
  theme(legend.position='none') +
  ggtitle('Uncertainty in future data')
```



Illustrate uncertainty in future value using the 2-dimensional distribution

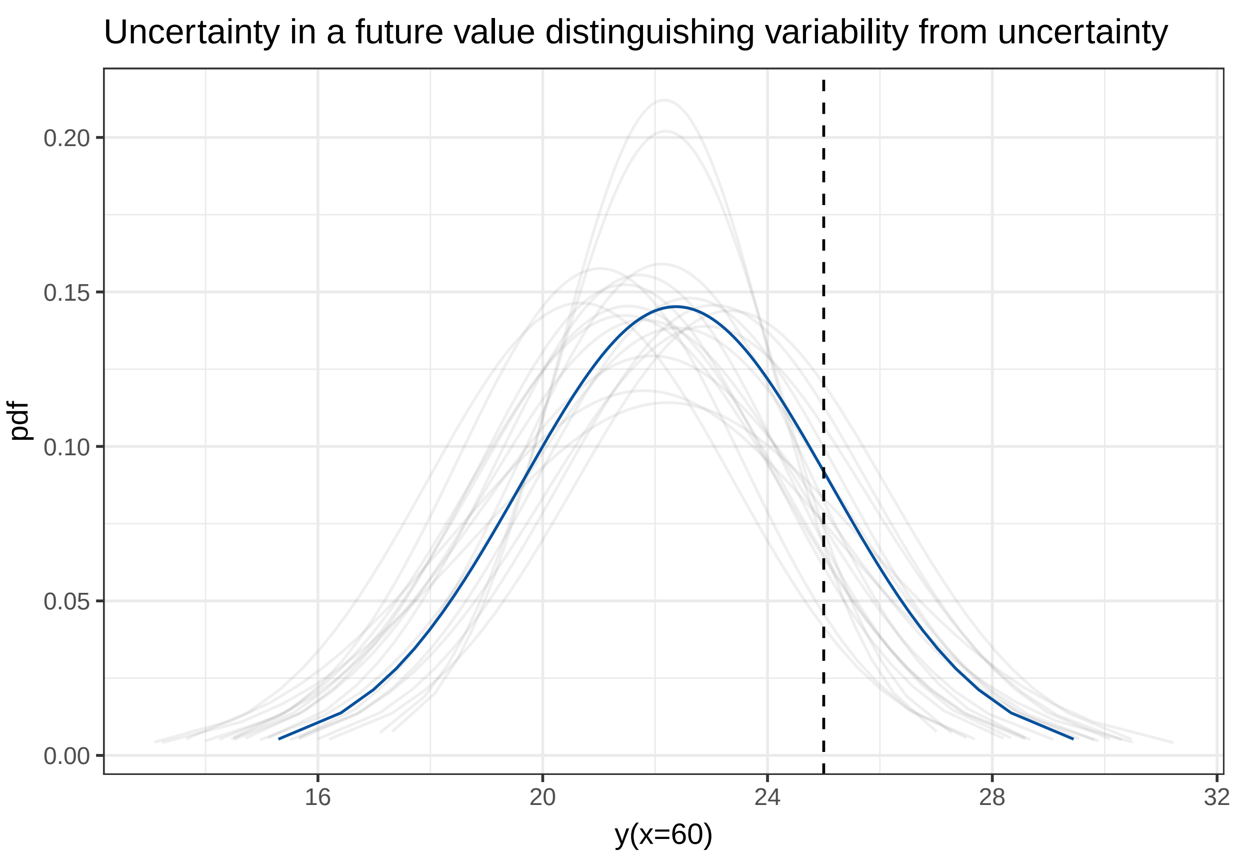
Consider that we are interested in how variable y varies. If so, we can illustrate uncertainty about this variability by propagating uncertainty distinguishing variability from uncertainty. This is done using 2-

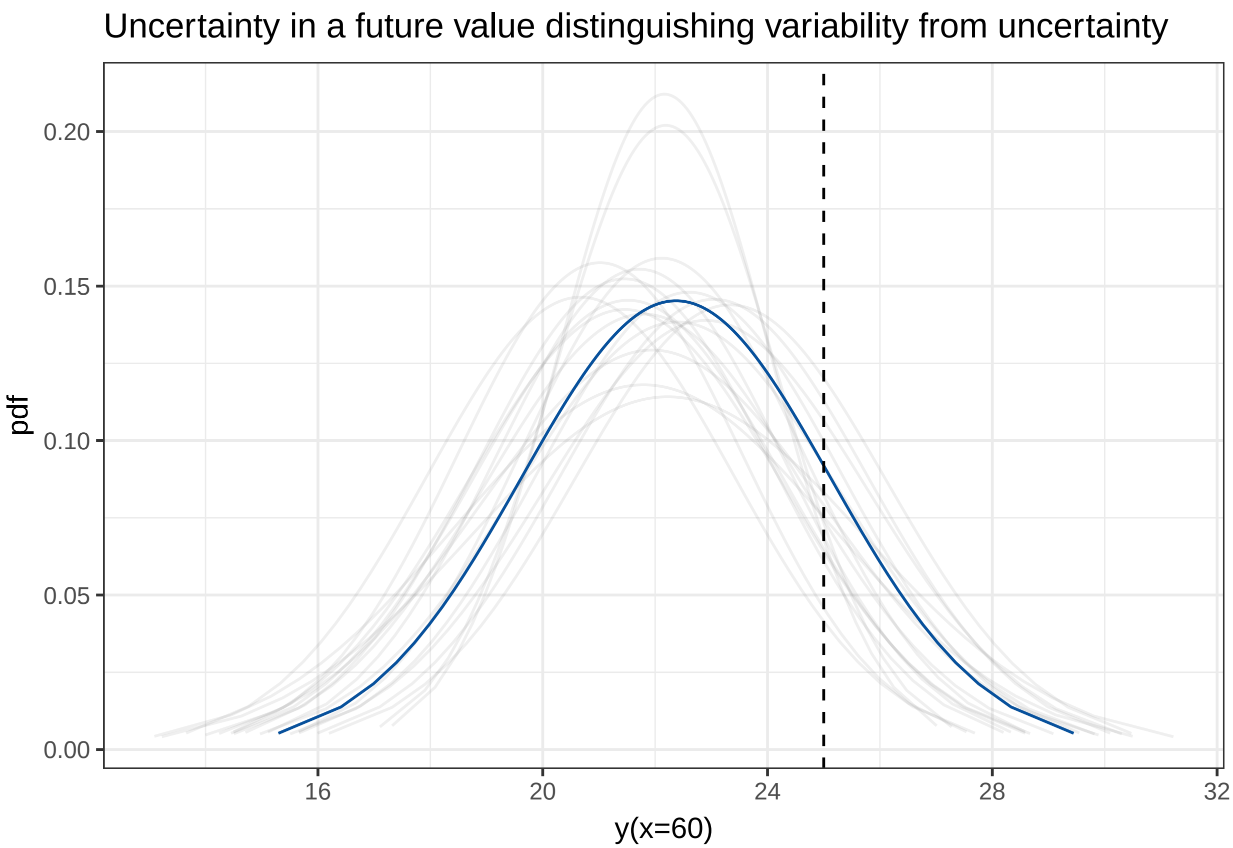
dimenstional Monte Carlo simulation. The resulting graph is describing a 2-D distribution or a spaghetti plot.

```
## derive quantity of interest from the posterior sample
y_sample_draws <- do.call('rbind',lapply(1:20,function(j){
  i <- sample.int(nrow(mcmc_sample),1)
  x <- 60
  pp <- ppoints(100)
  qq <- qnorm(pp,mcmc_sample[i,"a"] + (x-50)/50 * mcmc_sample[i,"b"],mcmc_sample[i,"sigma"])

data.frame(pdf=dnorm(qq,mcmc_sample[i,"a"] + (x-50)/50 * mcmc_sample[i,"b"],mcmc_sample[i,"sigma"]),
           q=qq,draw=j)
}))

ggplot(y_sample_draws,aes(x = q,y = pdf)) +
  geom_line(aes(group = draw), color = "#08519C") +
  geom_vline(xintercept = c(25), linetype = "dashed") +
  ylab('pdf') +
  xlab('y(x=60)') +
  theme(legend.position='none') +
  theme_bw() +
  transition_states(draw, 0, 0.2) +
  shadow_mark(past = TRUE, future = TRUE, alpha = 1/8, color = "gray50")+
  ggtitle('Uncertainty in a future value distinguishing variability from uncertainty')
```

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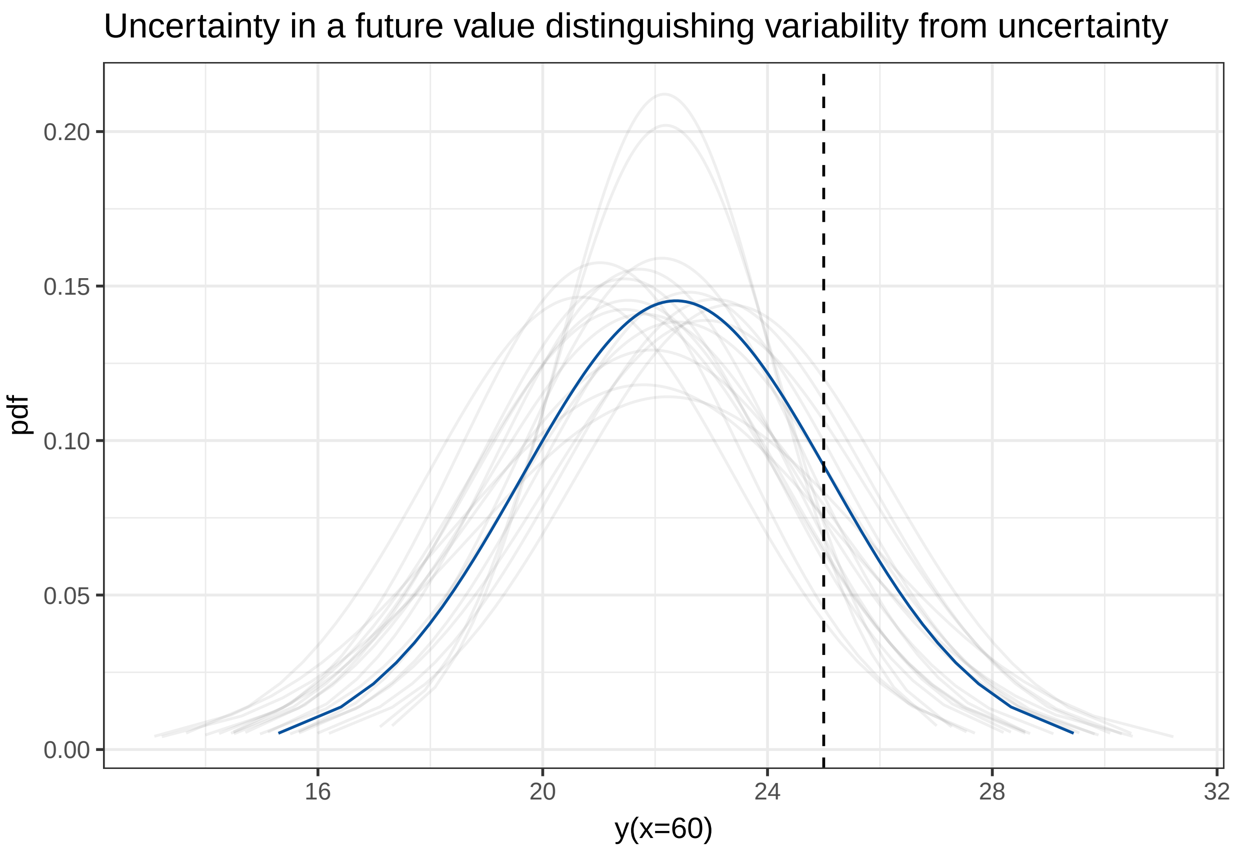
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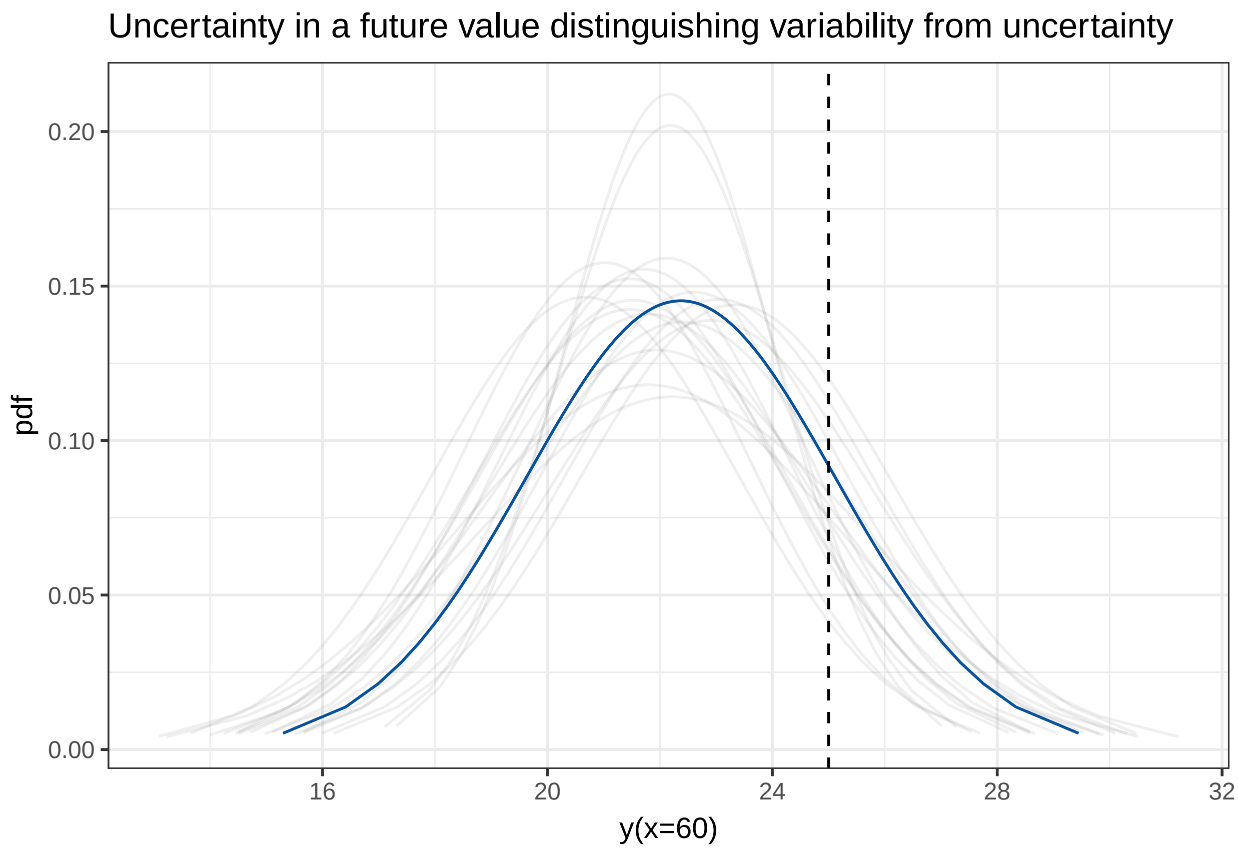
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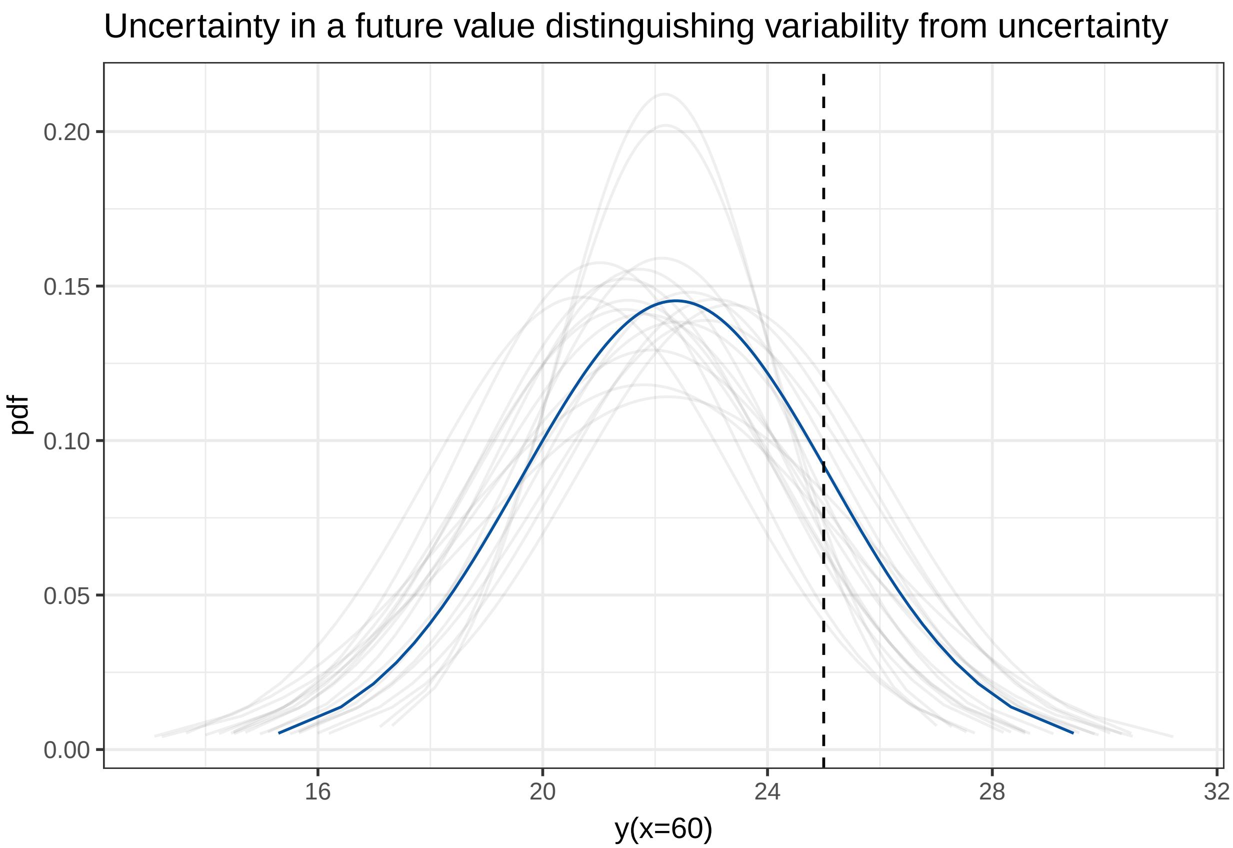
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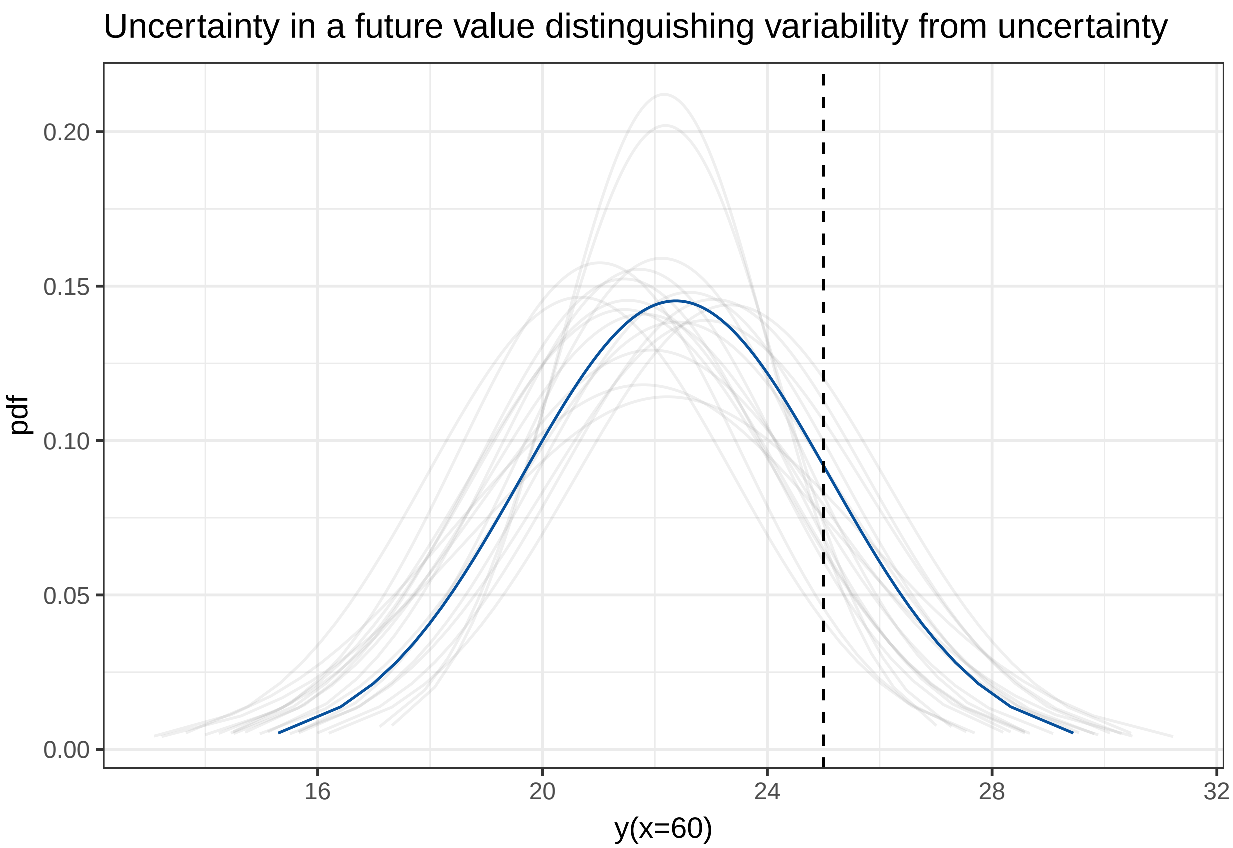
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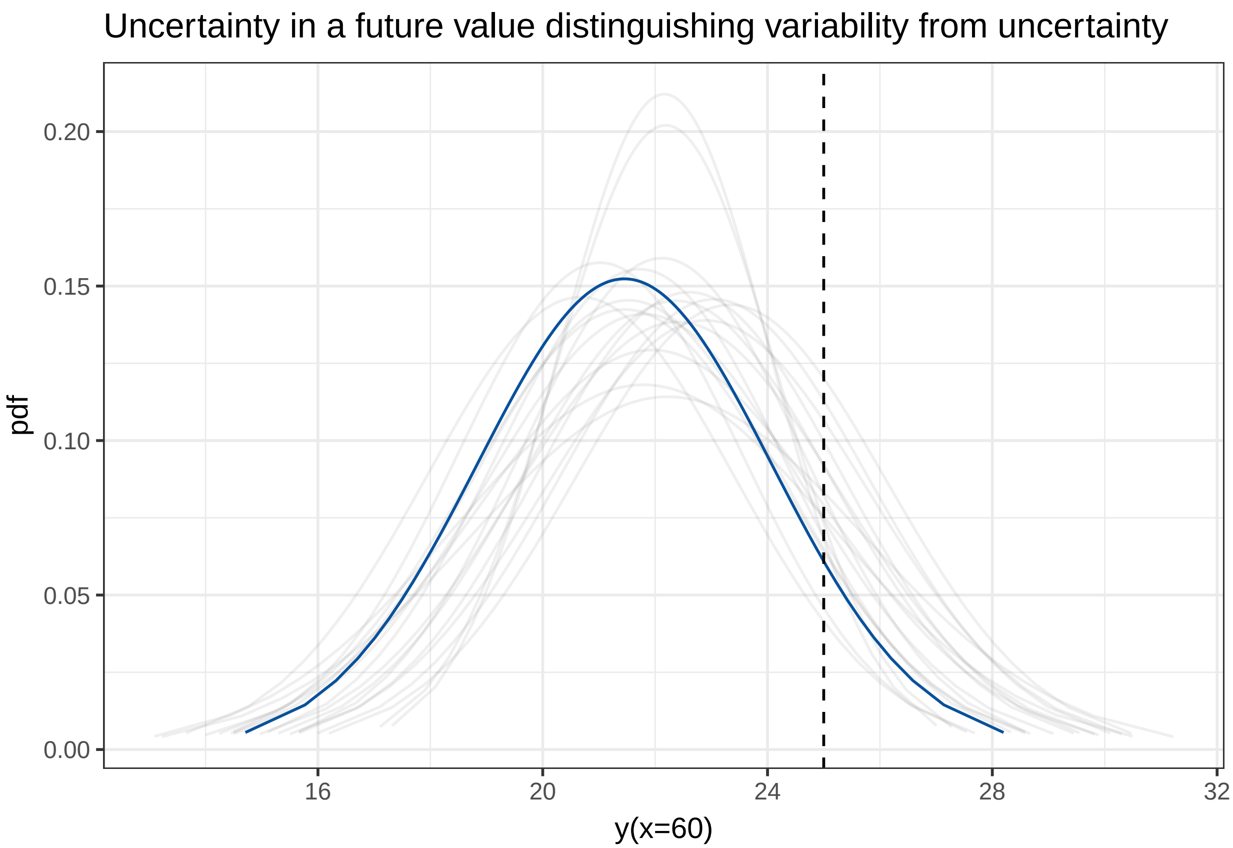

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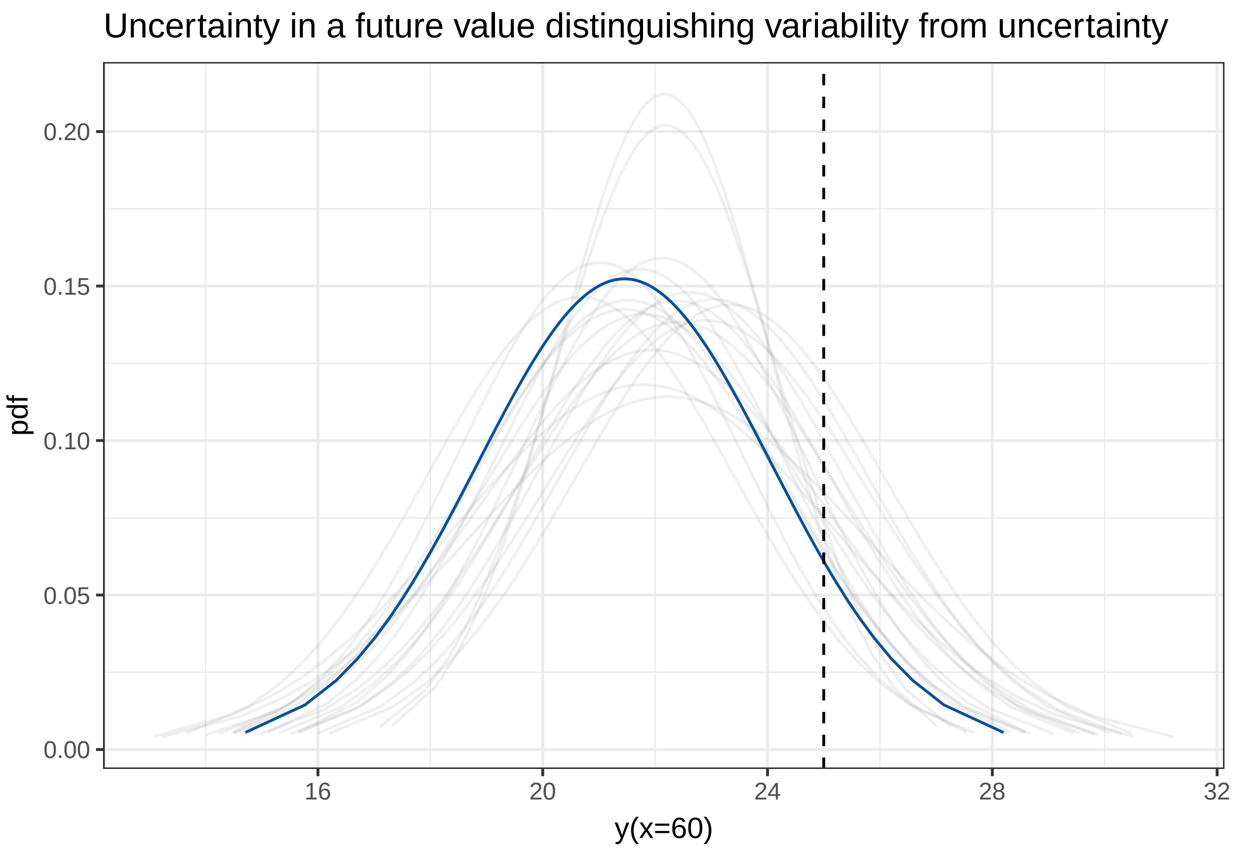
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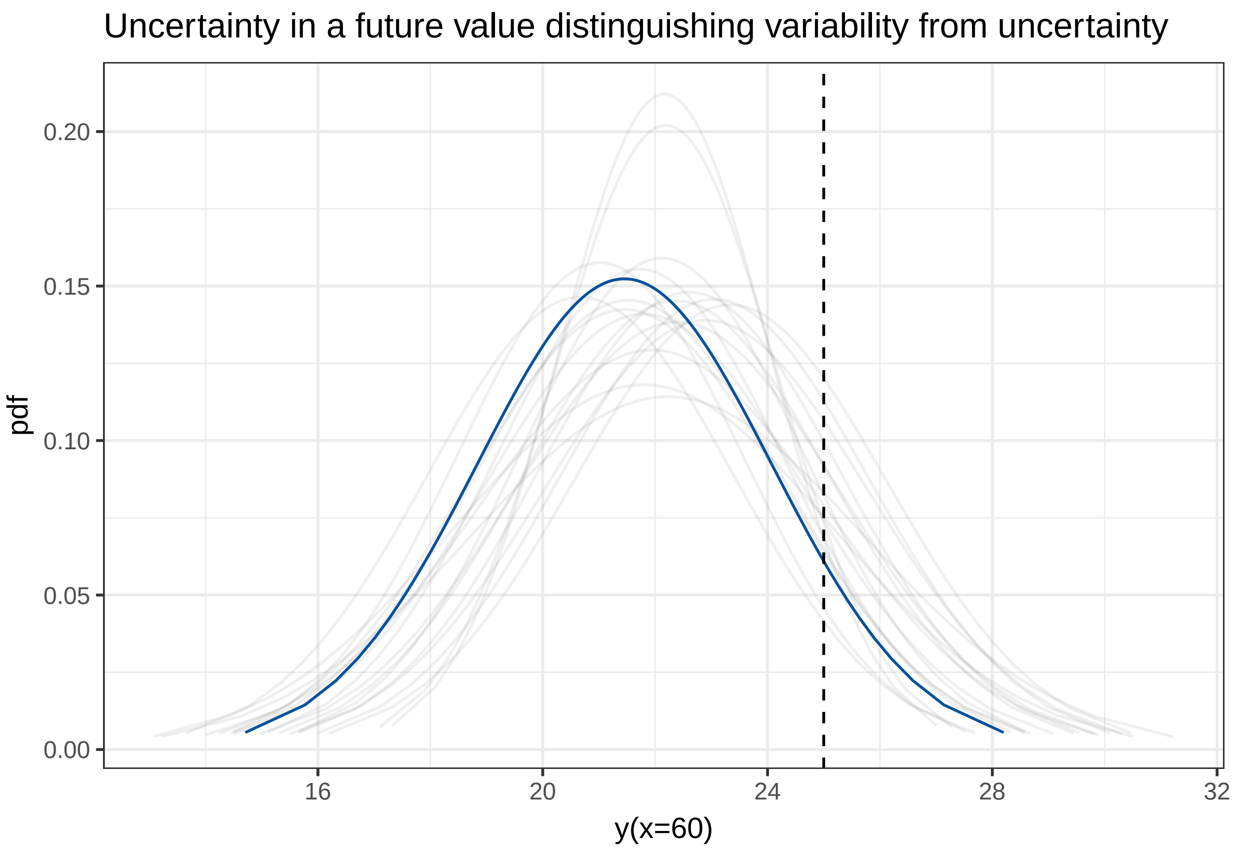
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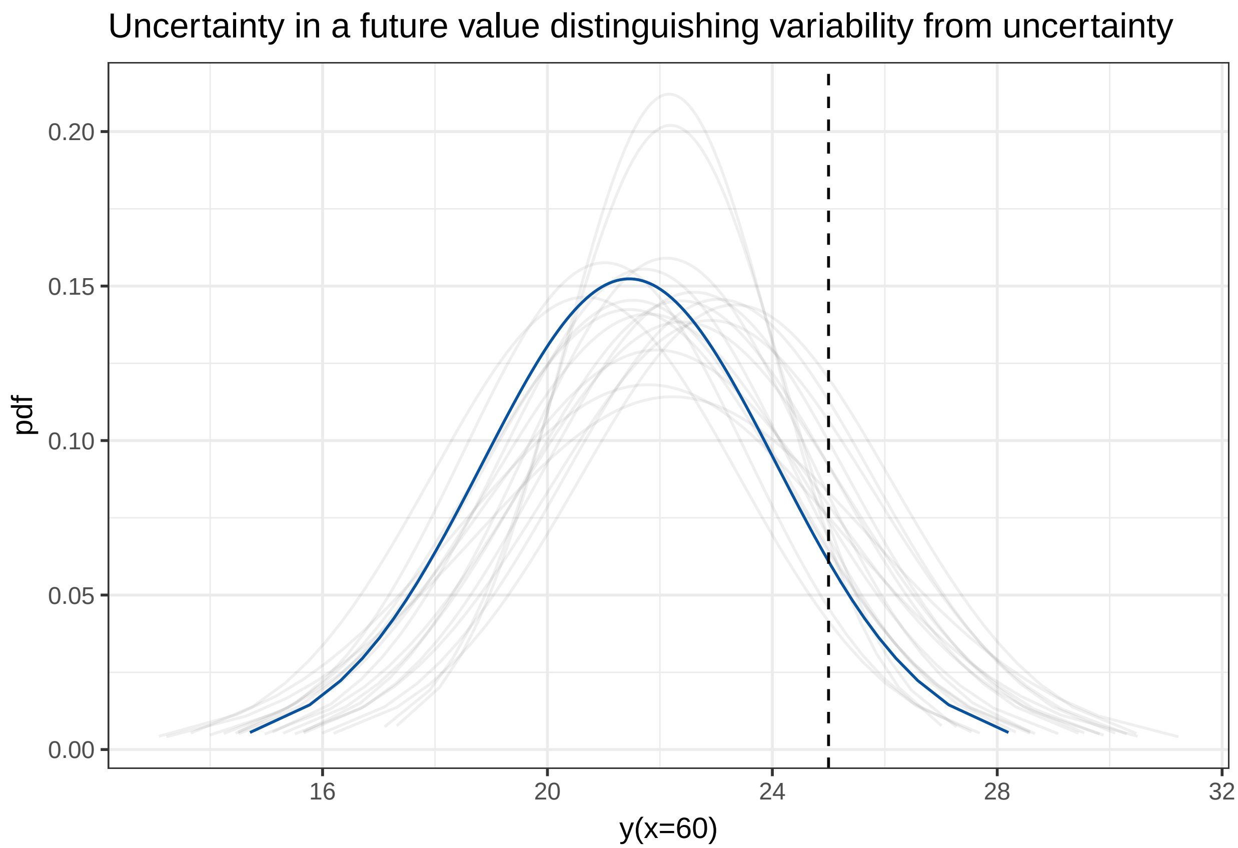
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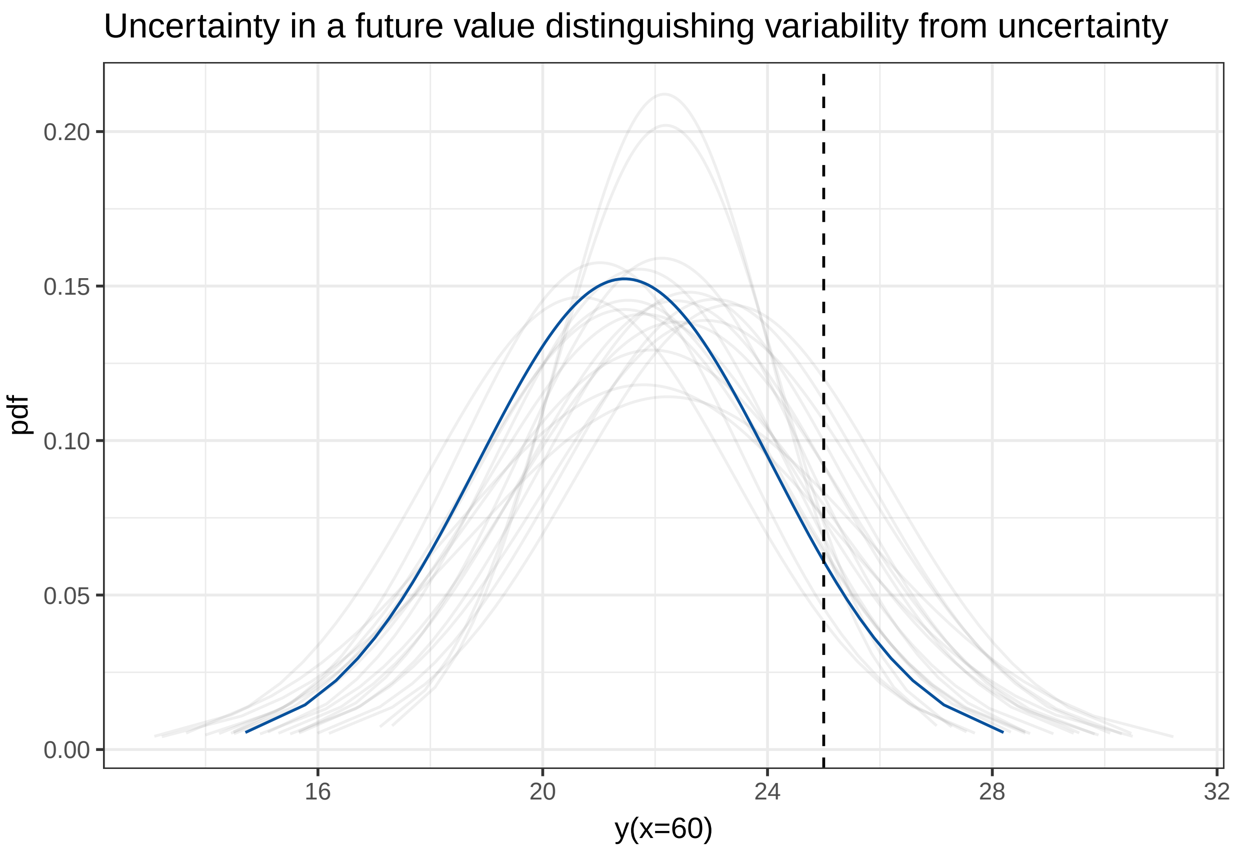

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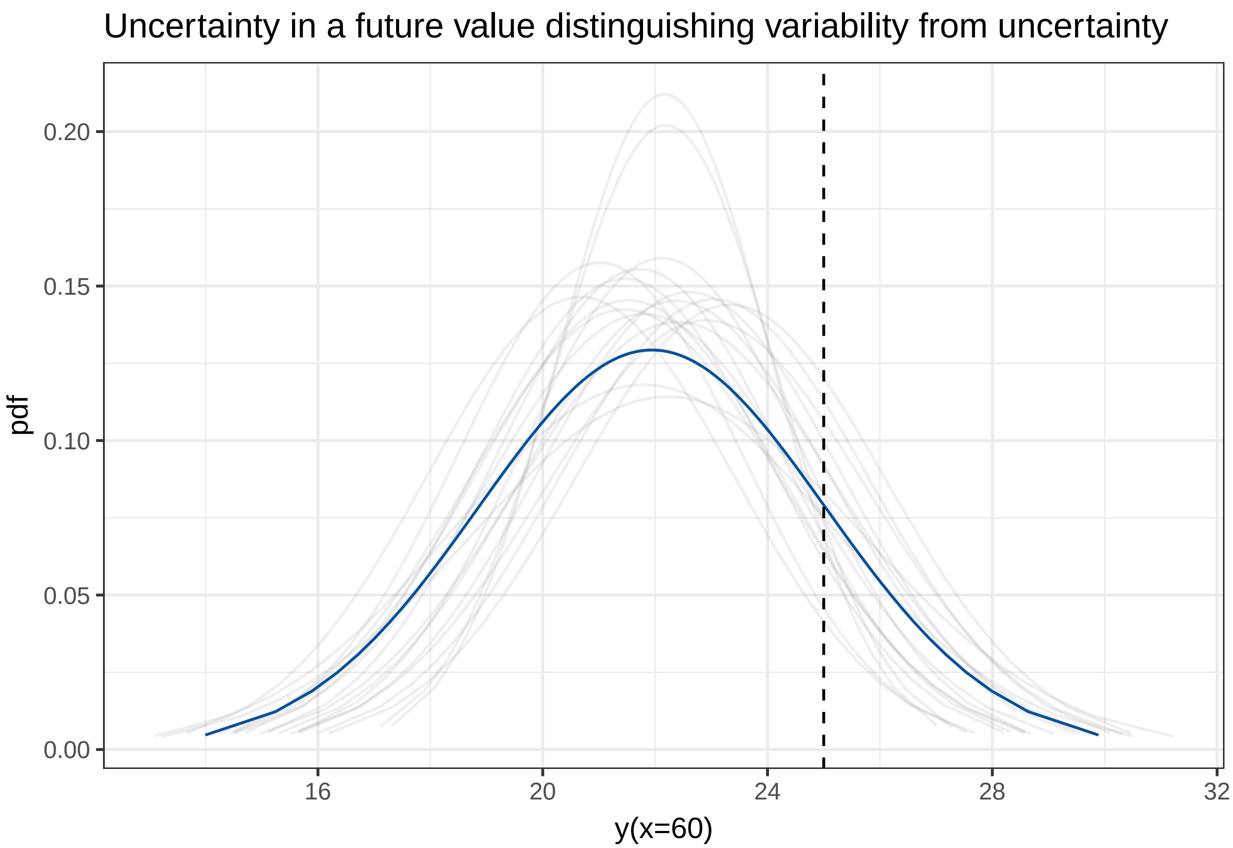
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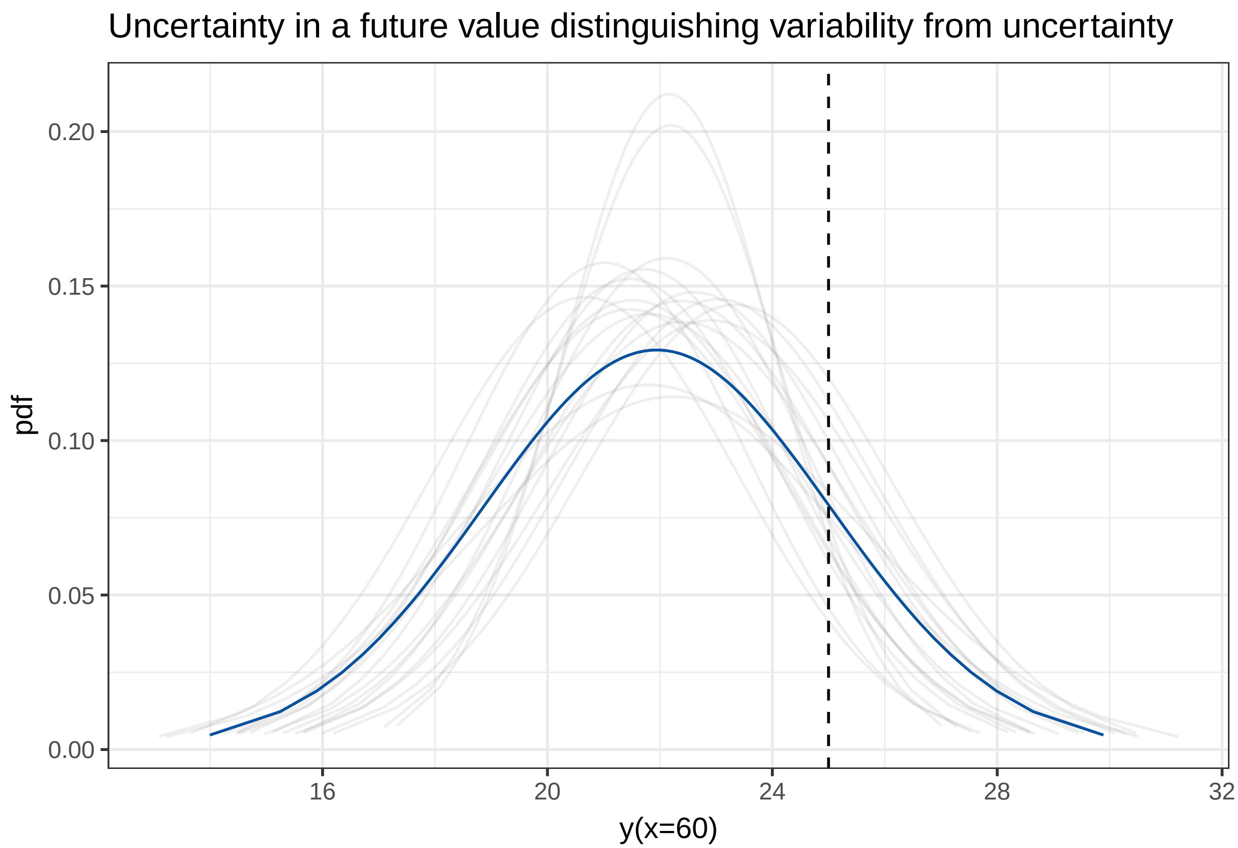
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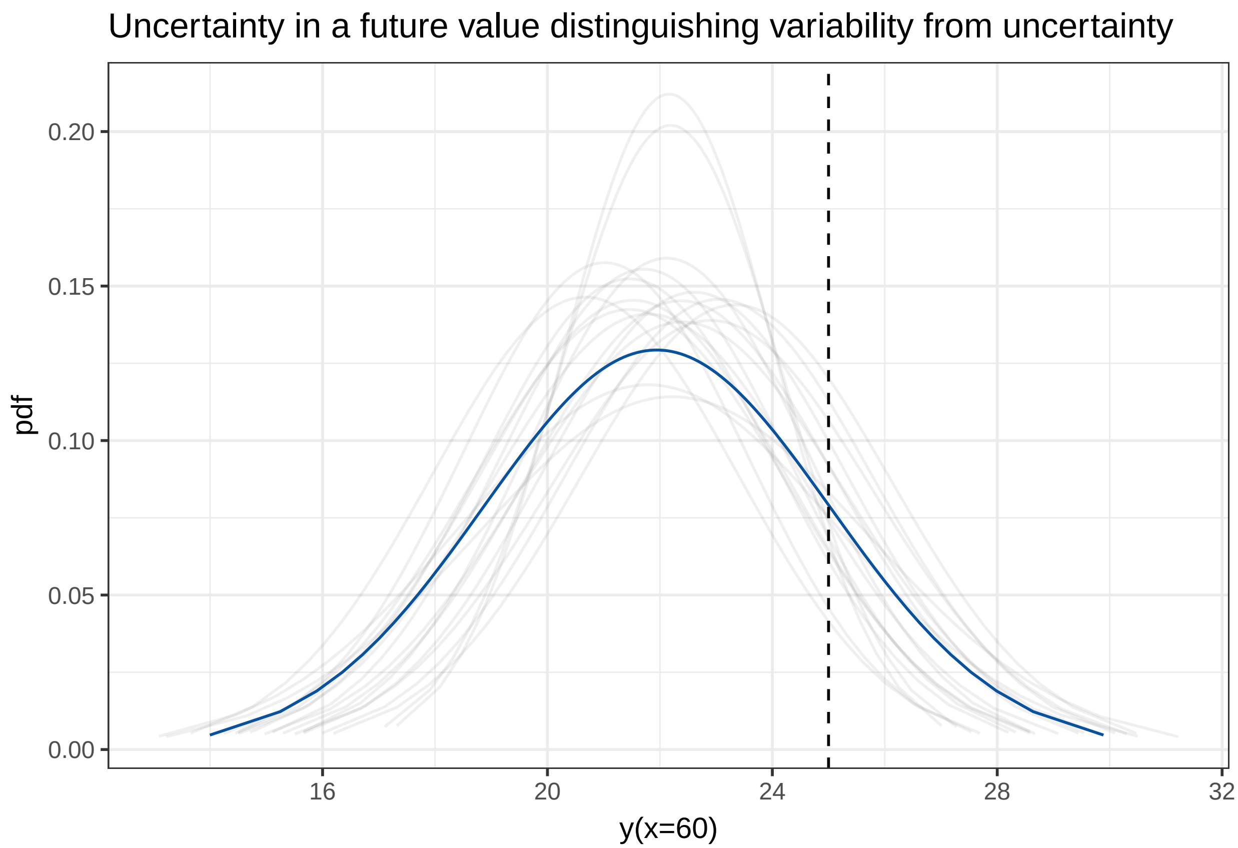

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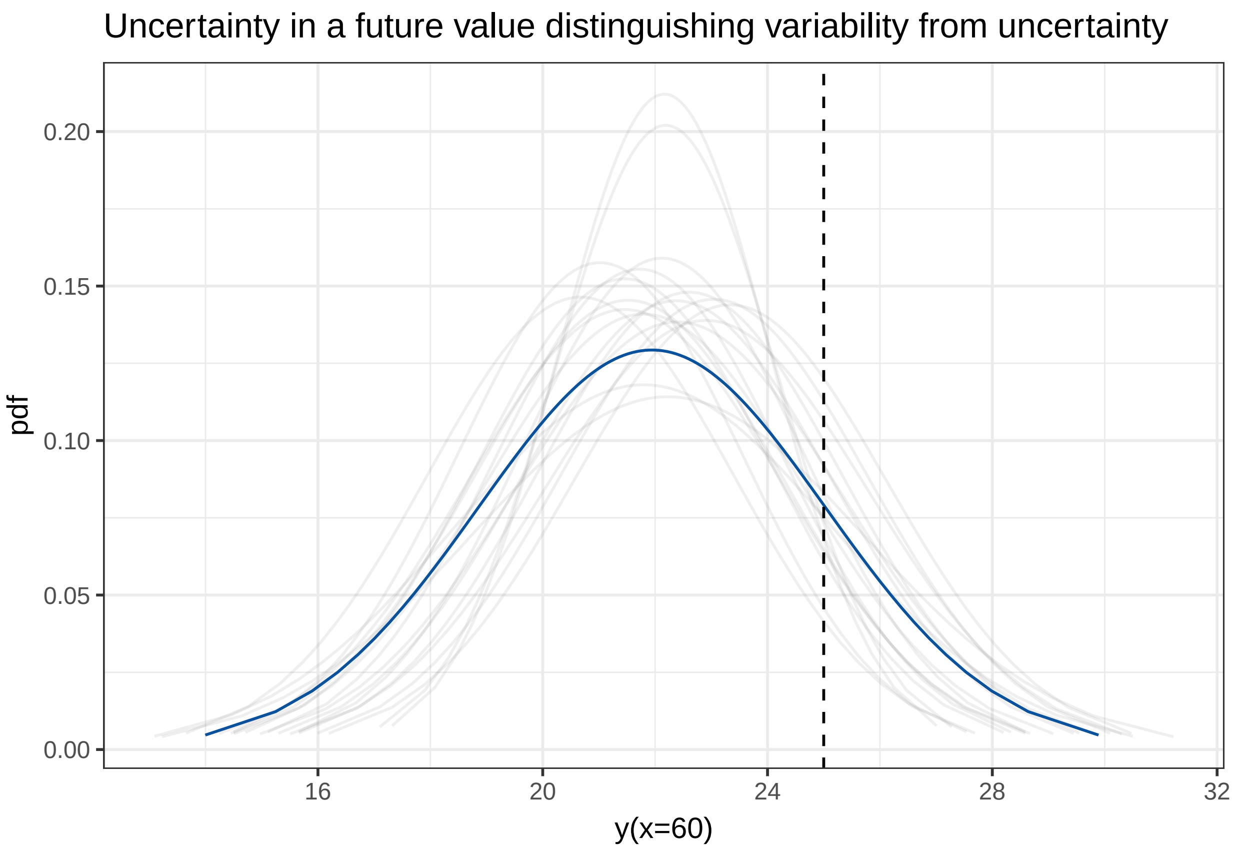
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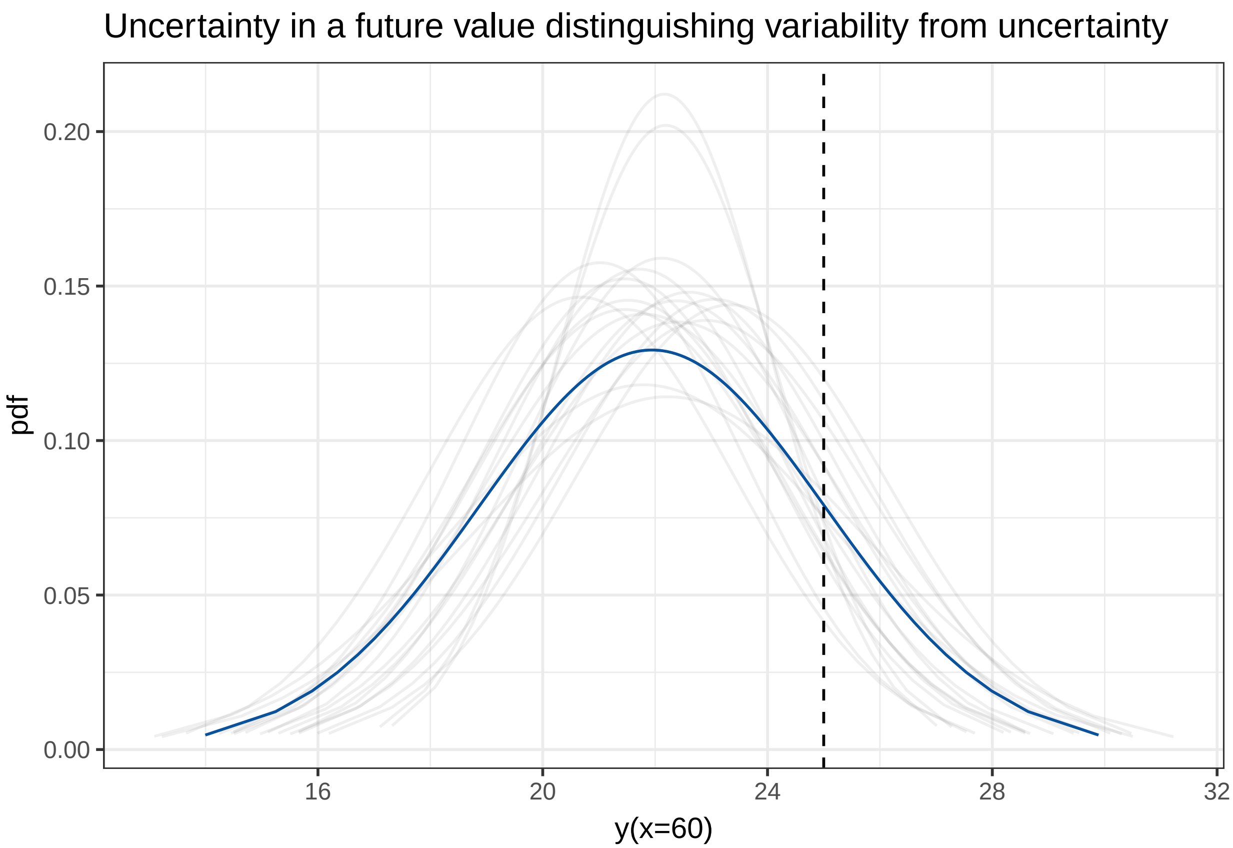
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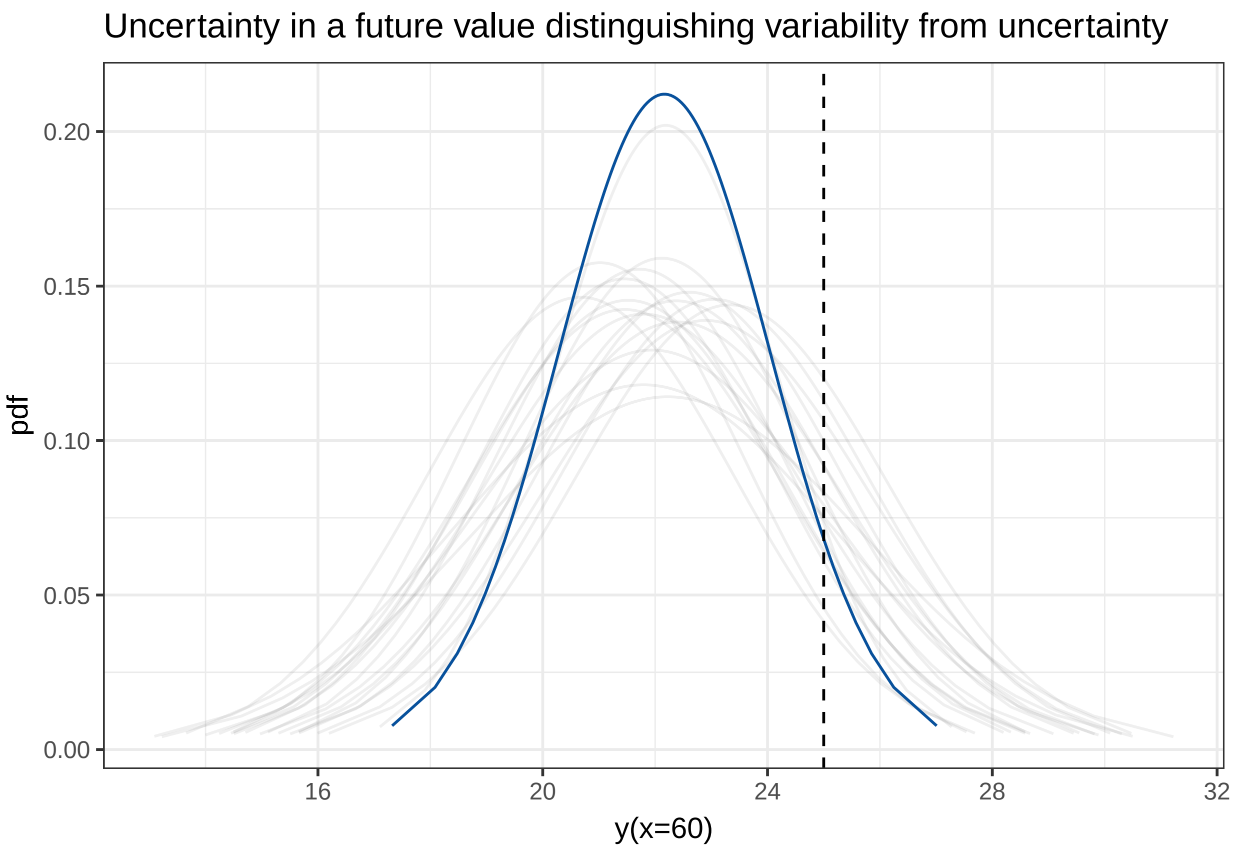

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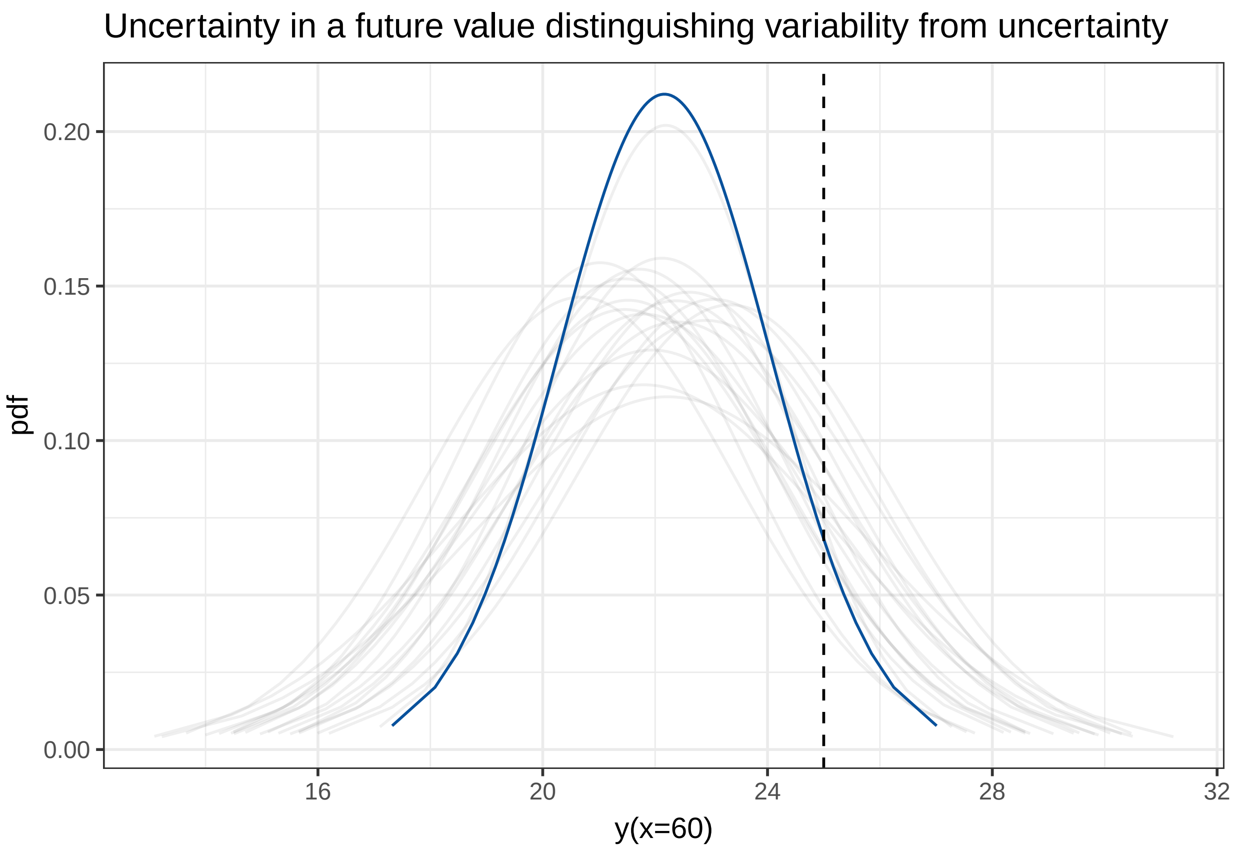
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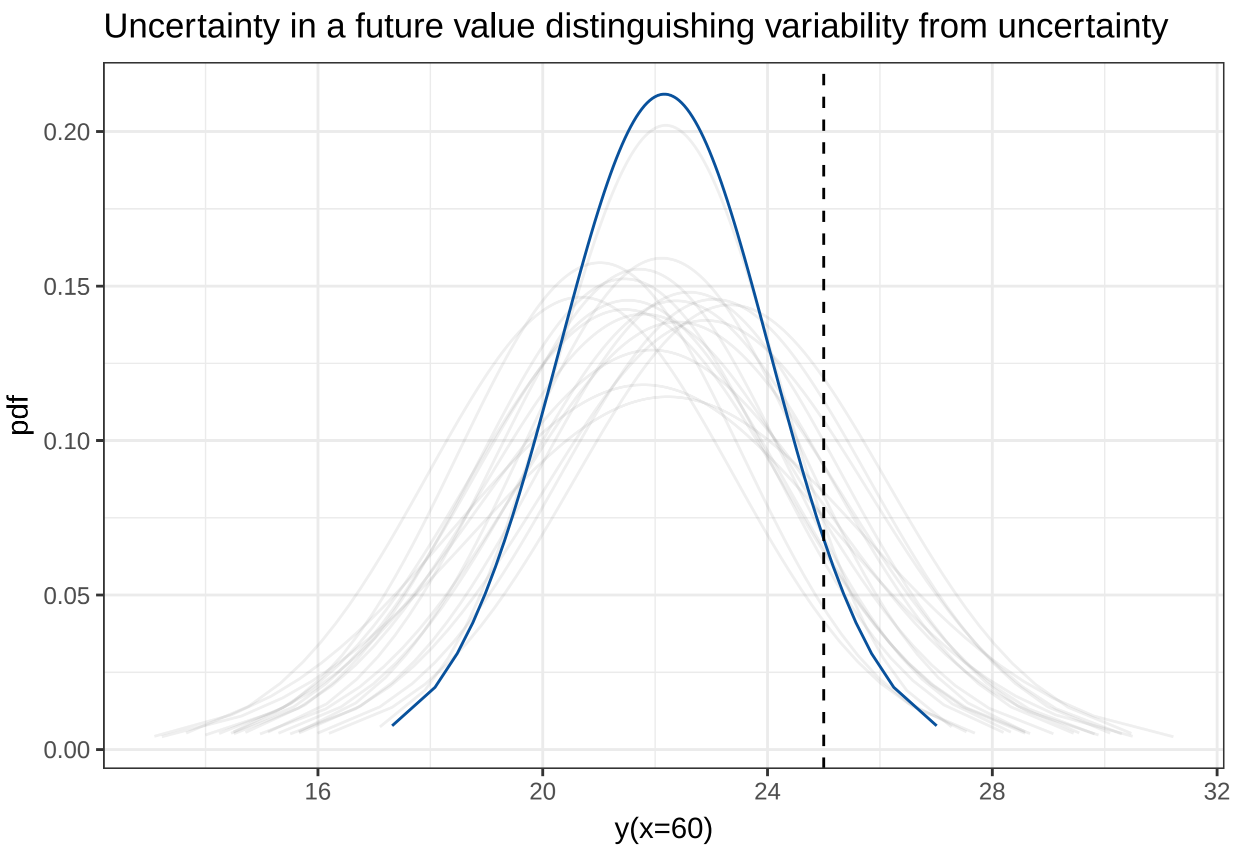
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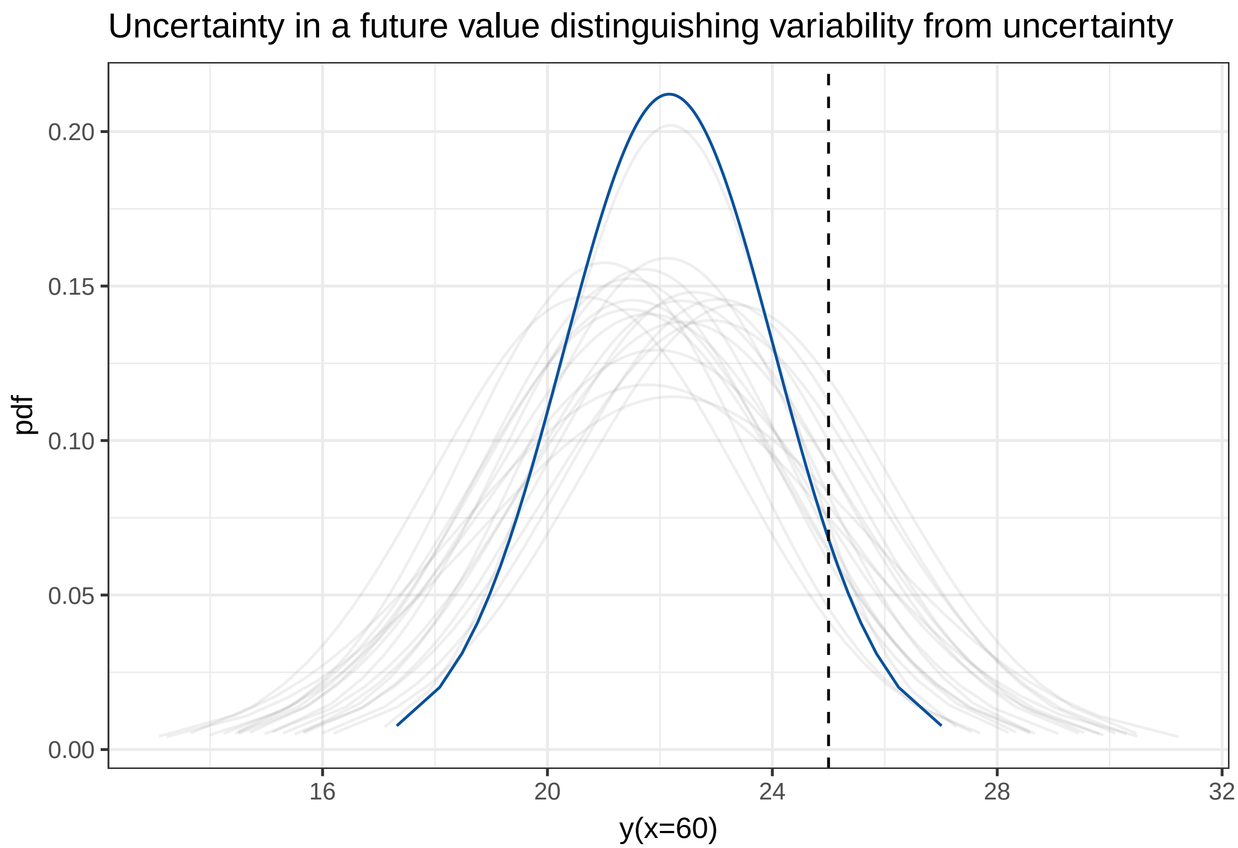
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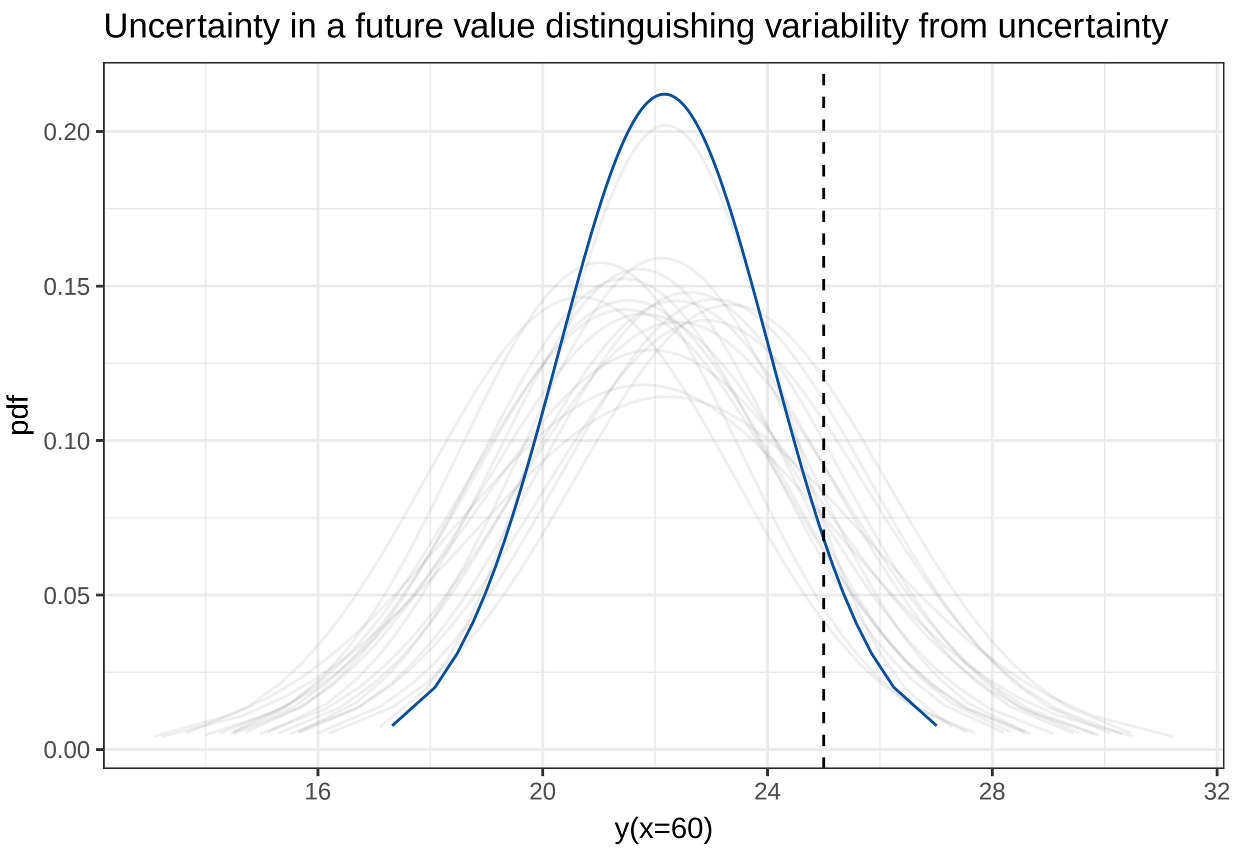
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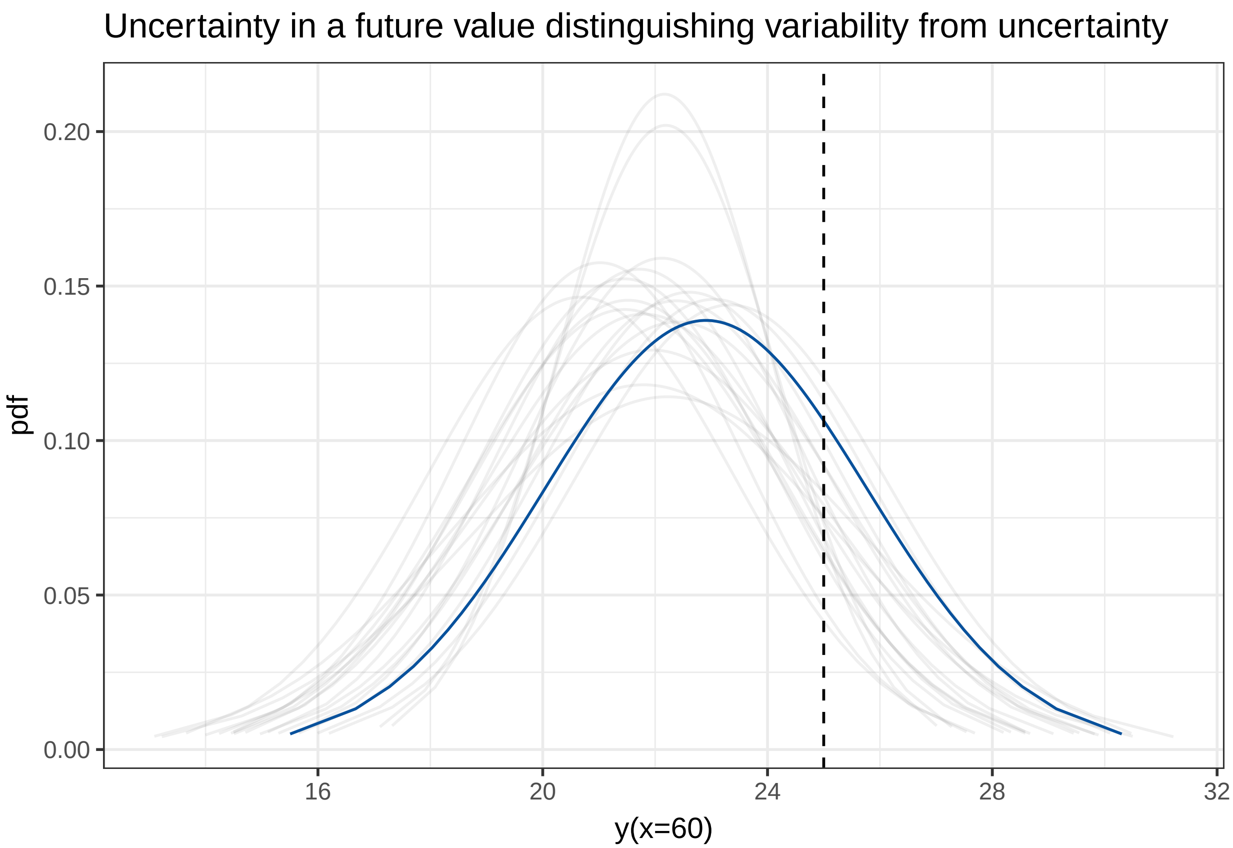

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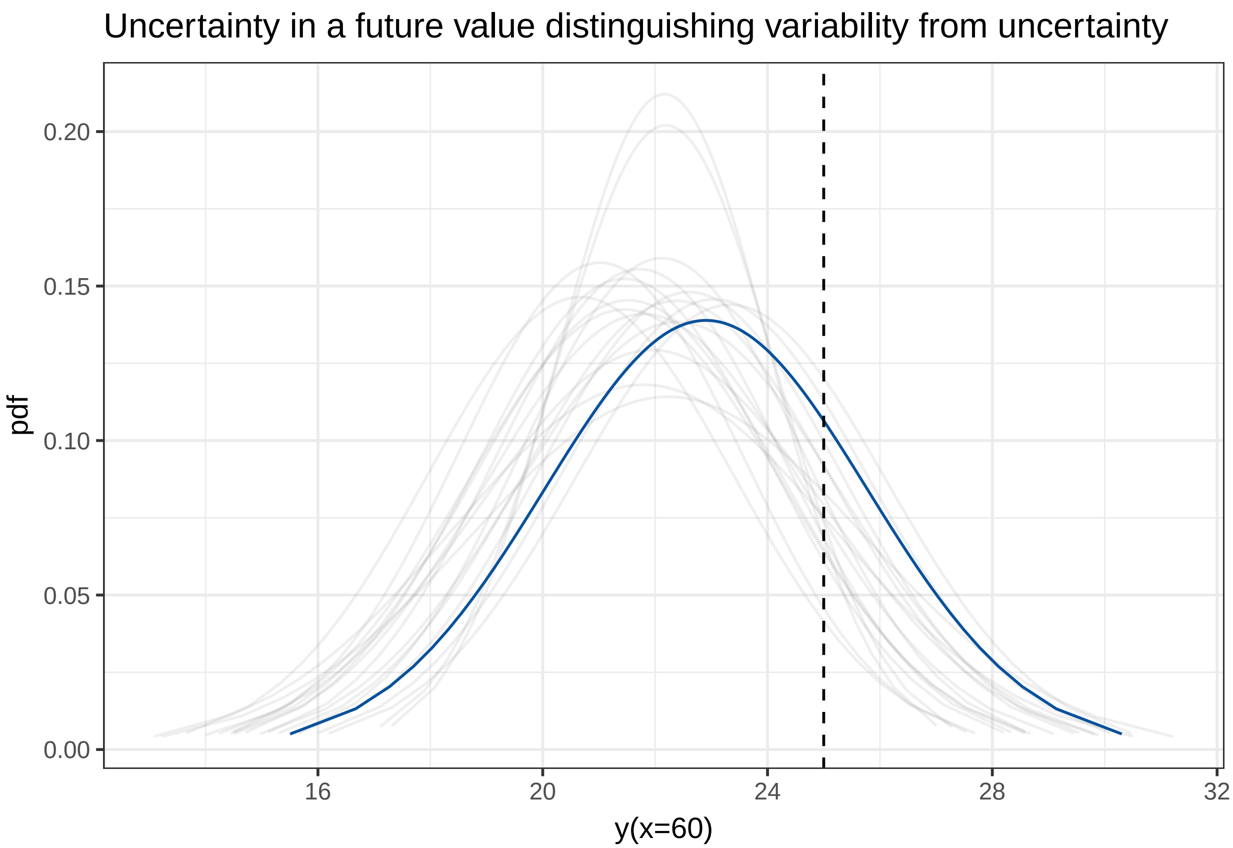

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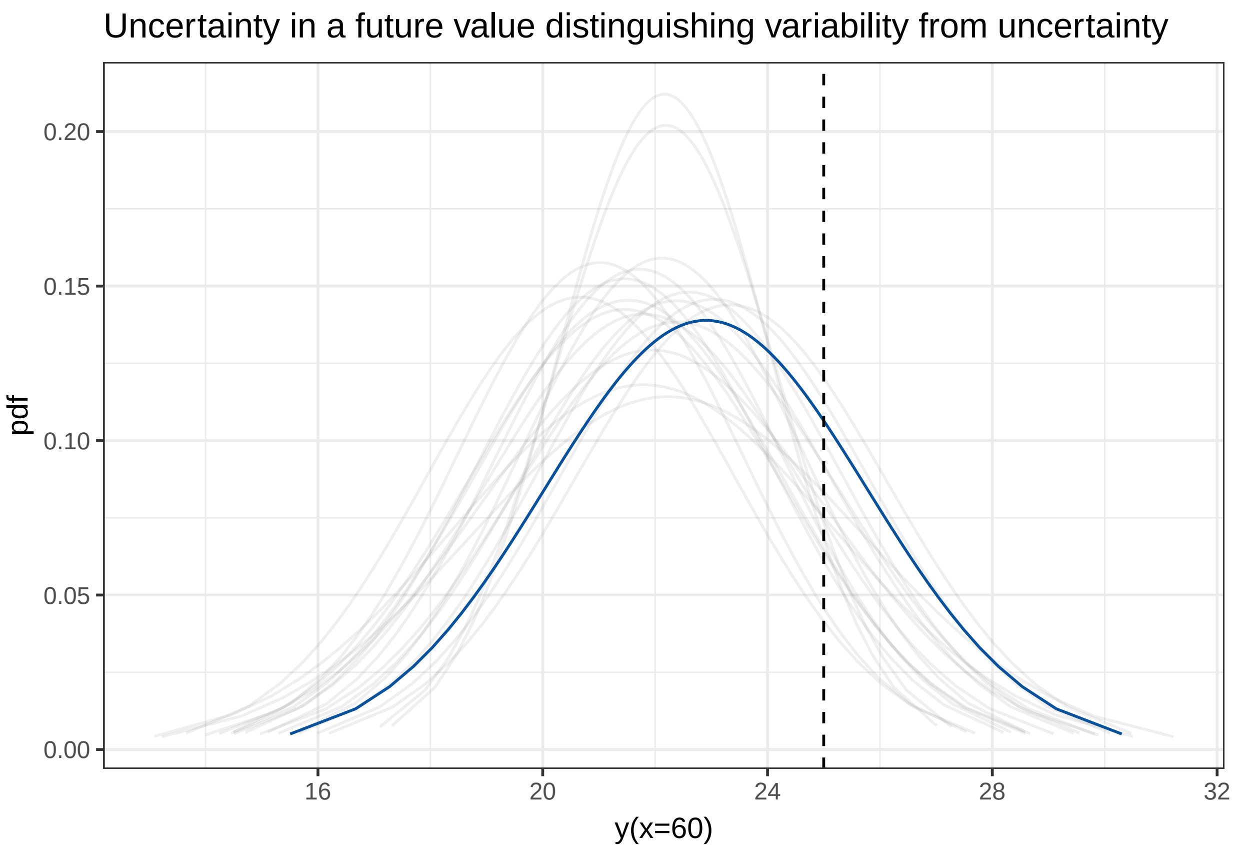
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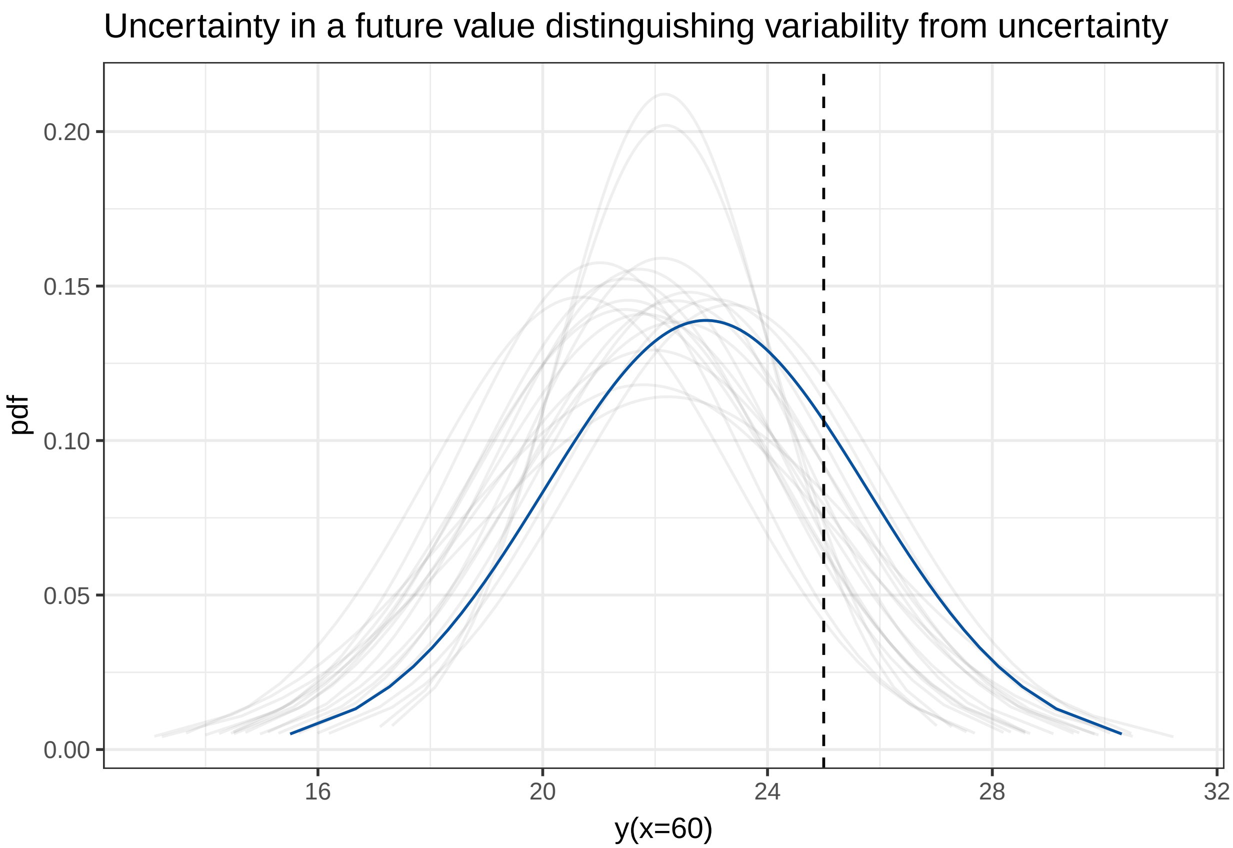
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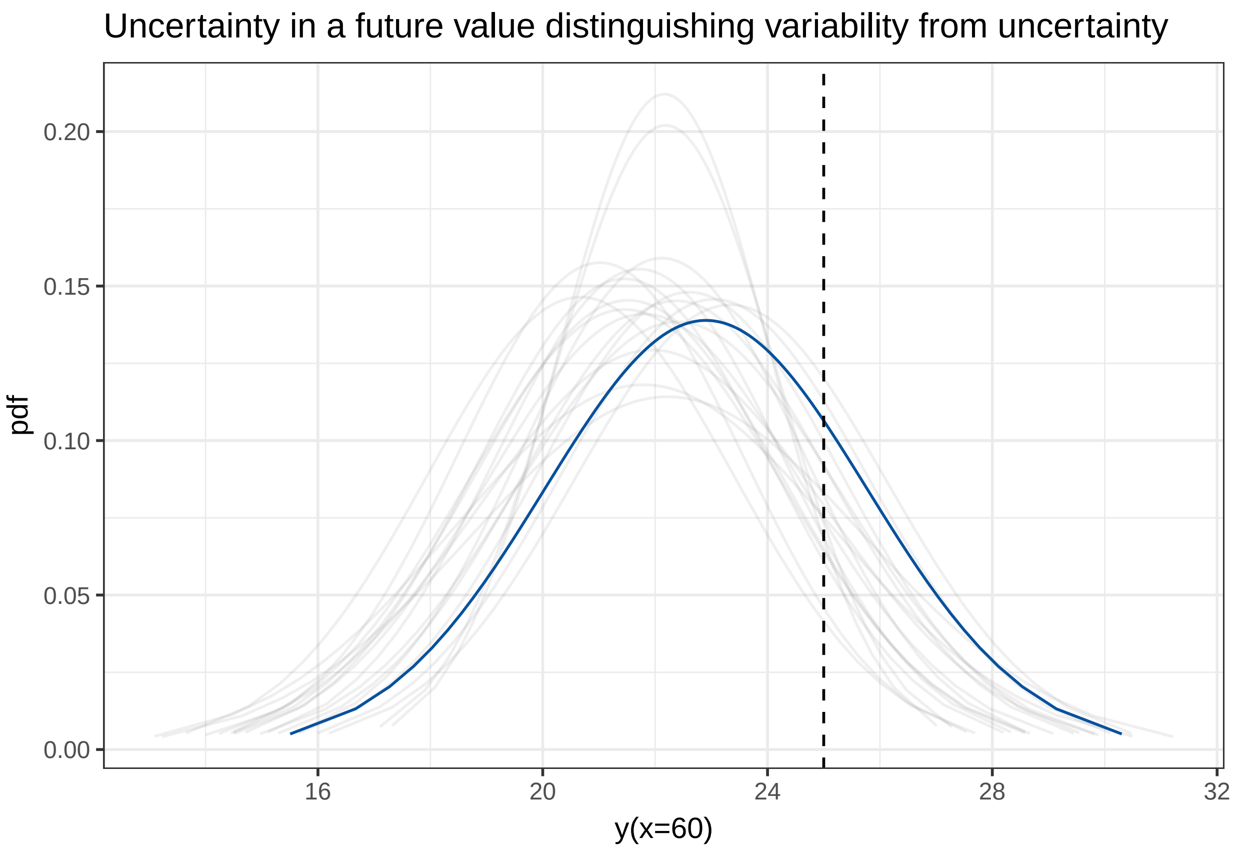
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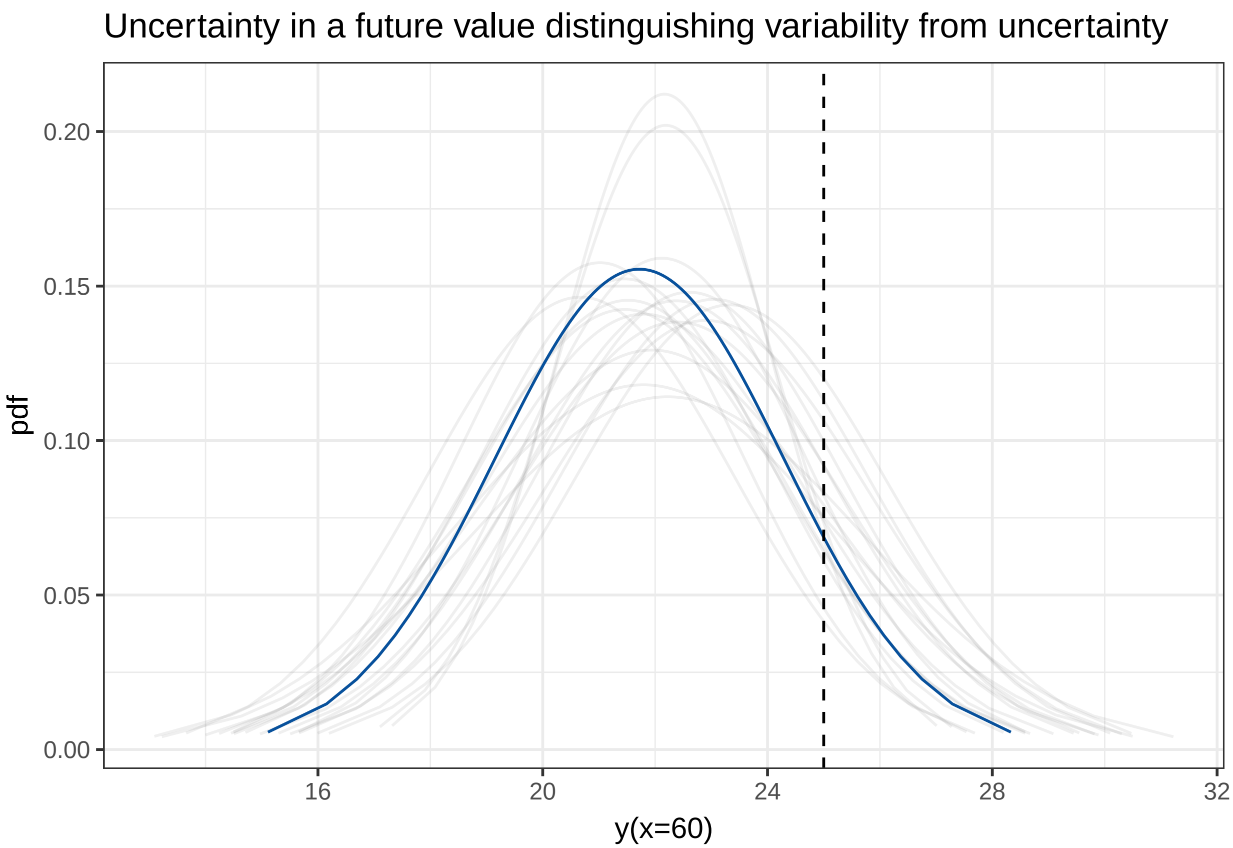
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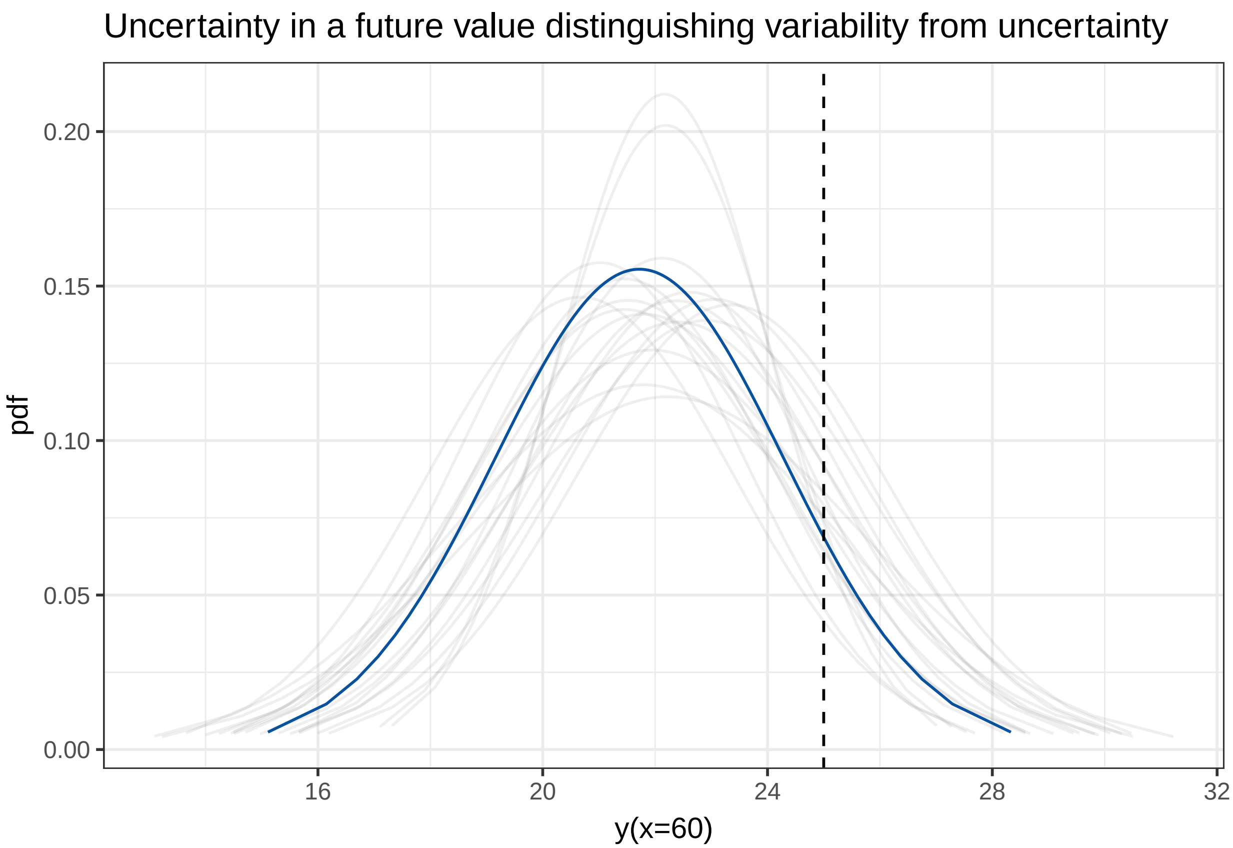
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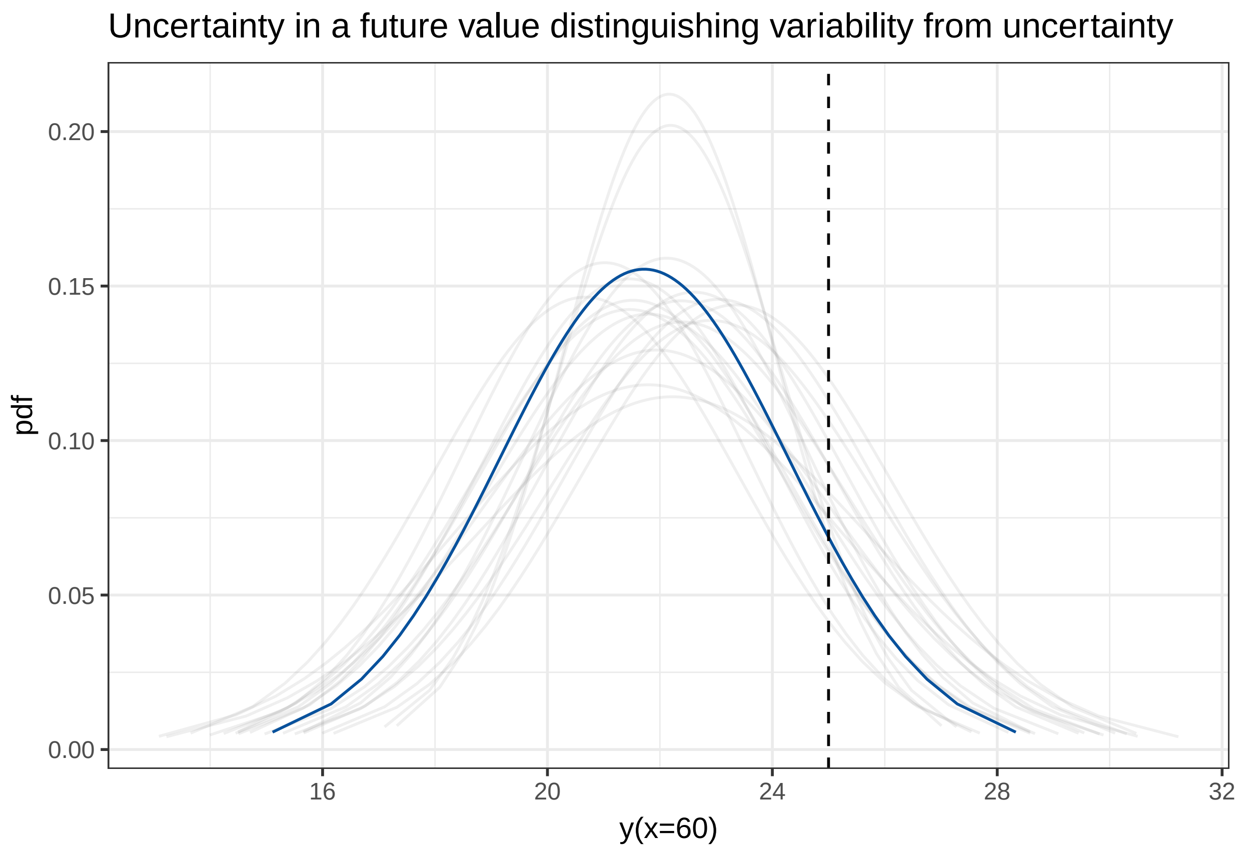
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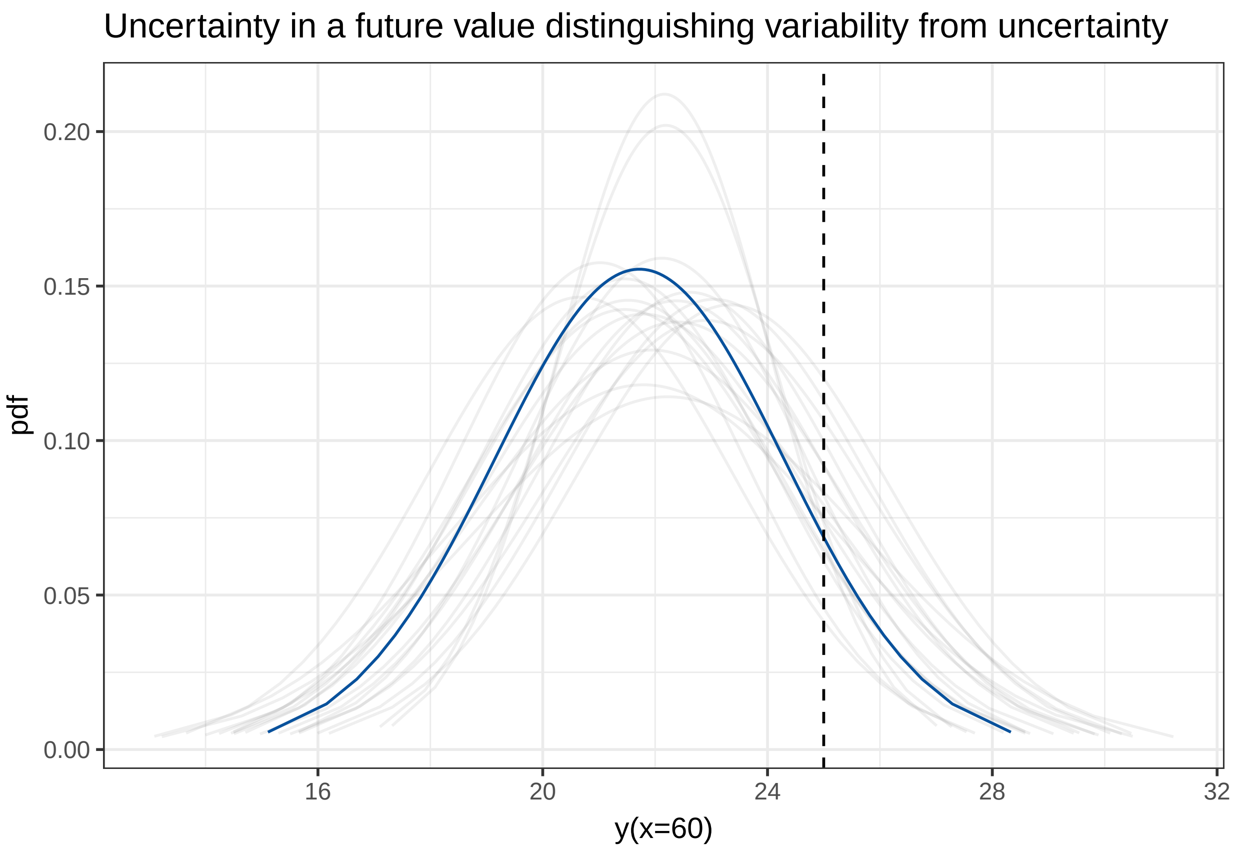
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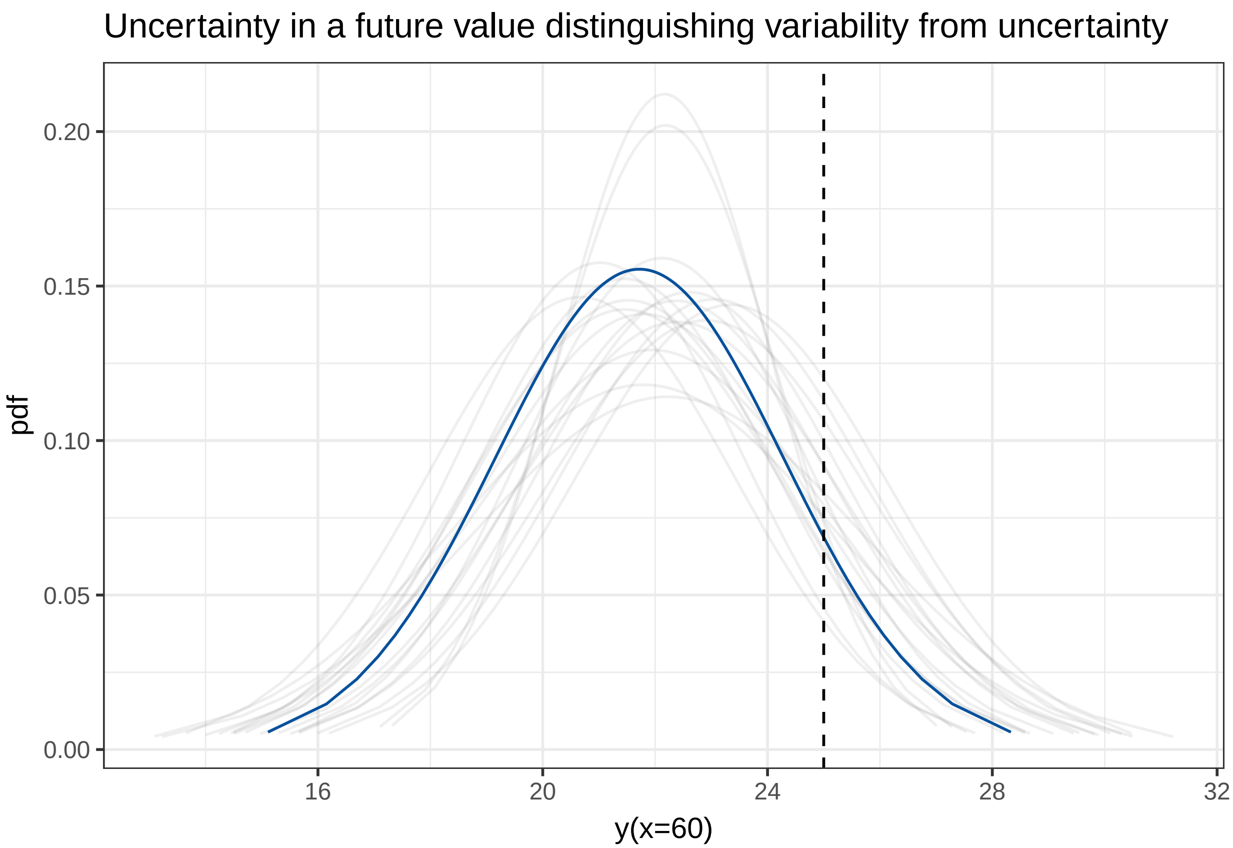
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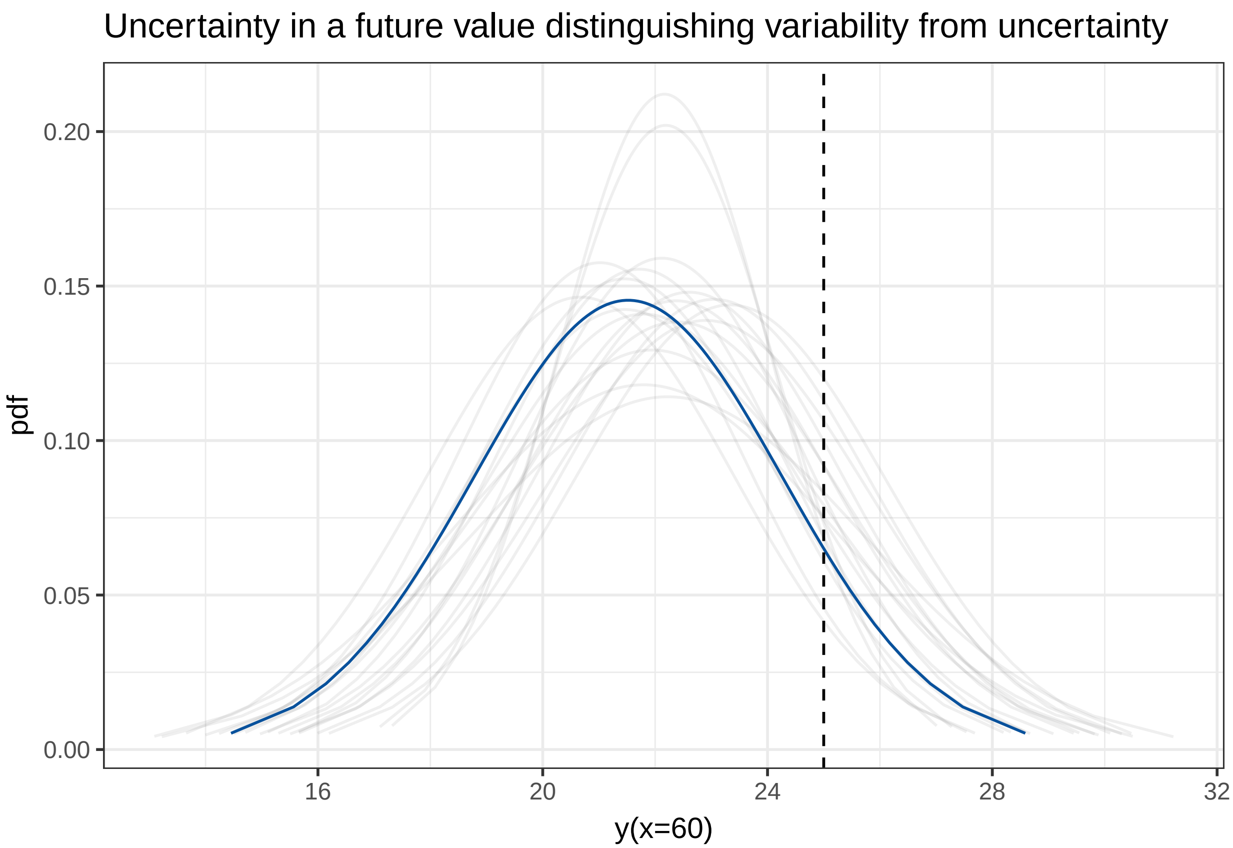
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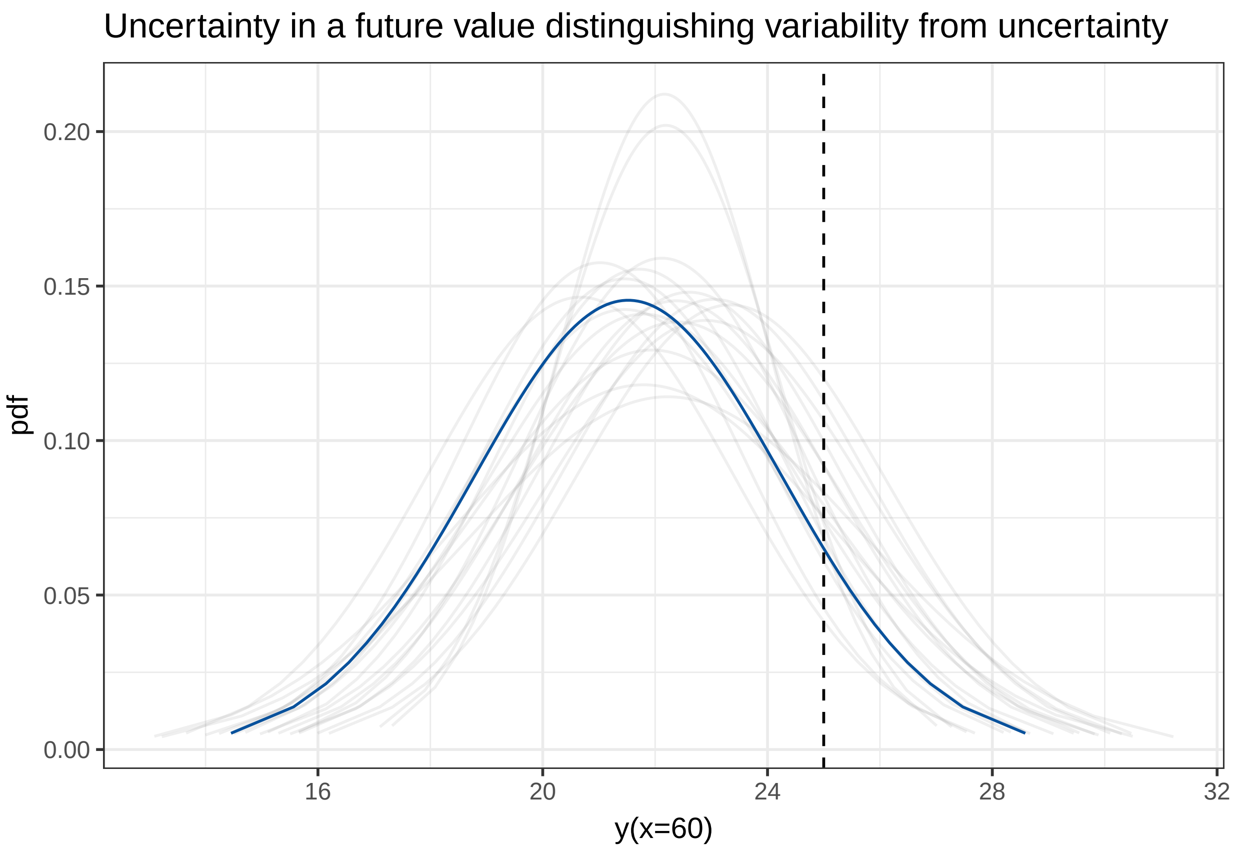

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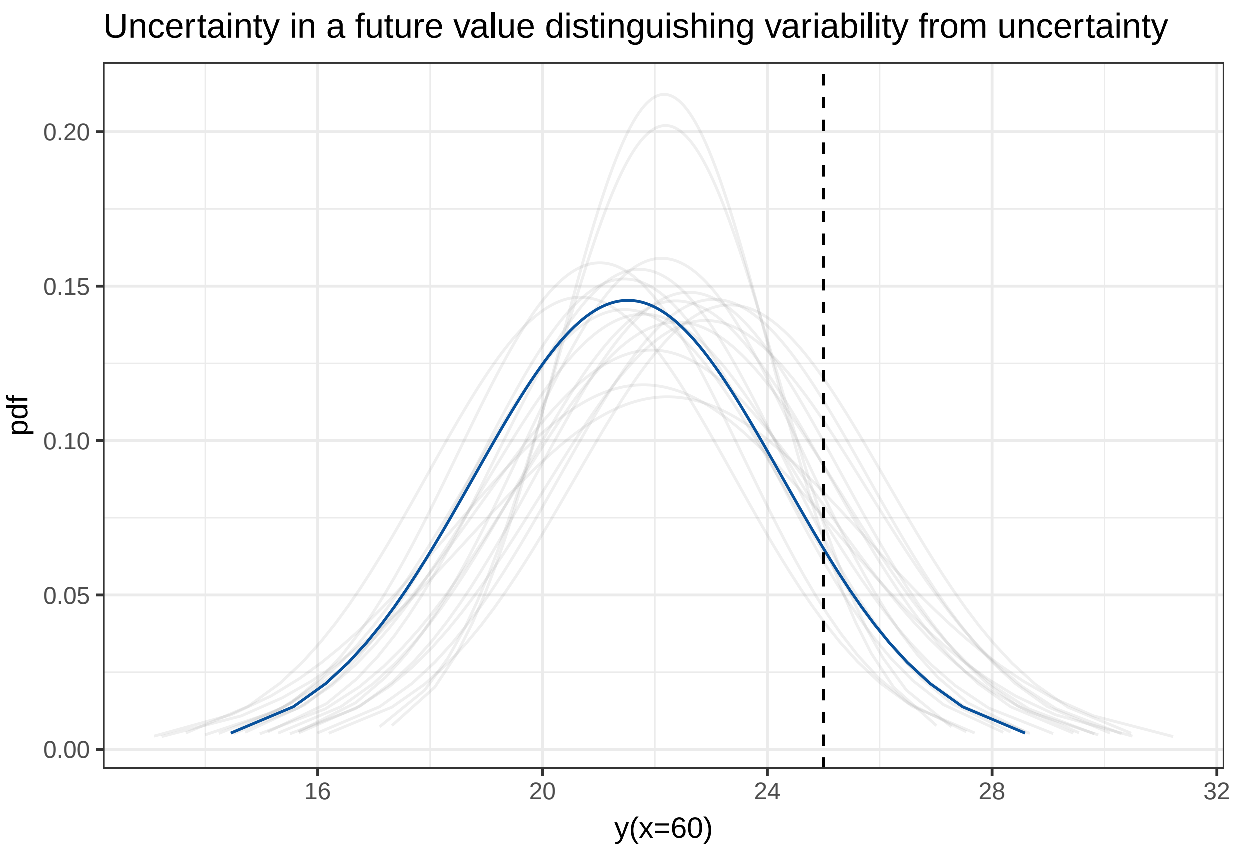

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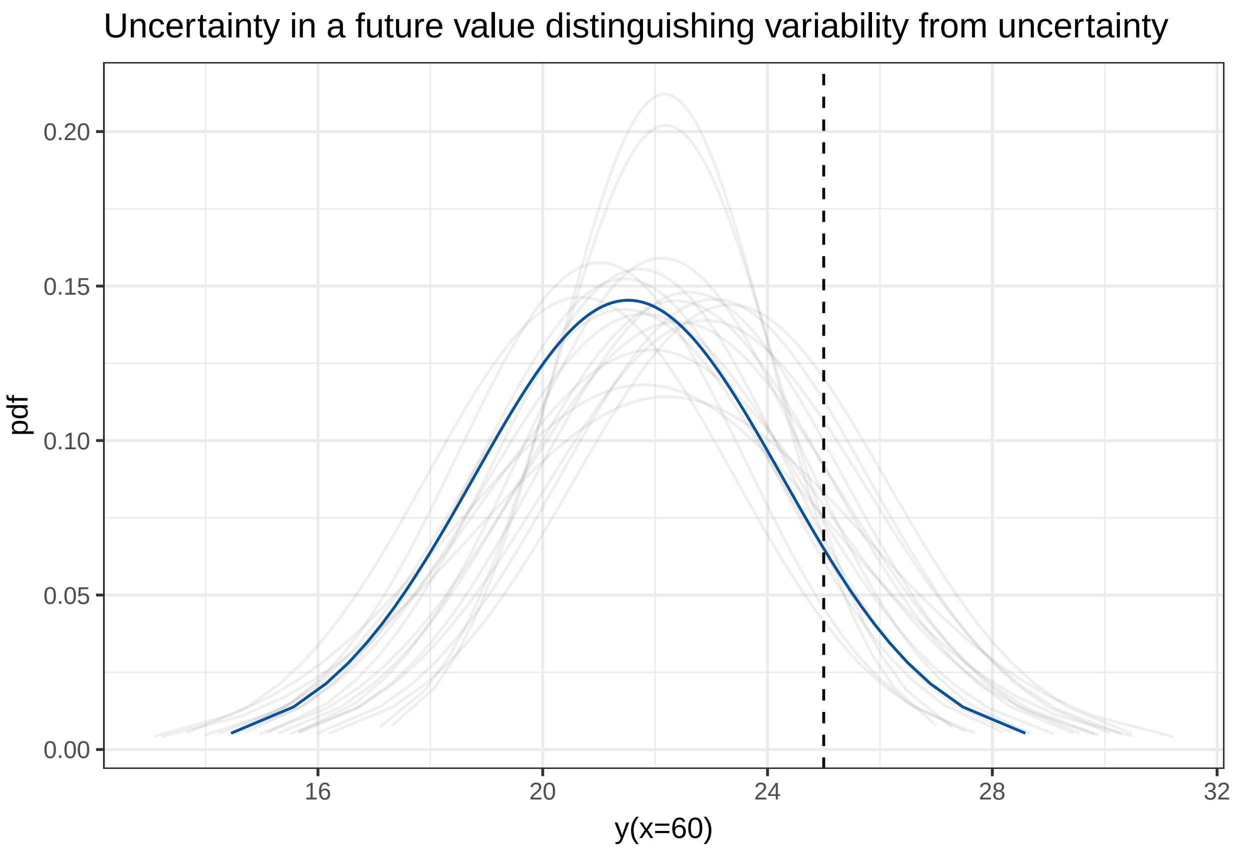

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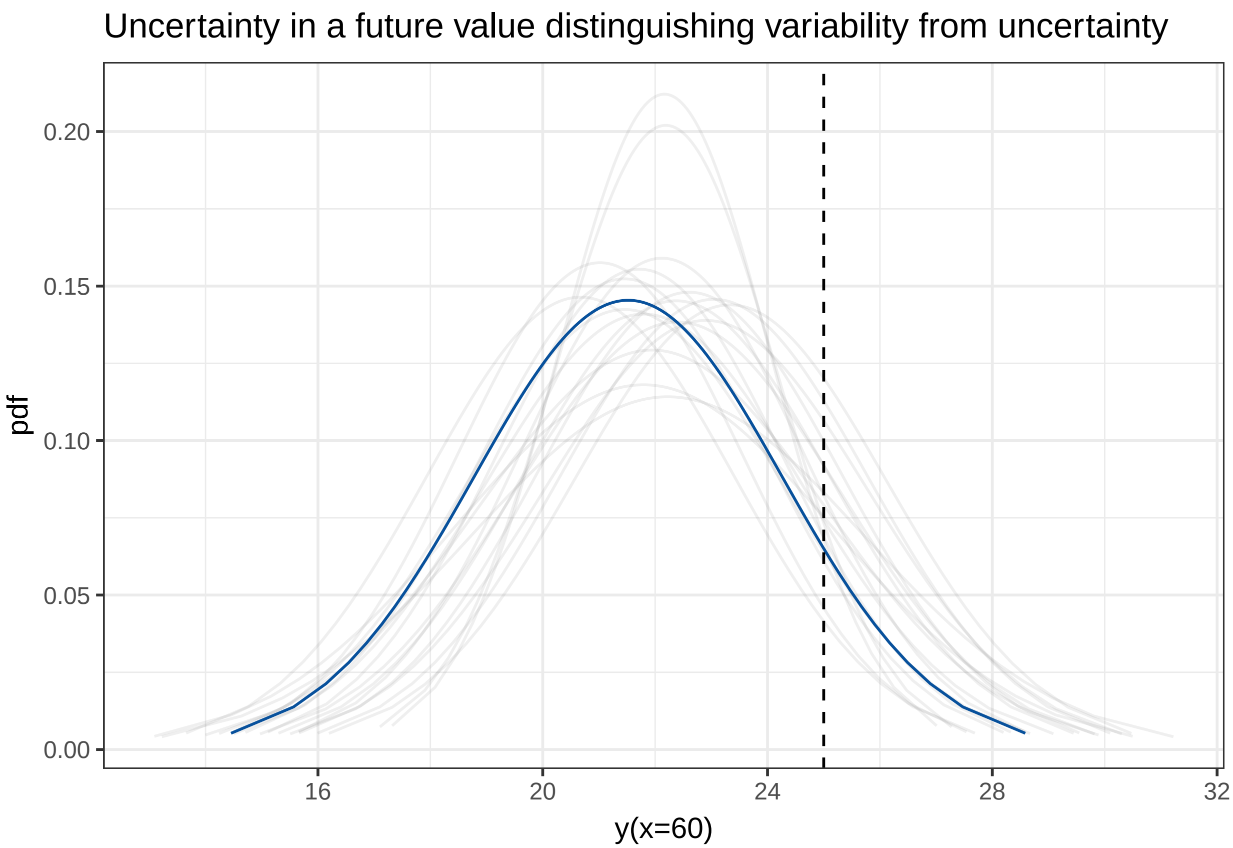
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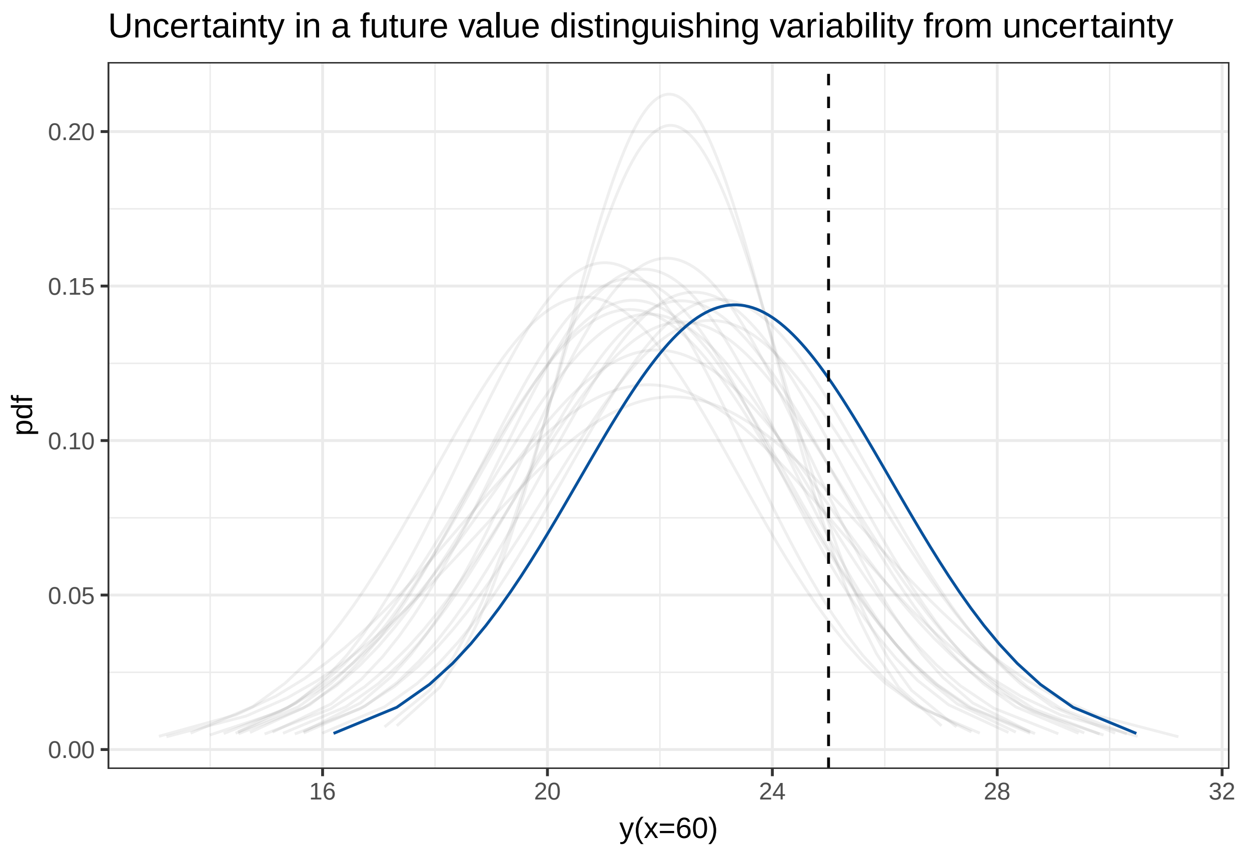
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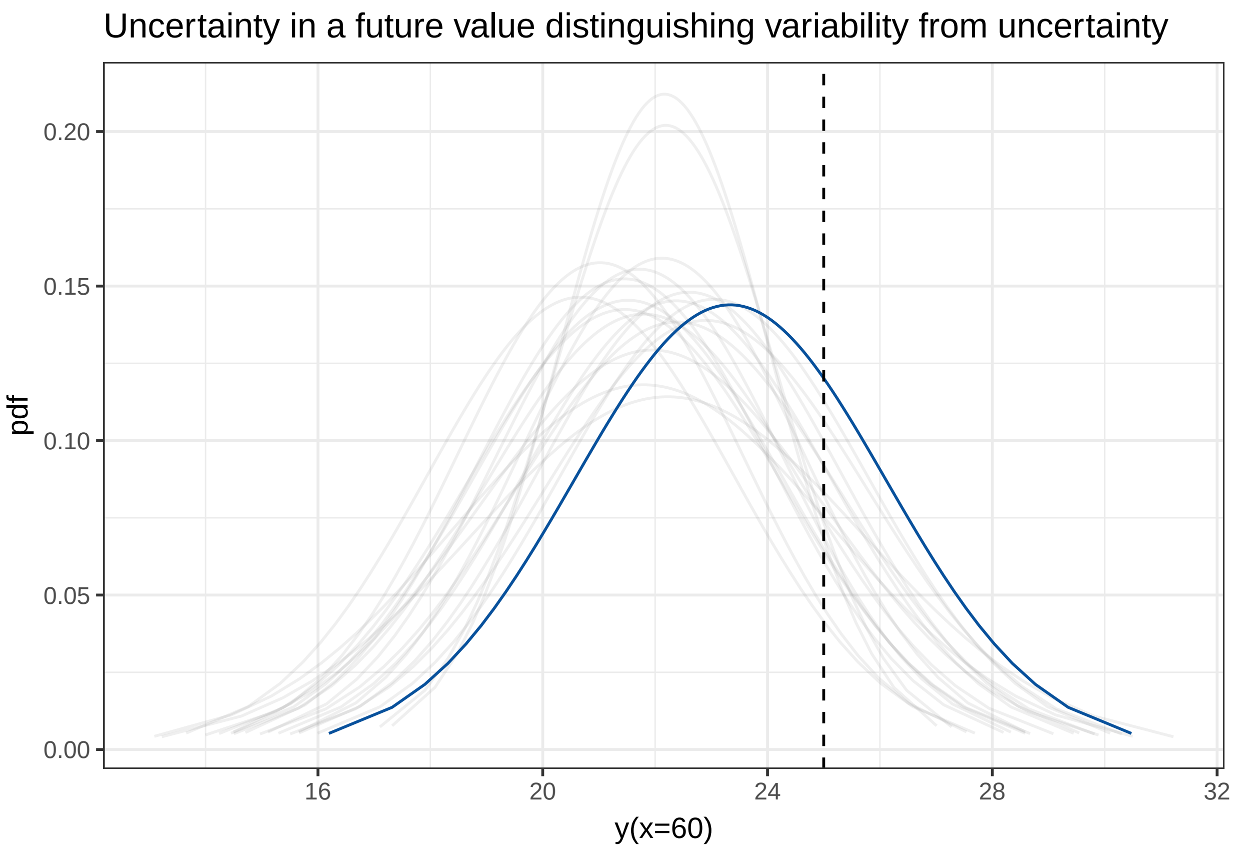
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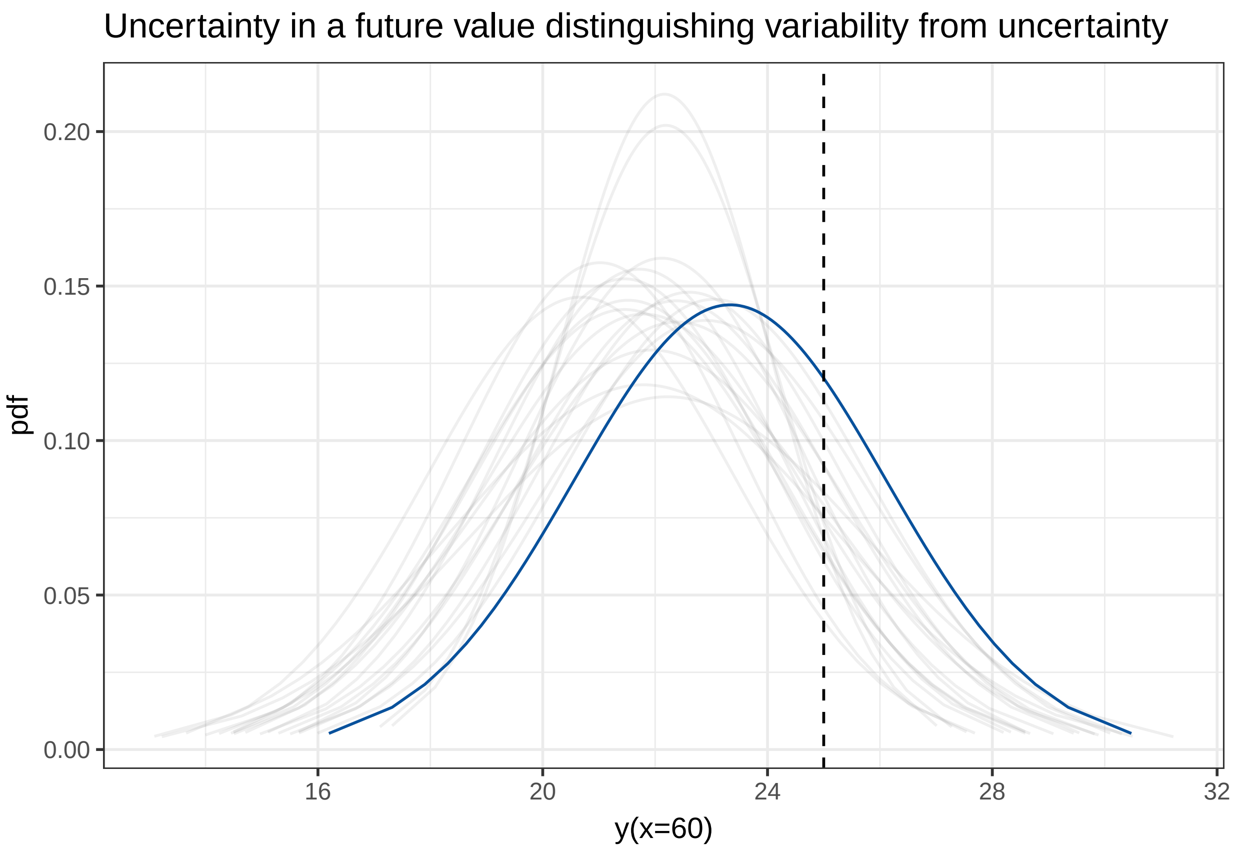

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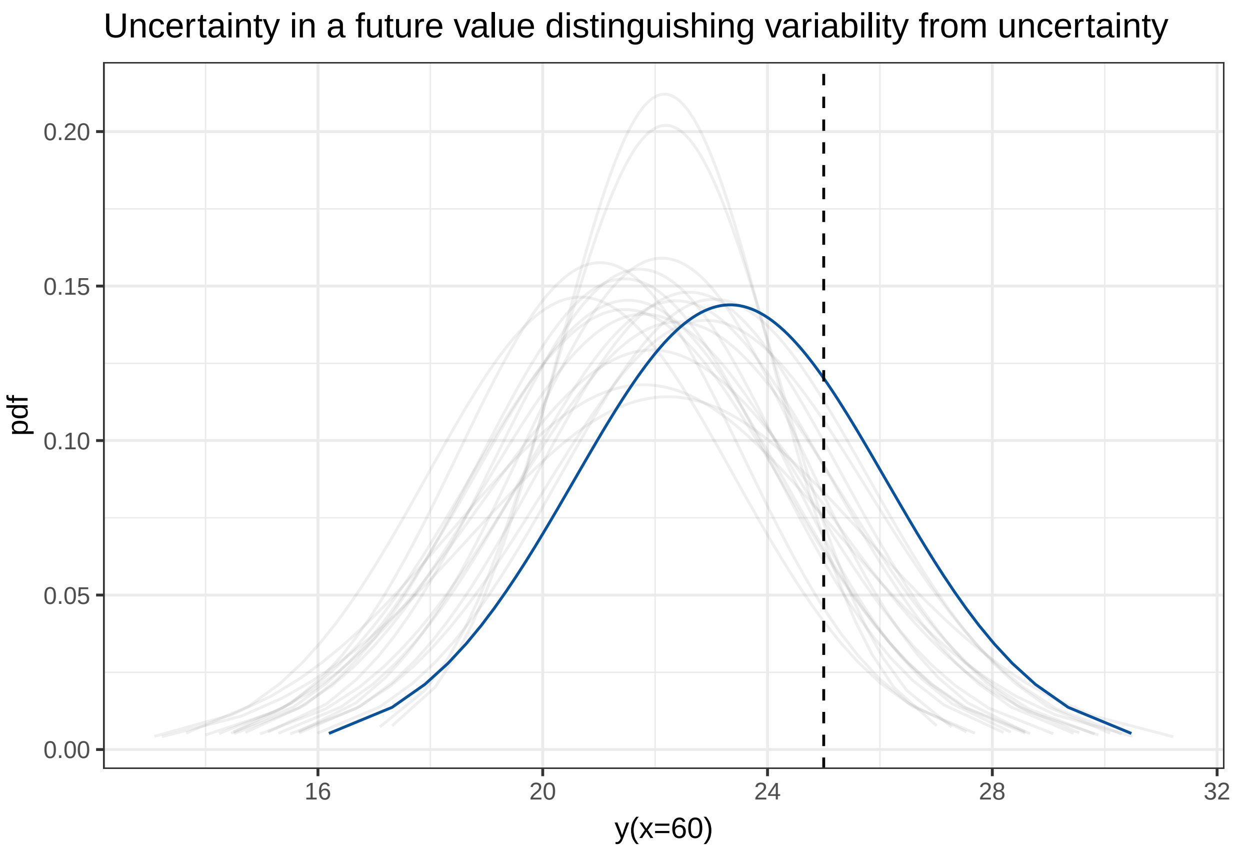
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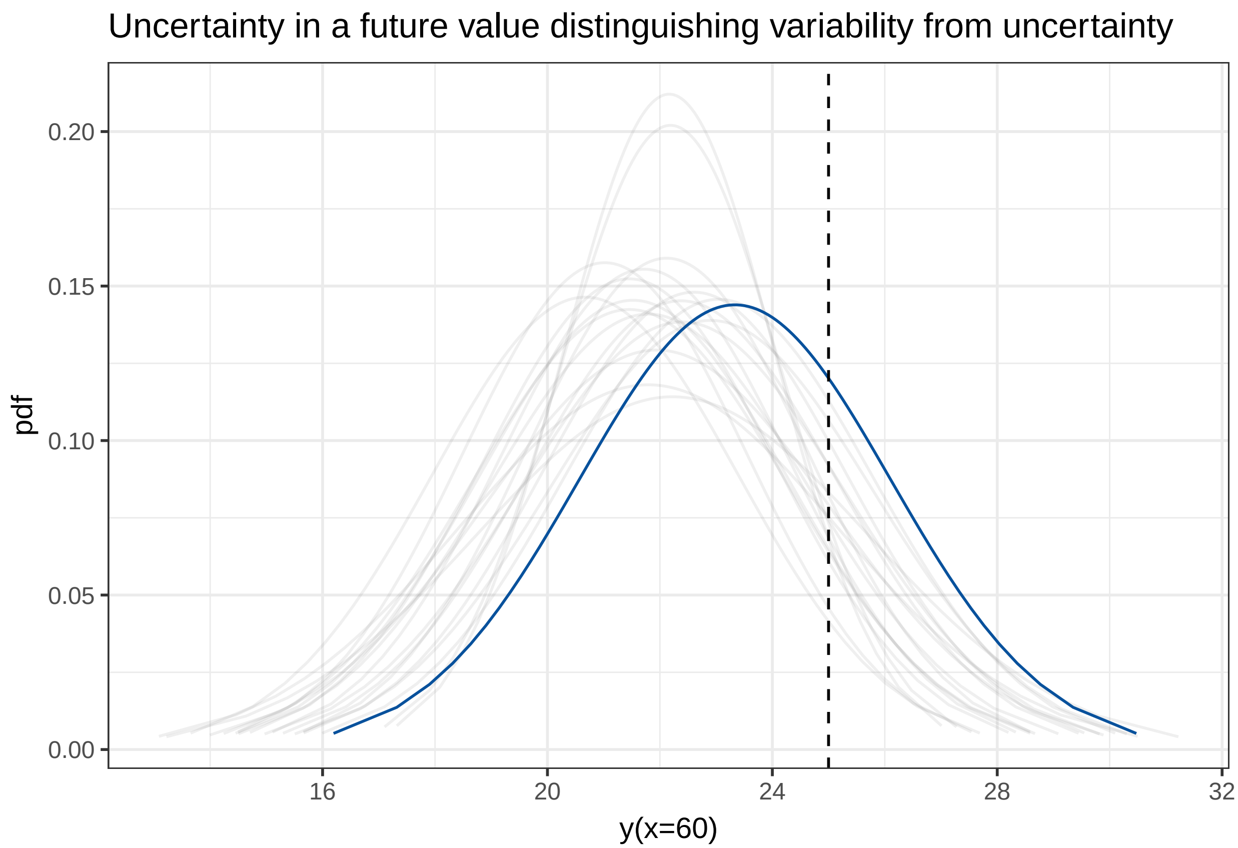

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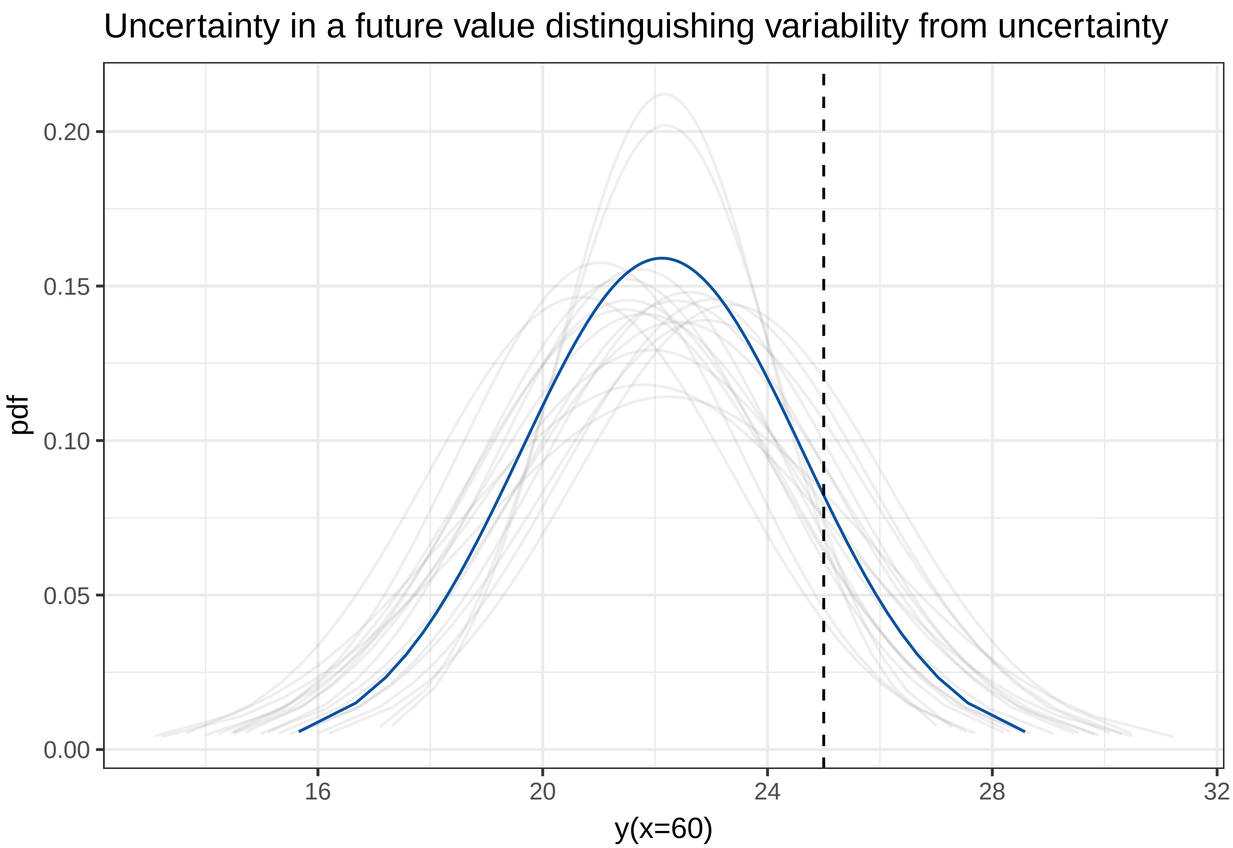
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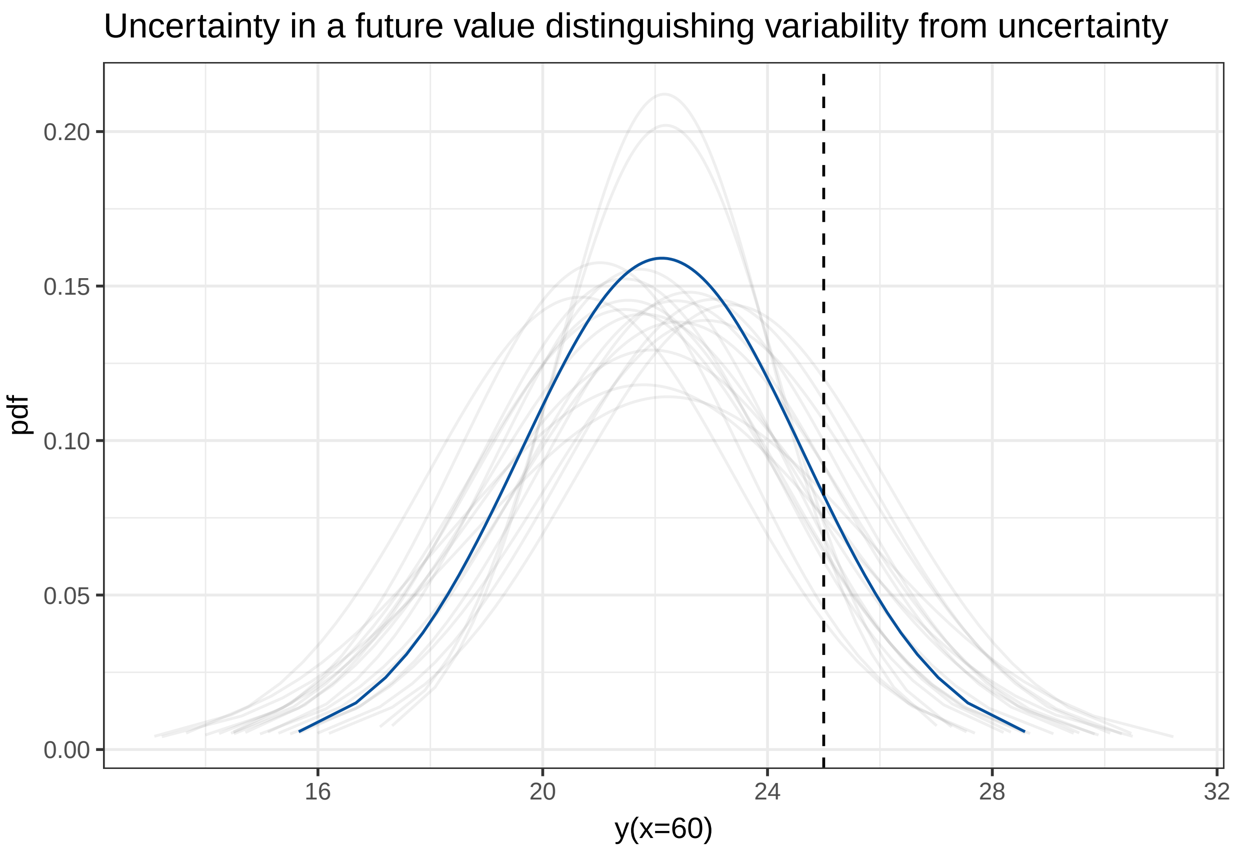
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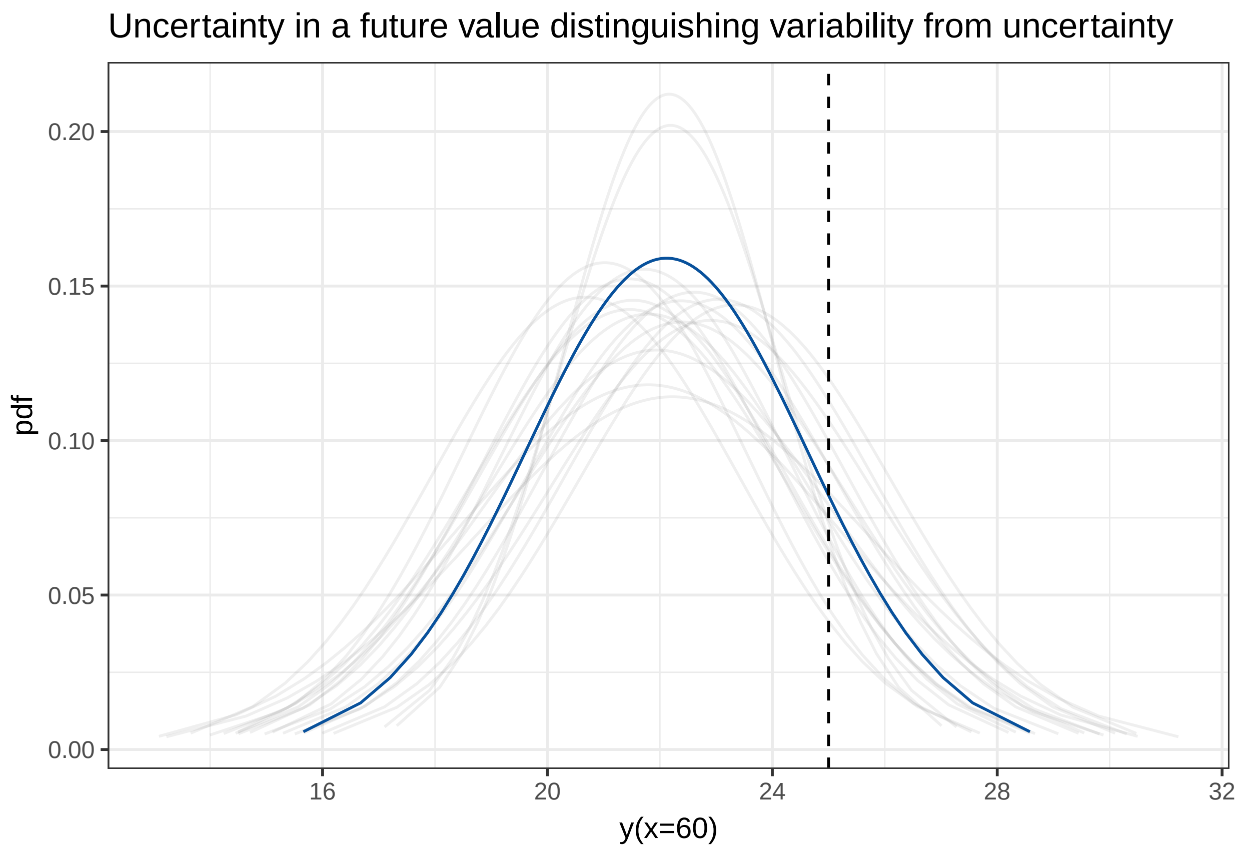

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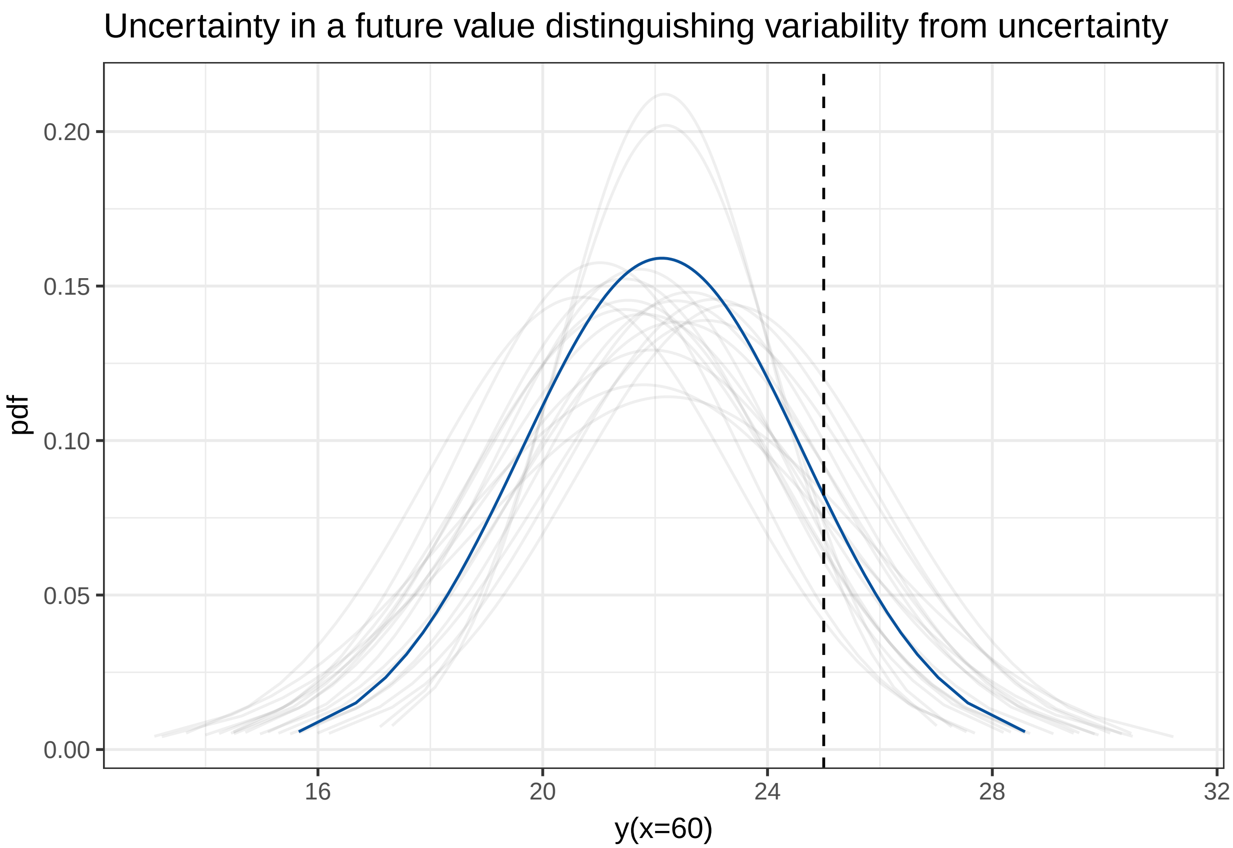
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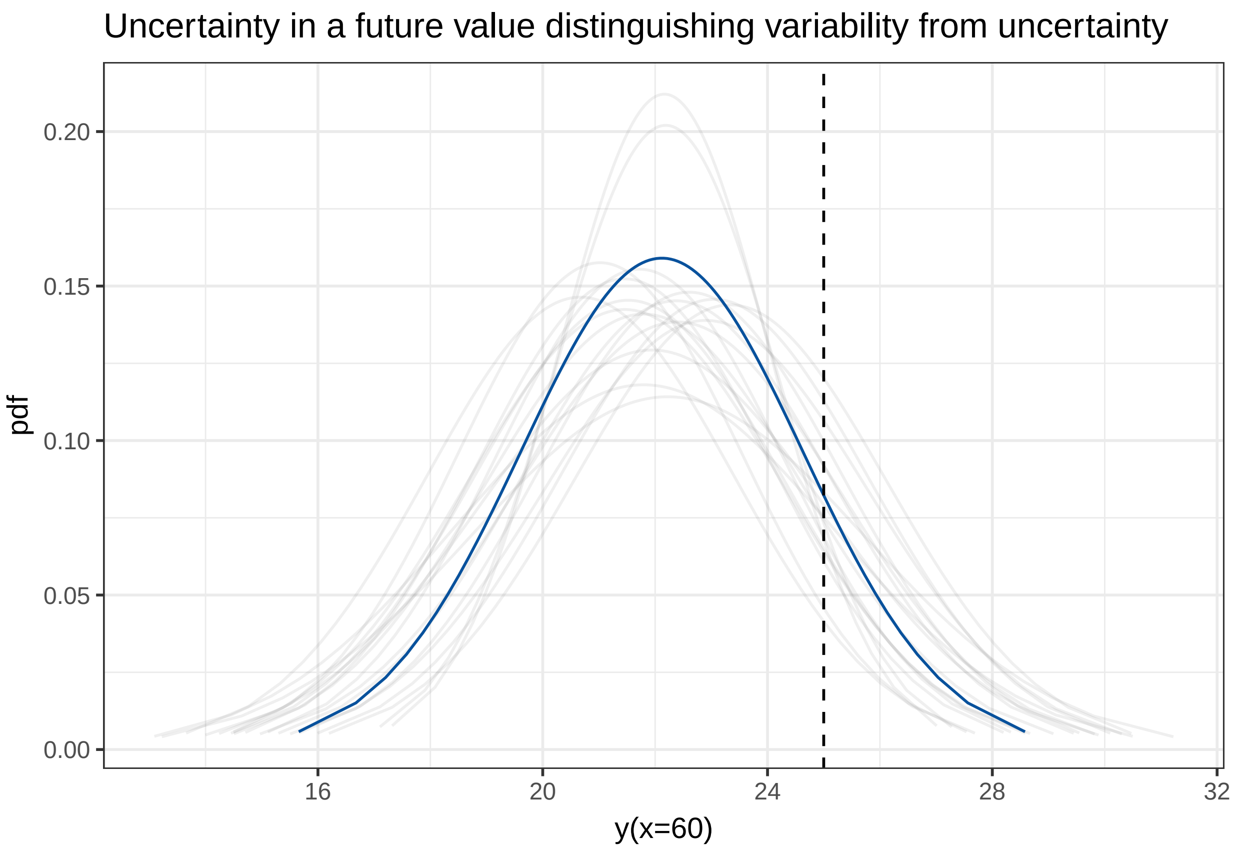

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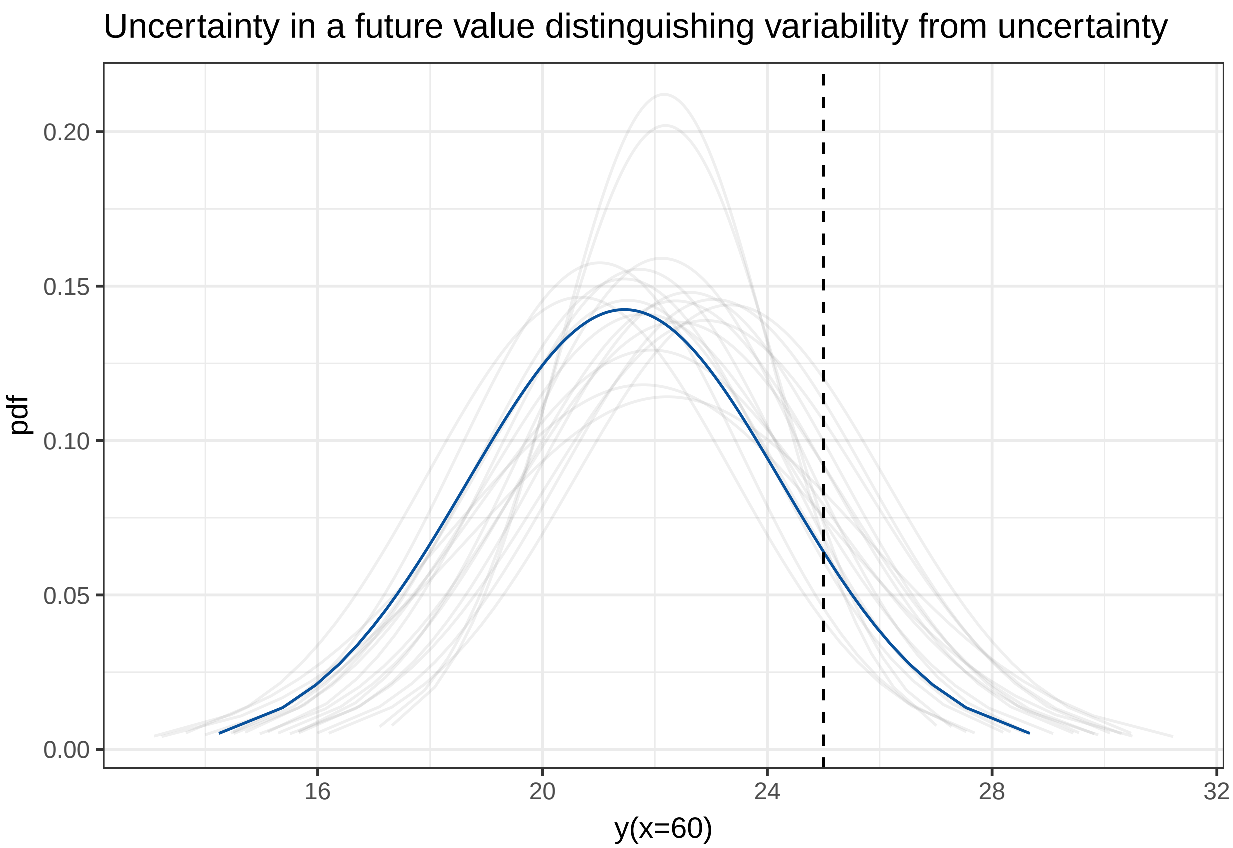
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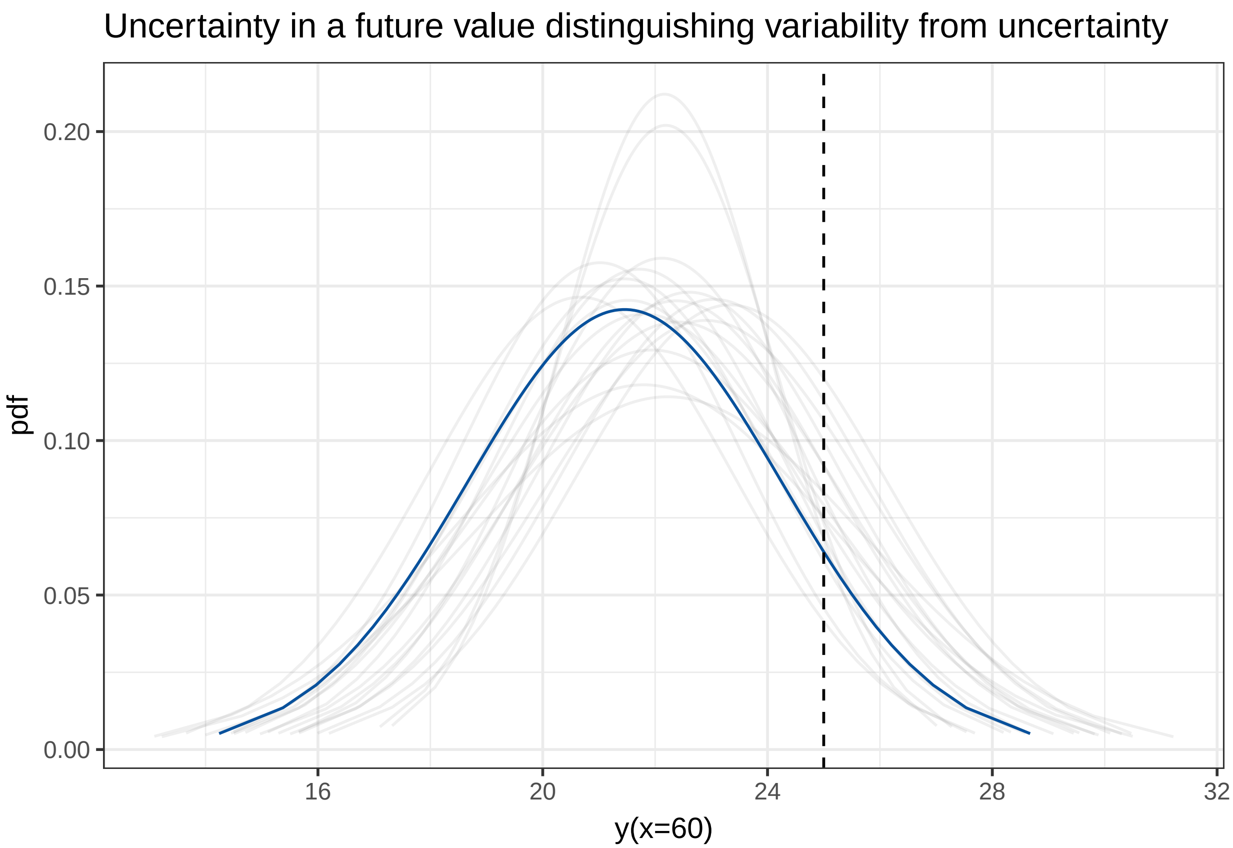

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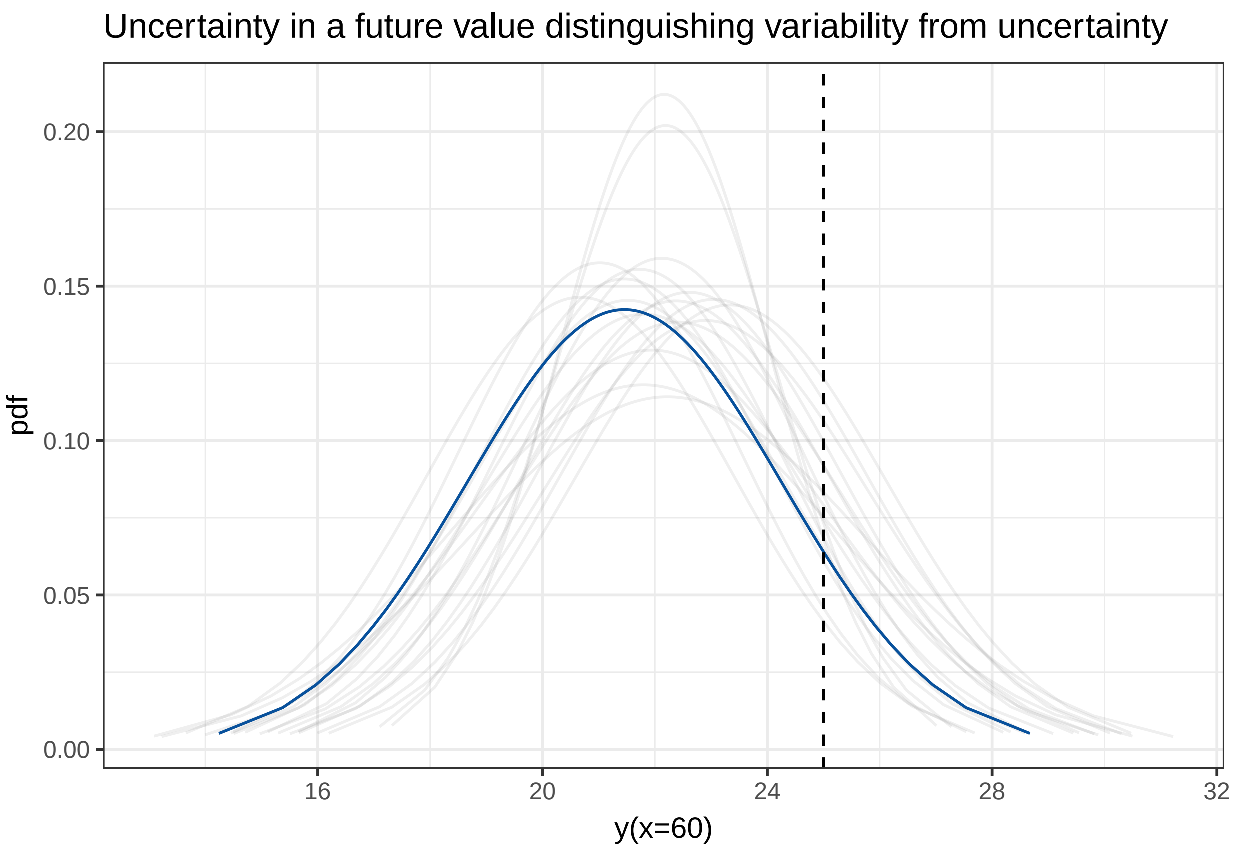
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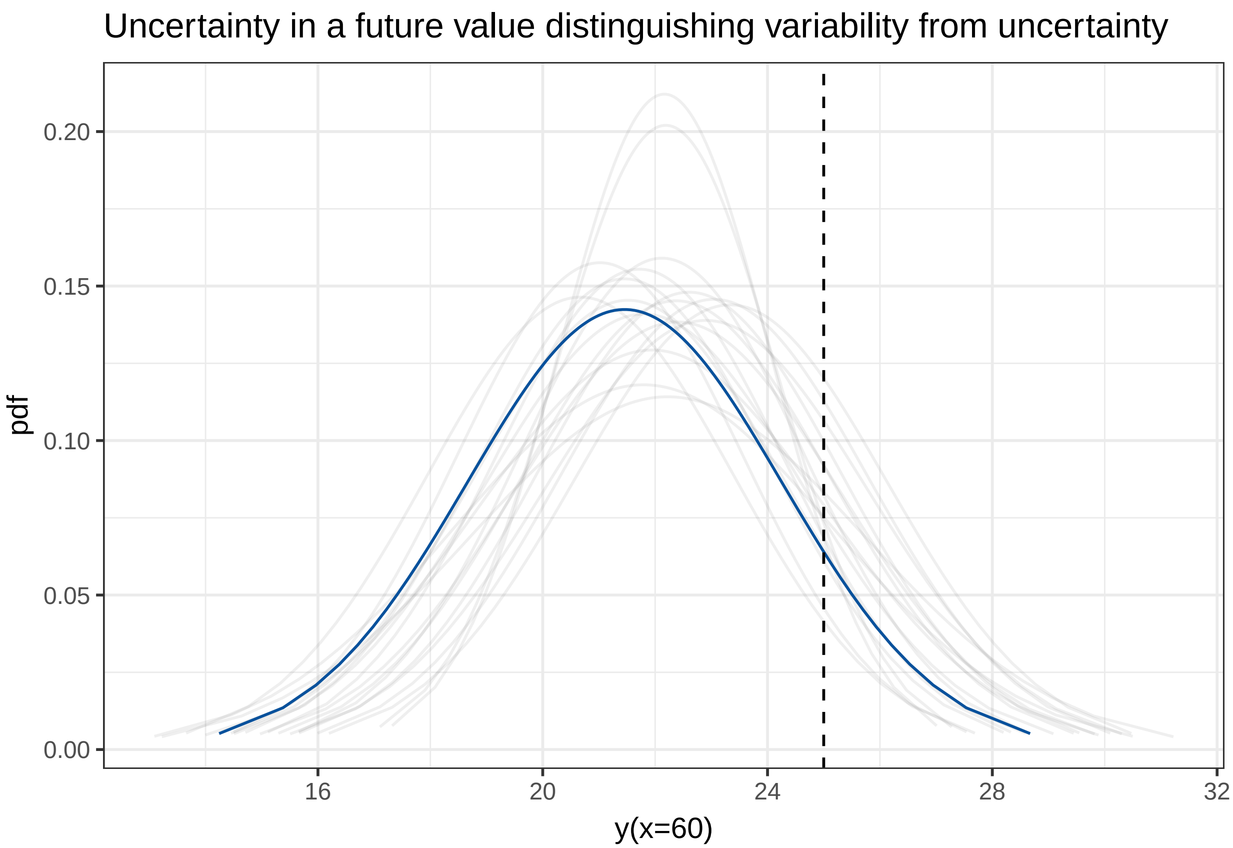
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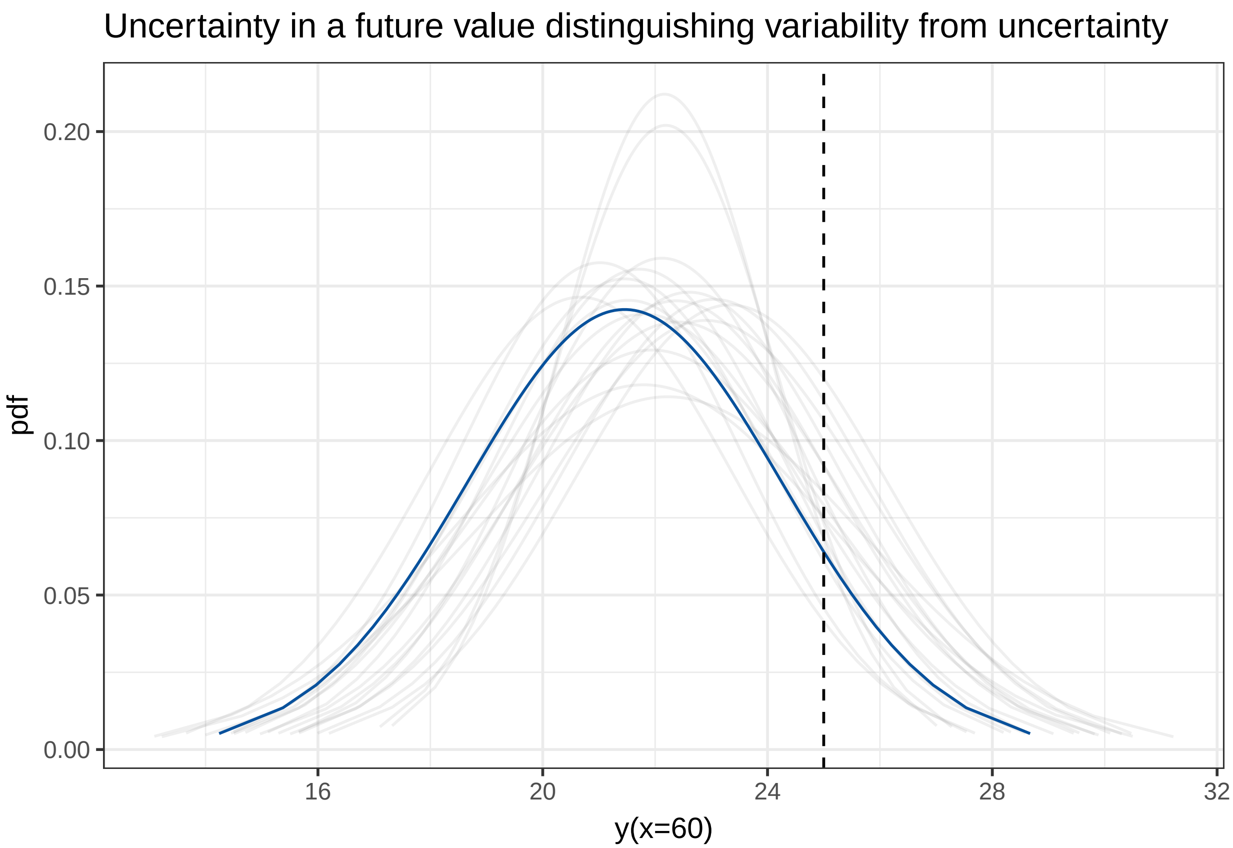
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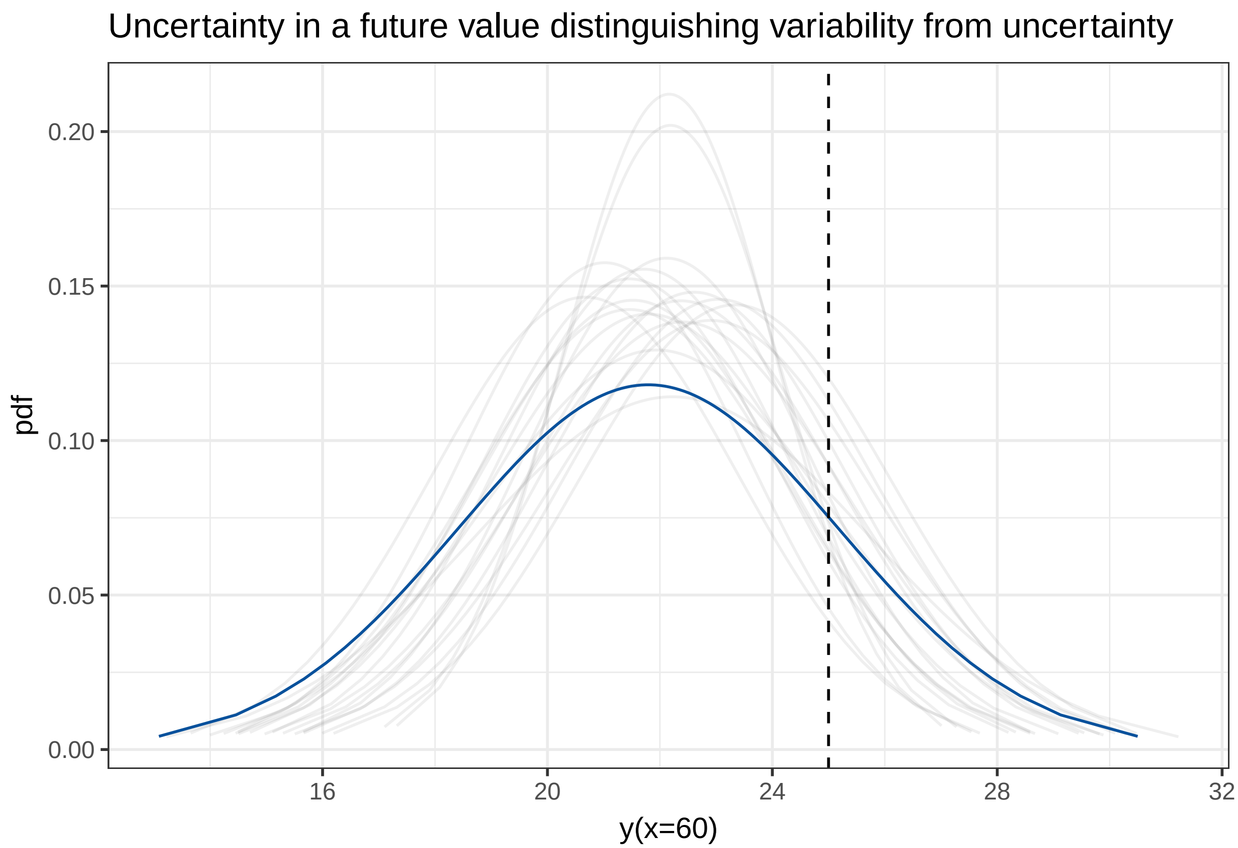
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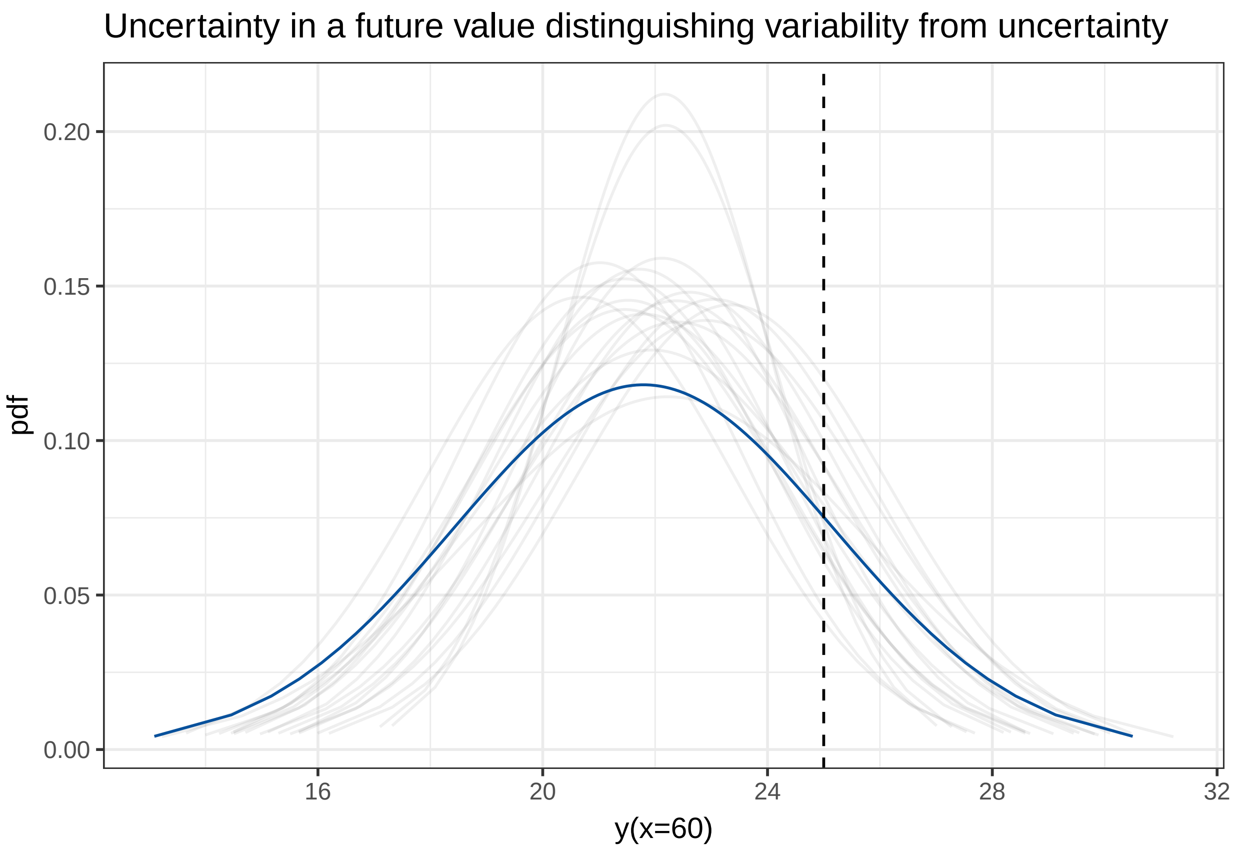
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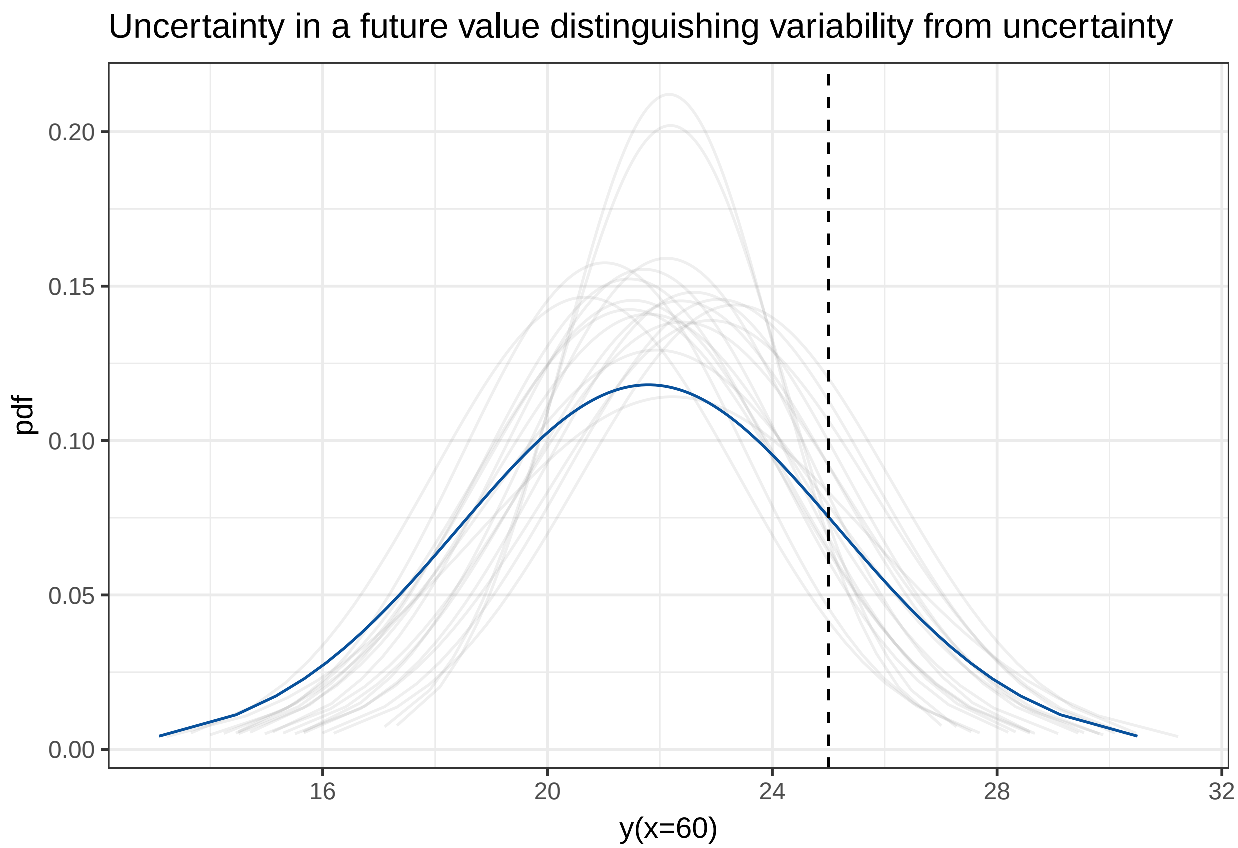
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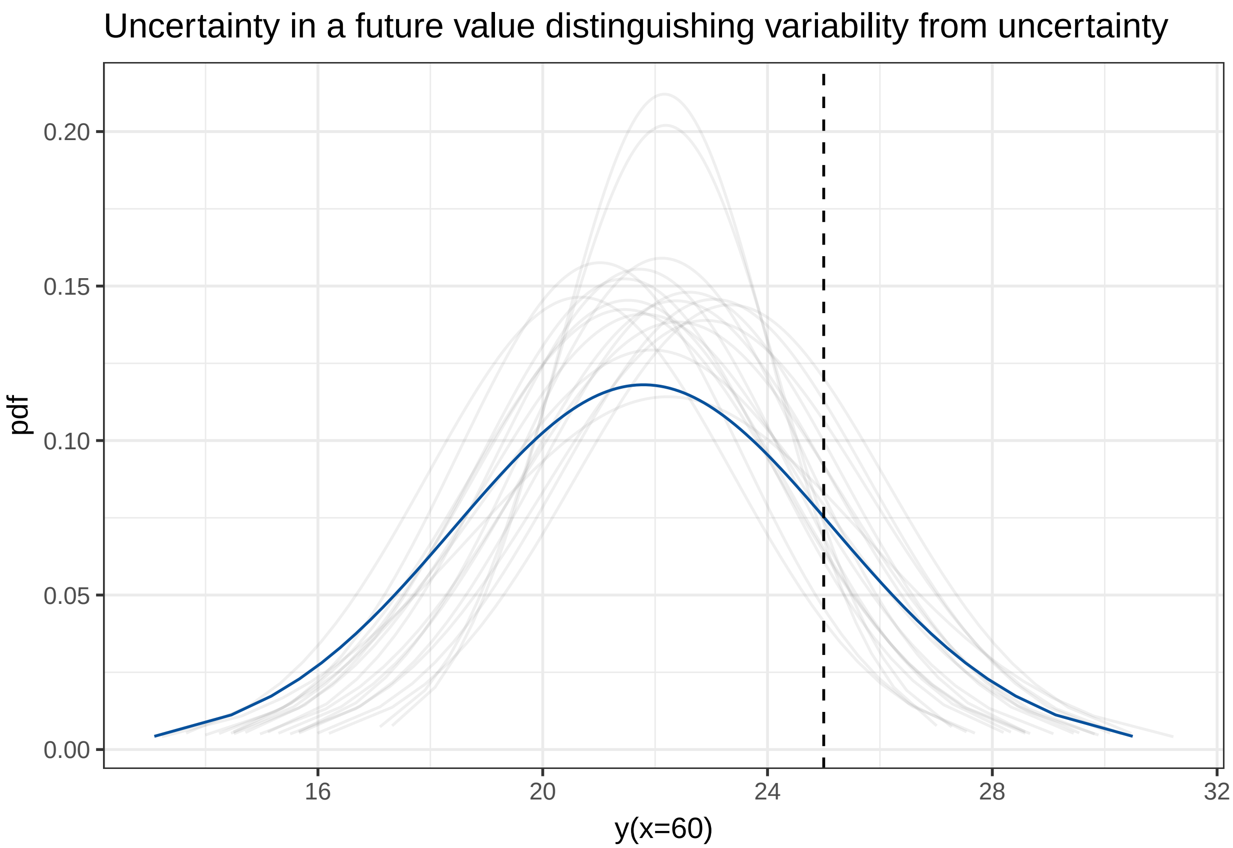
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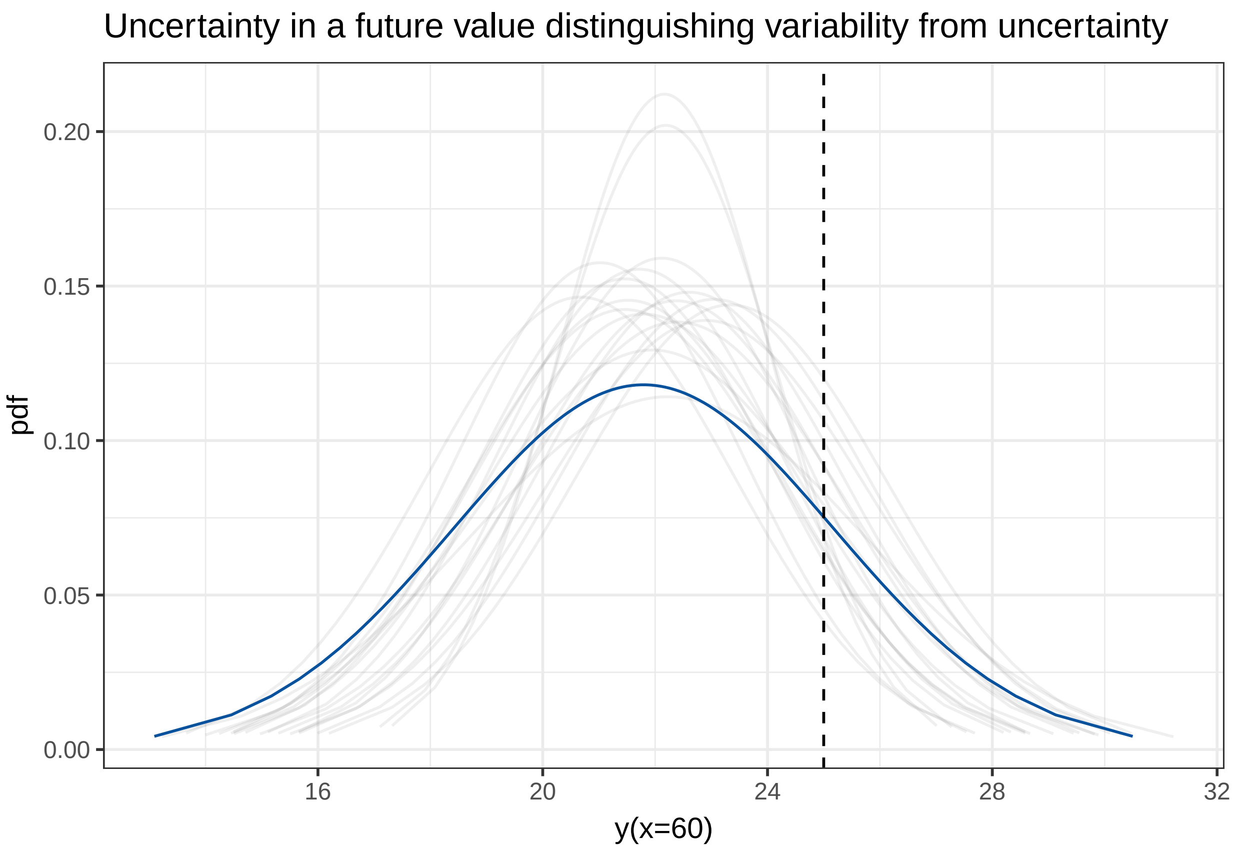
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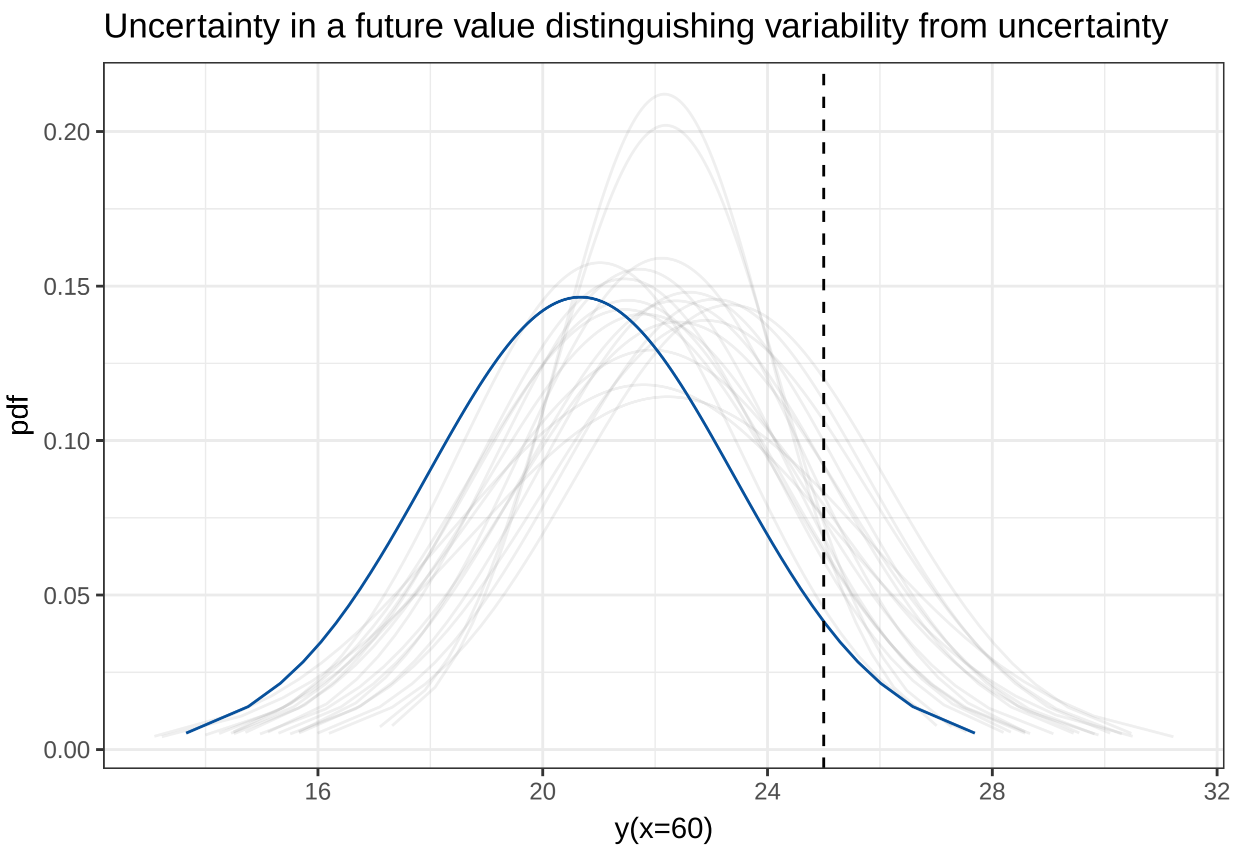
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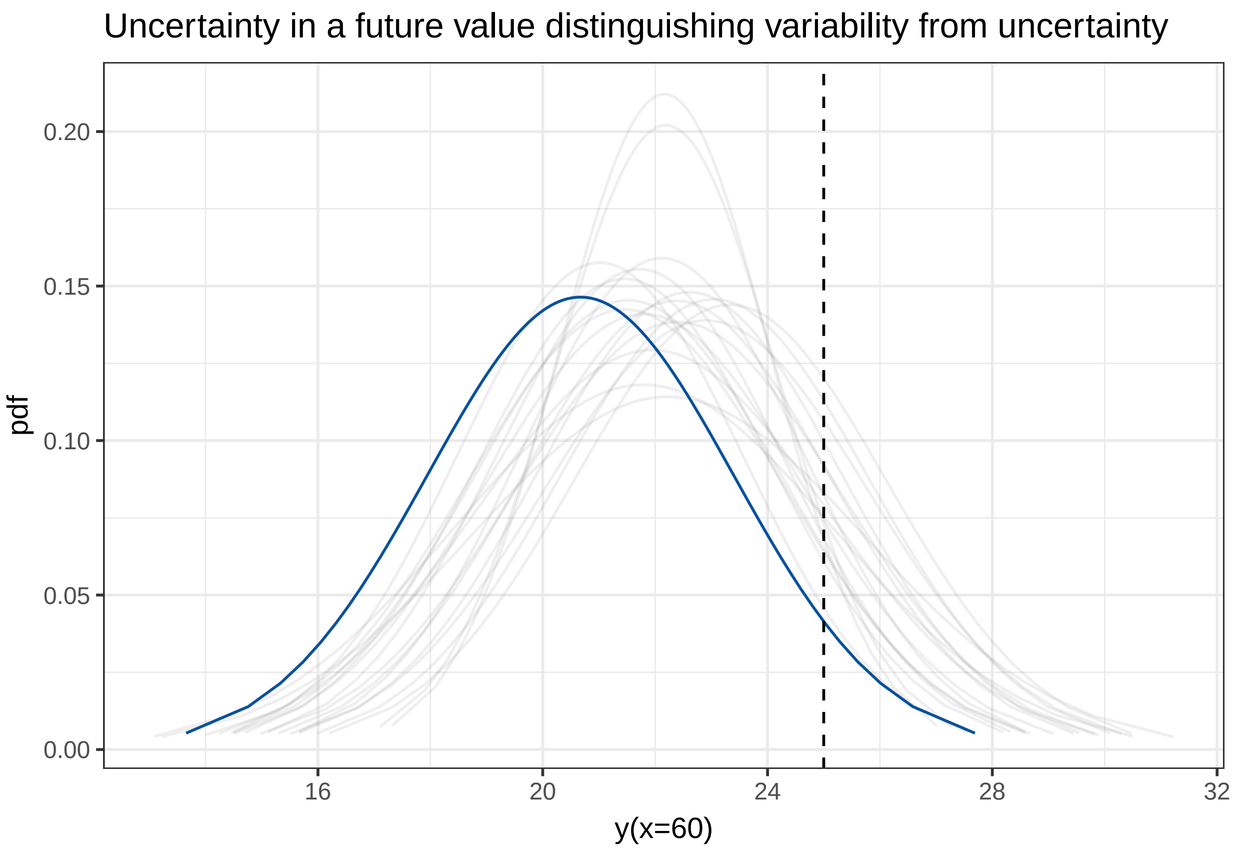
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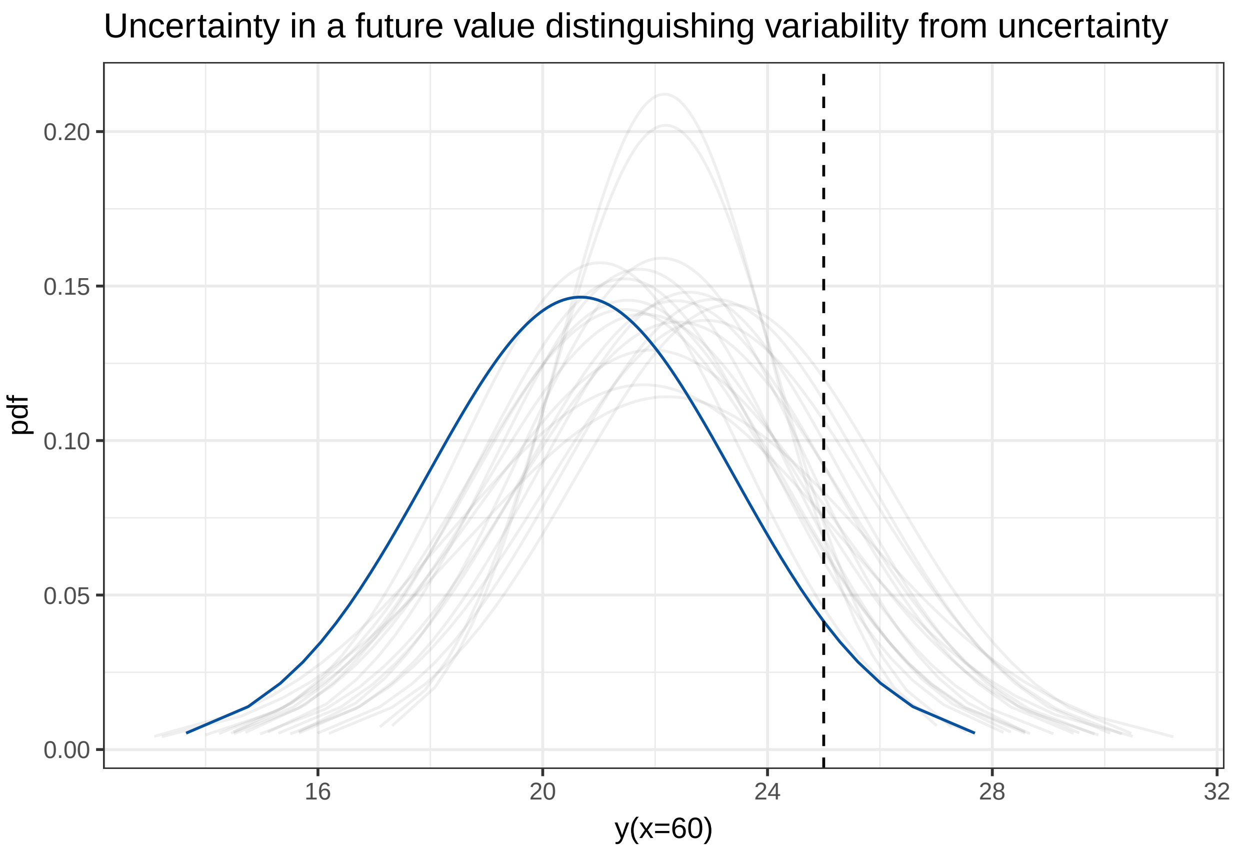
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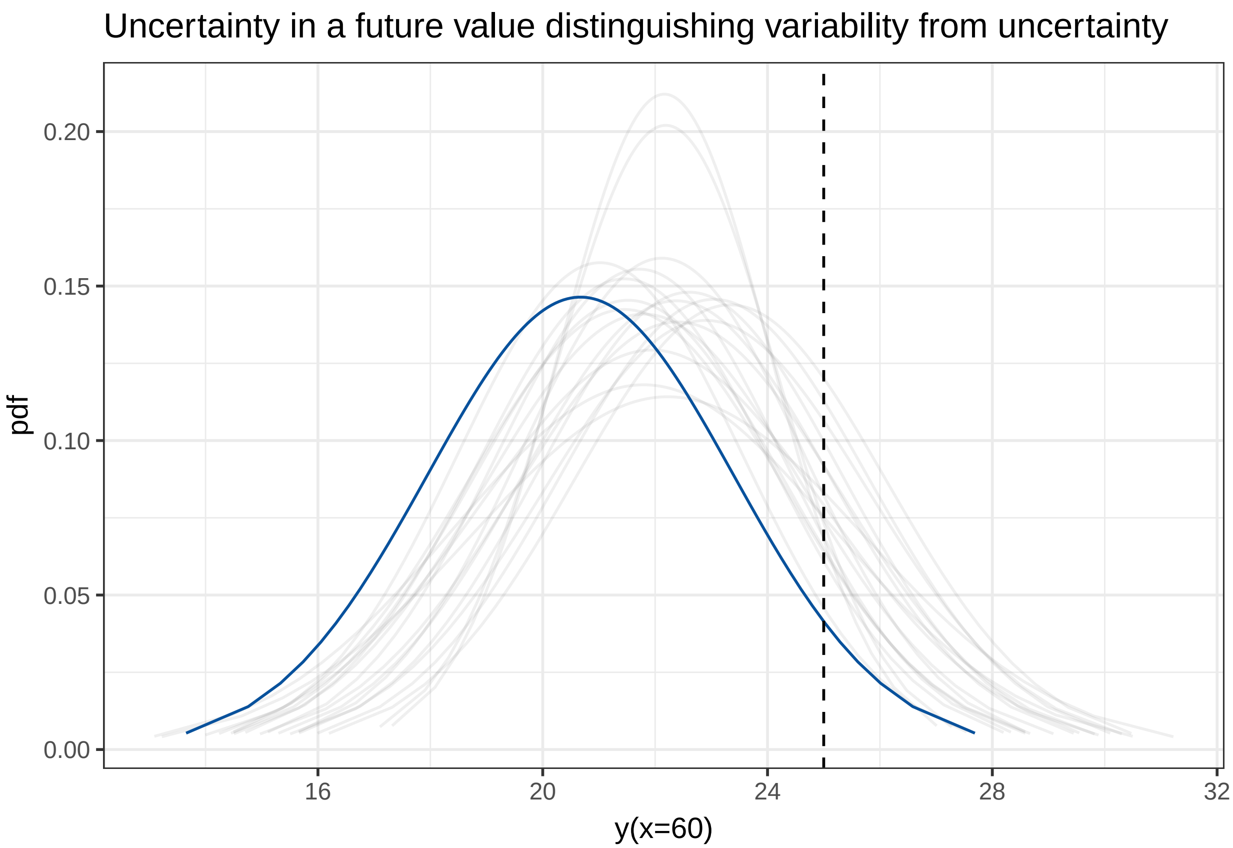
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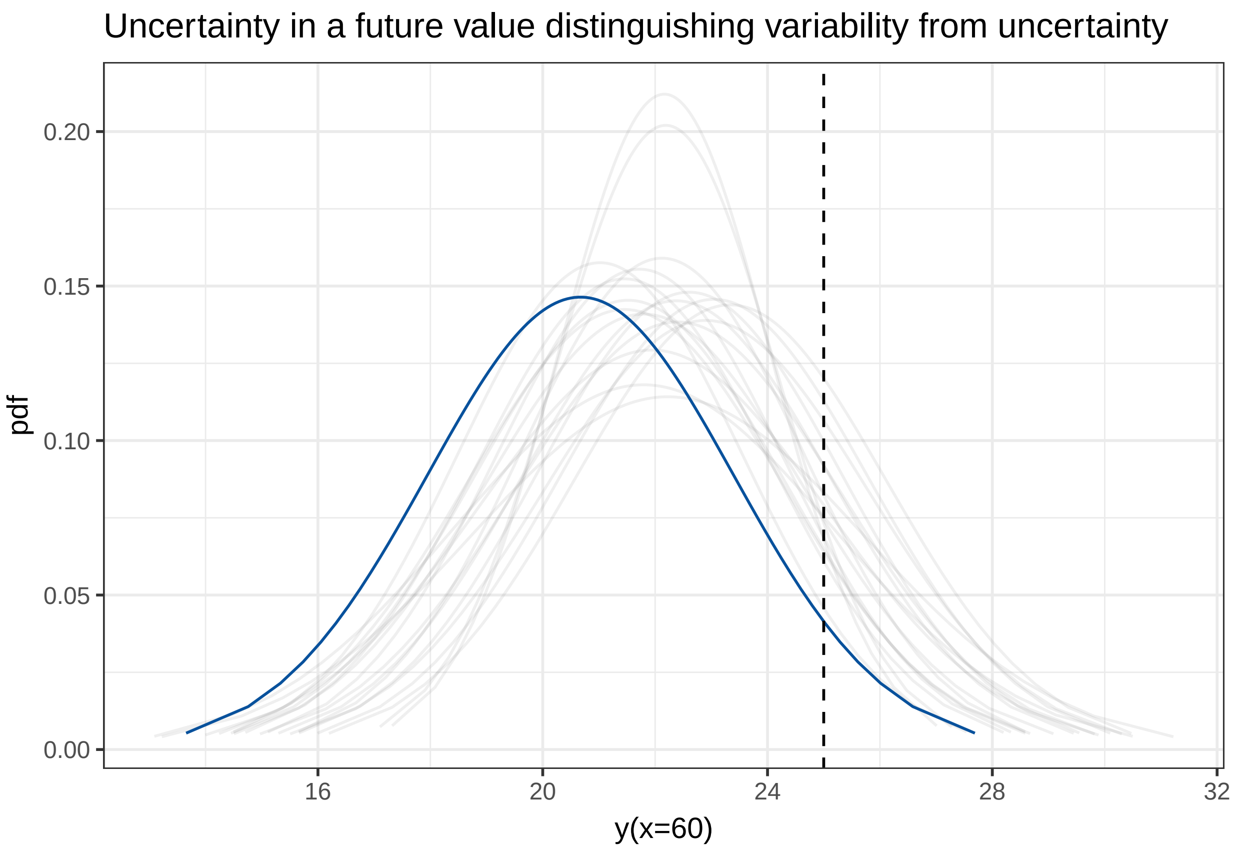

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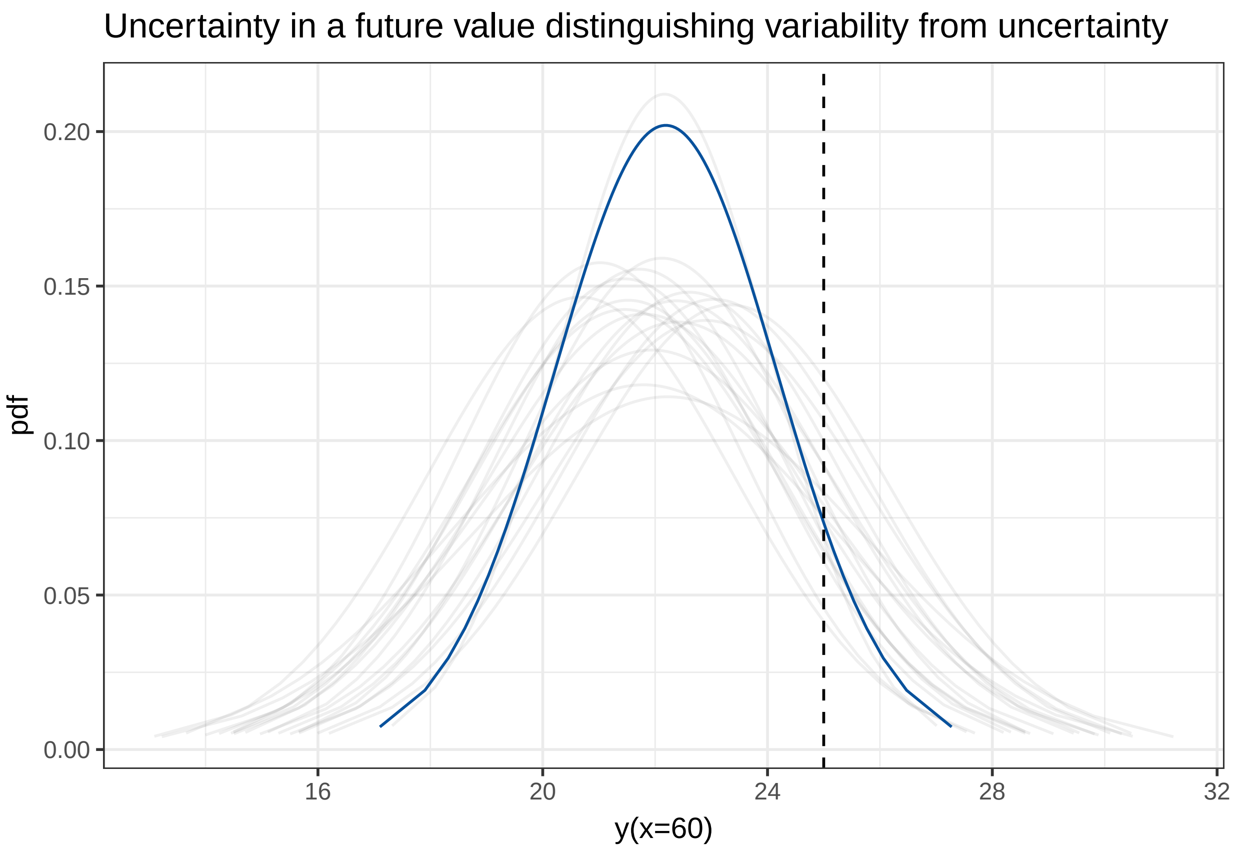
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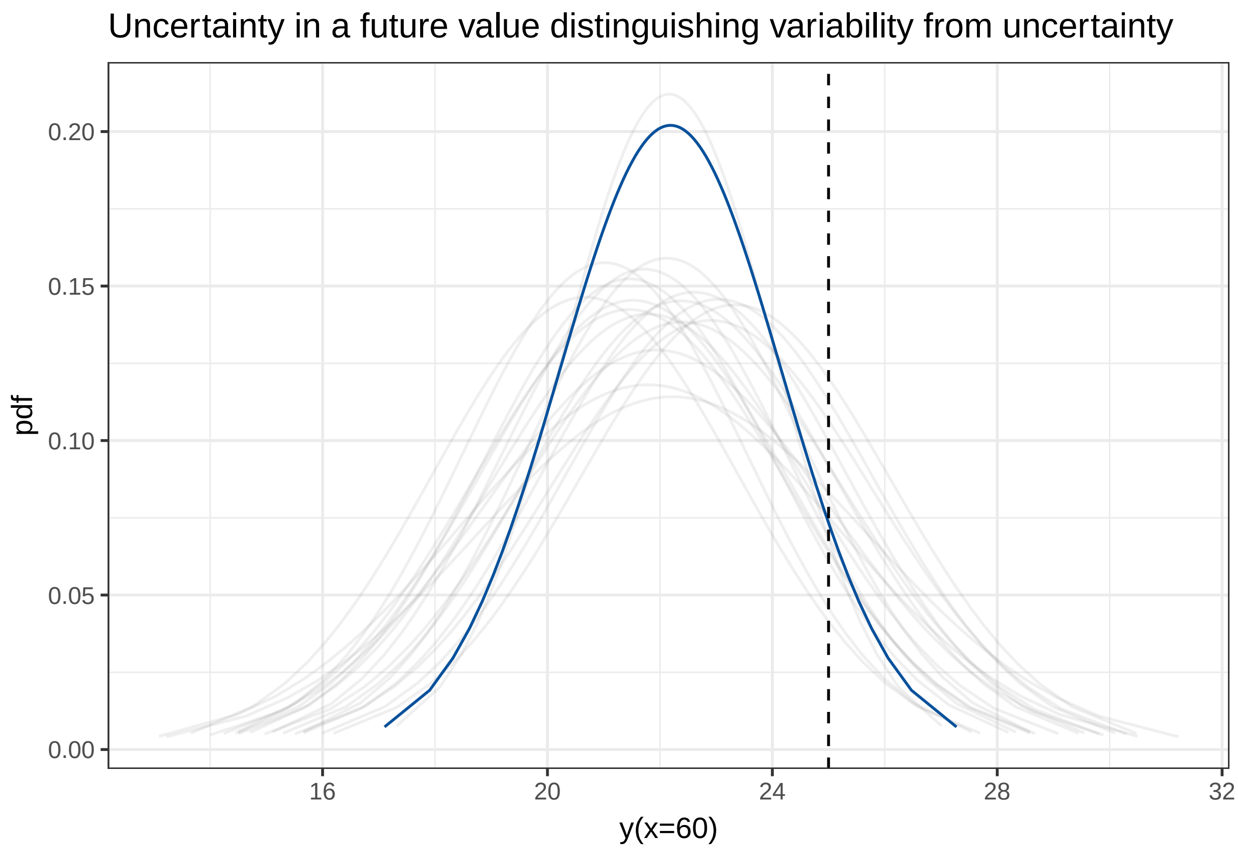
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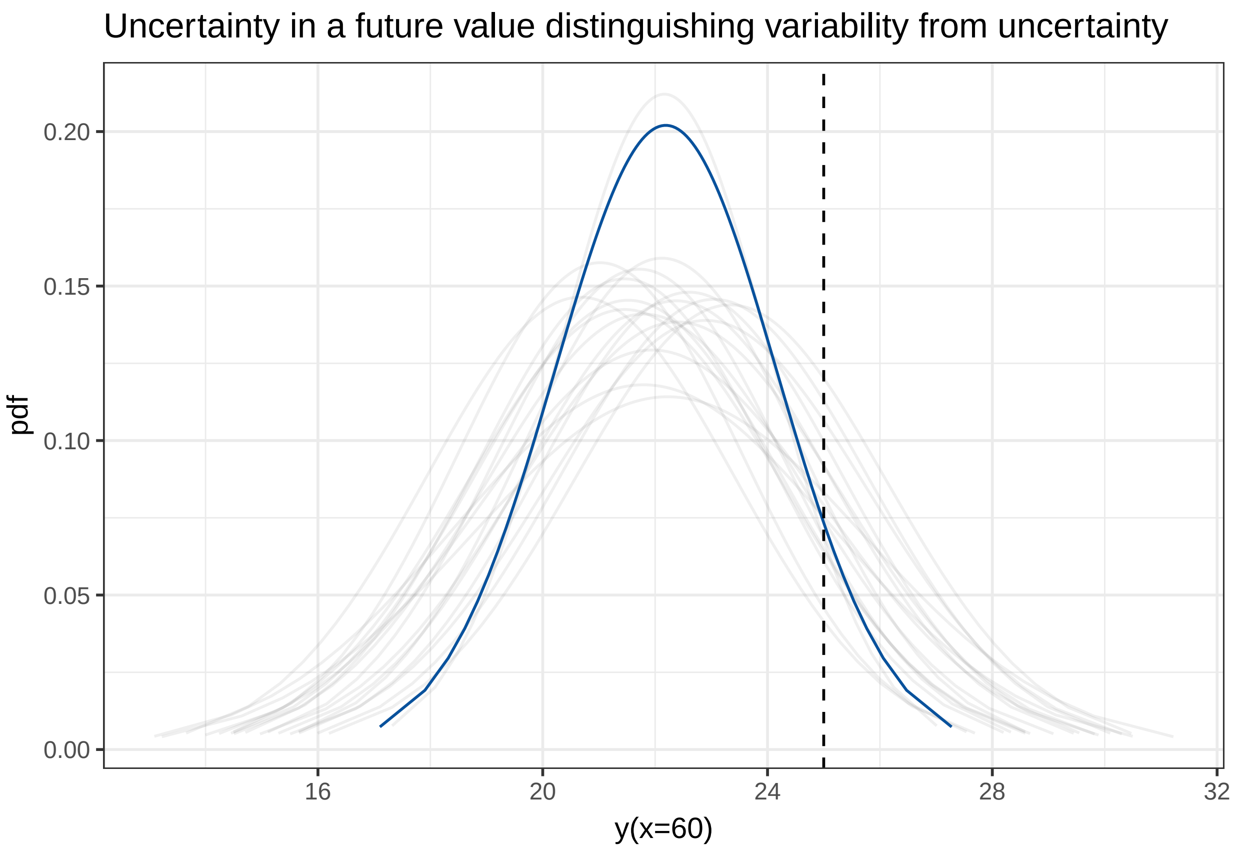
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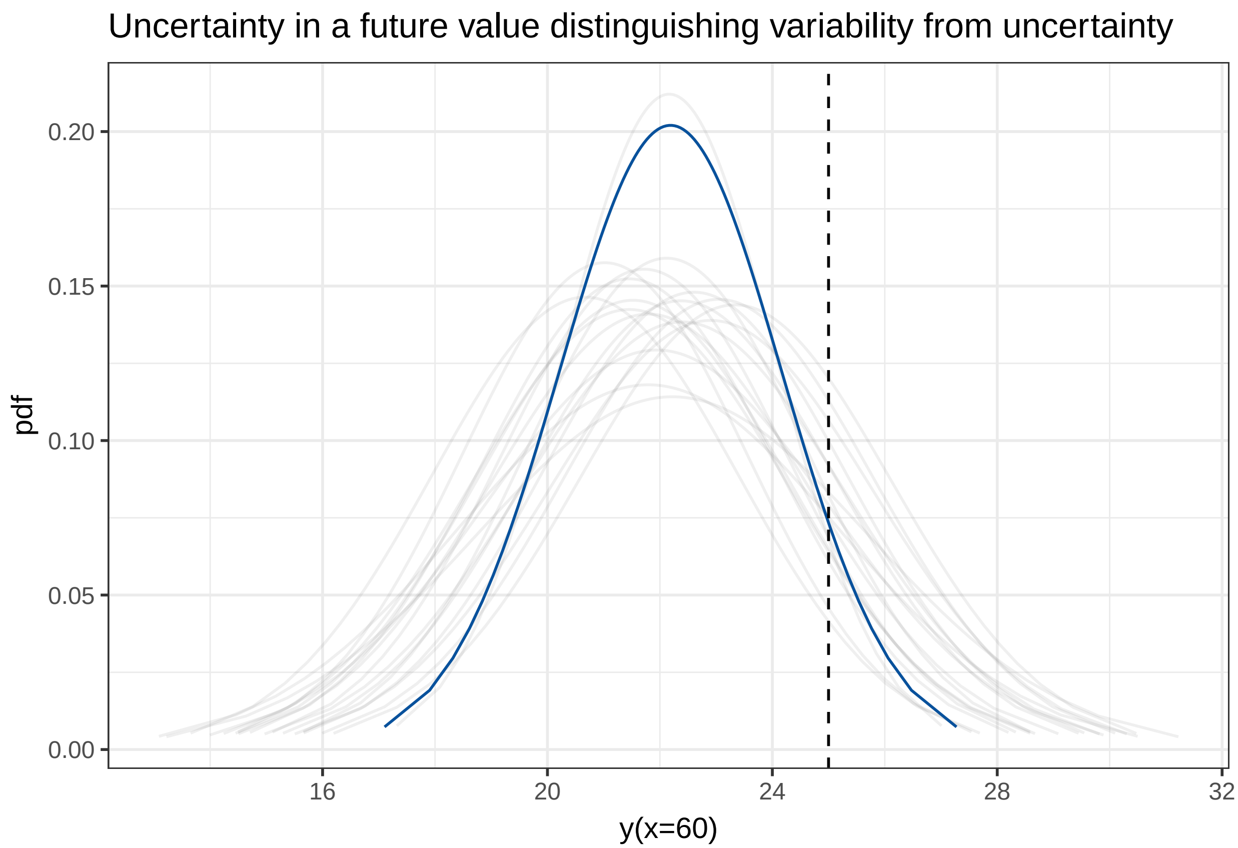
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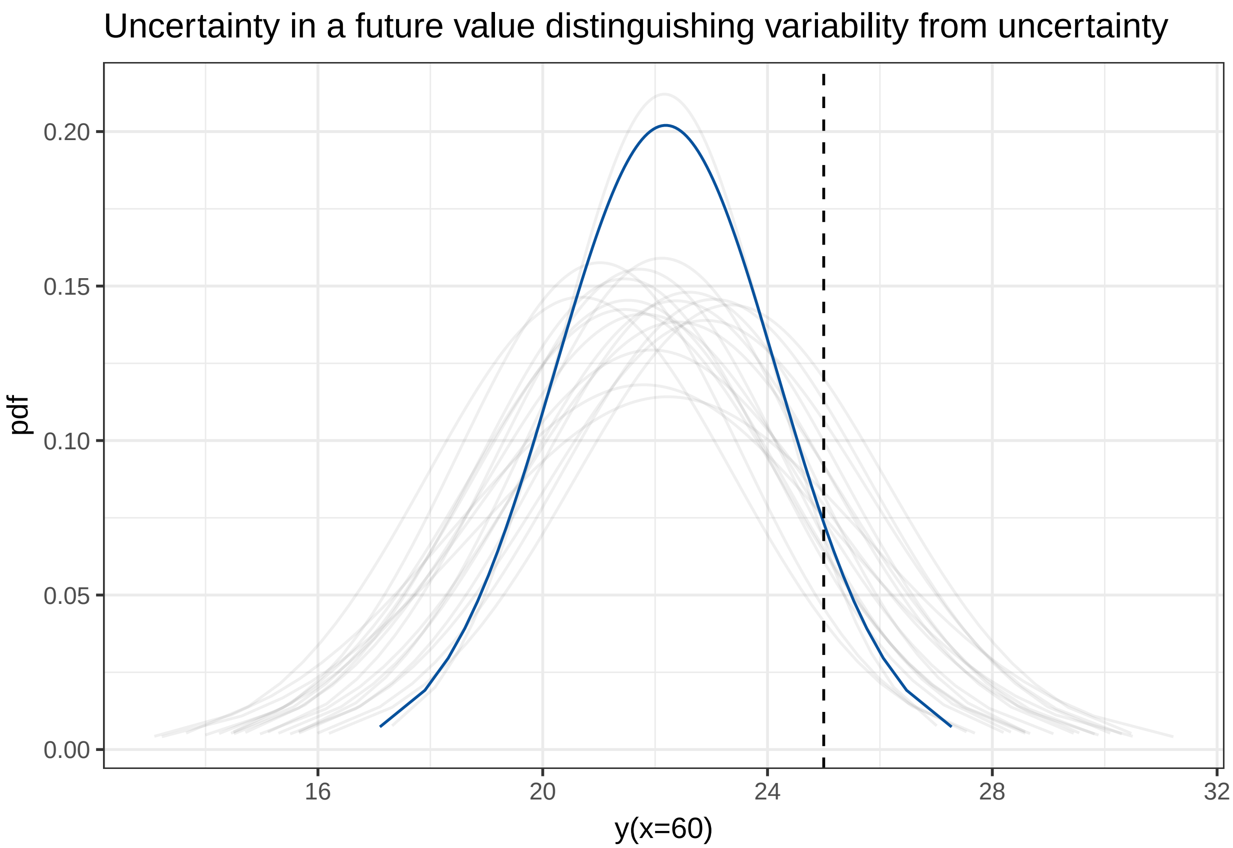
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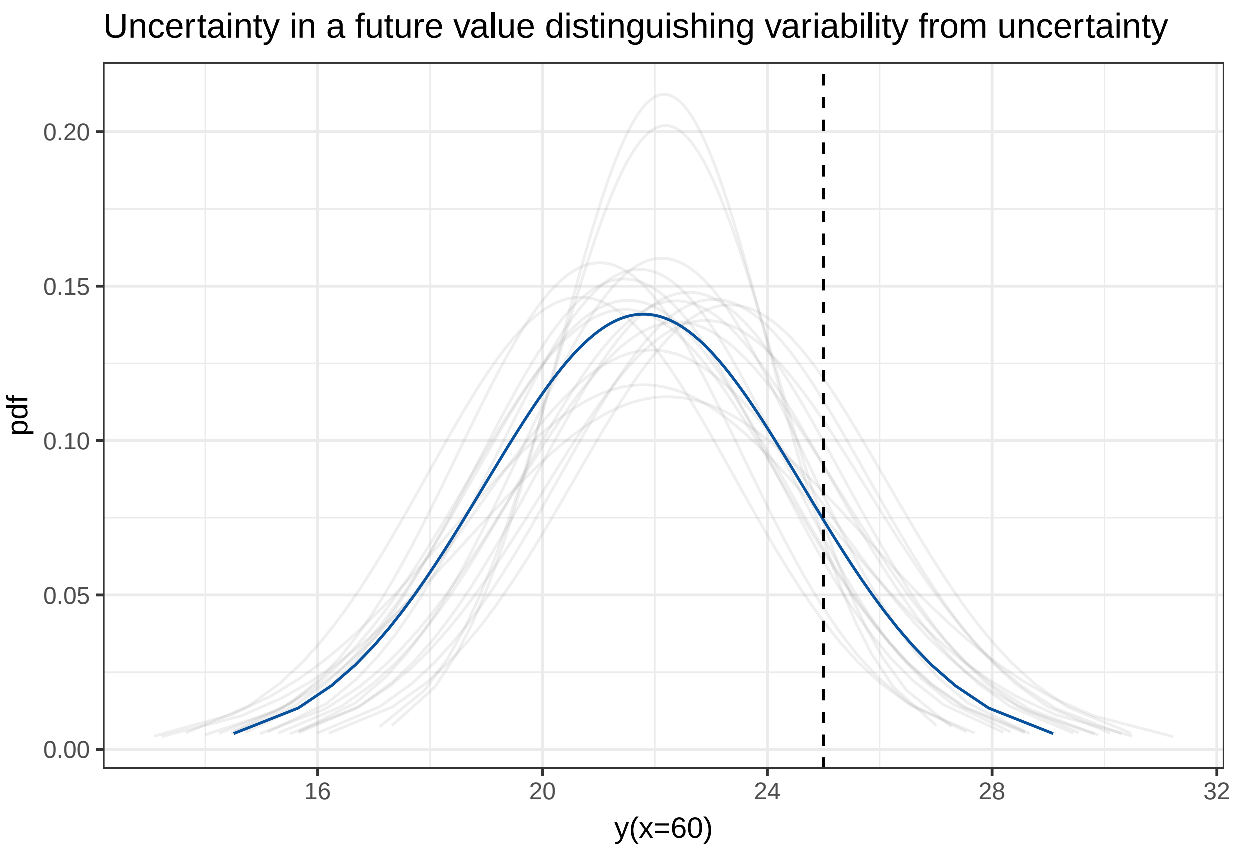
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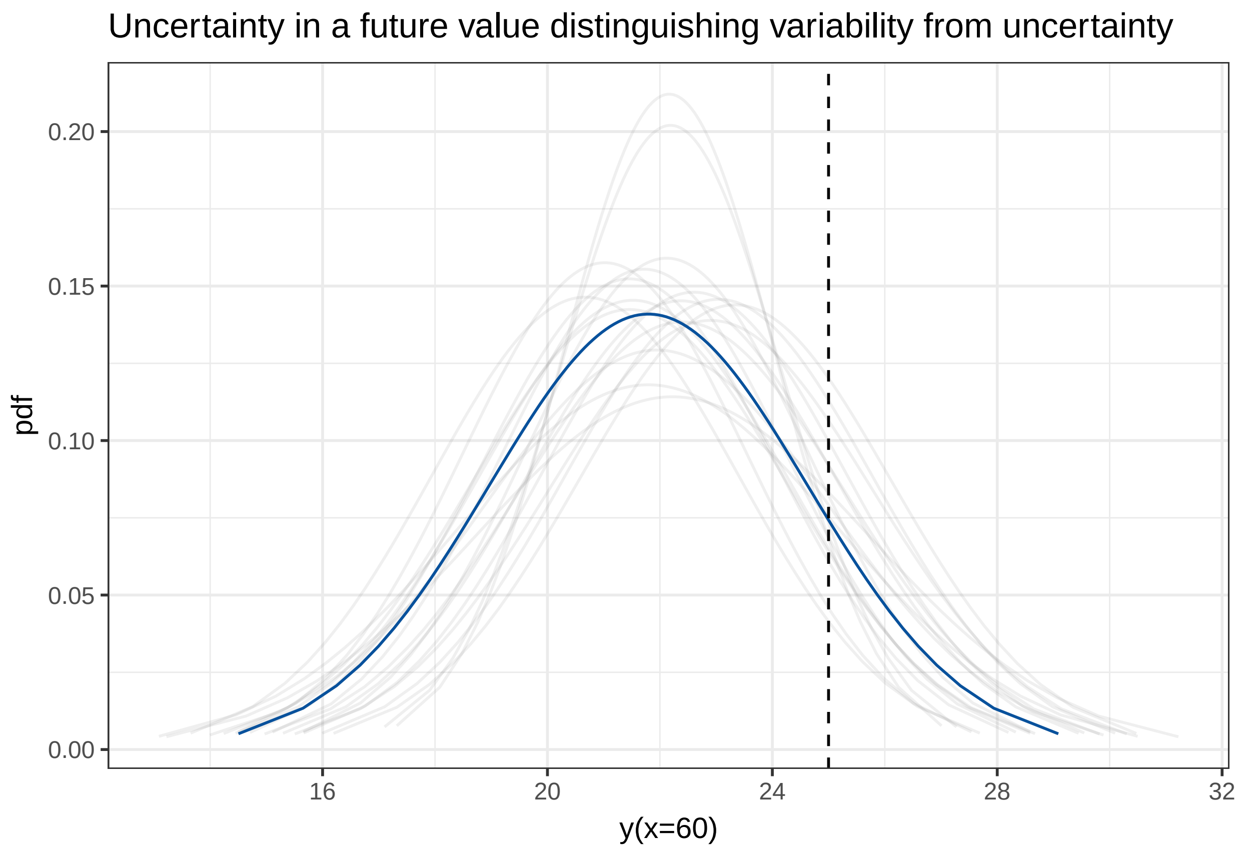

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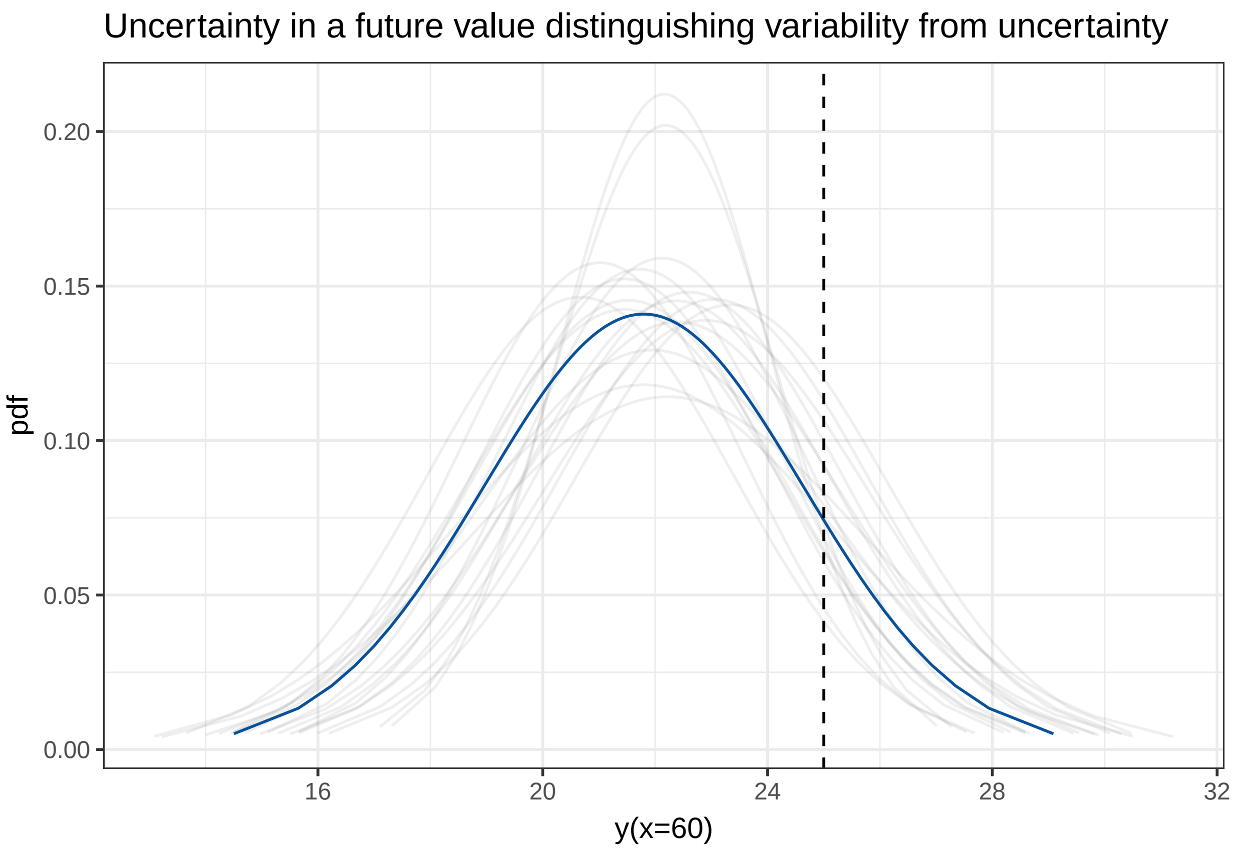

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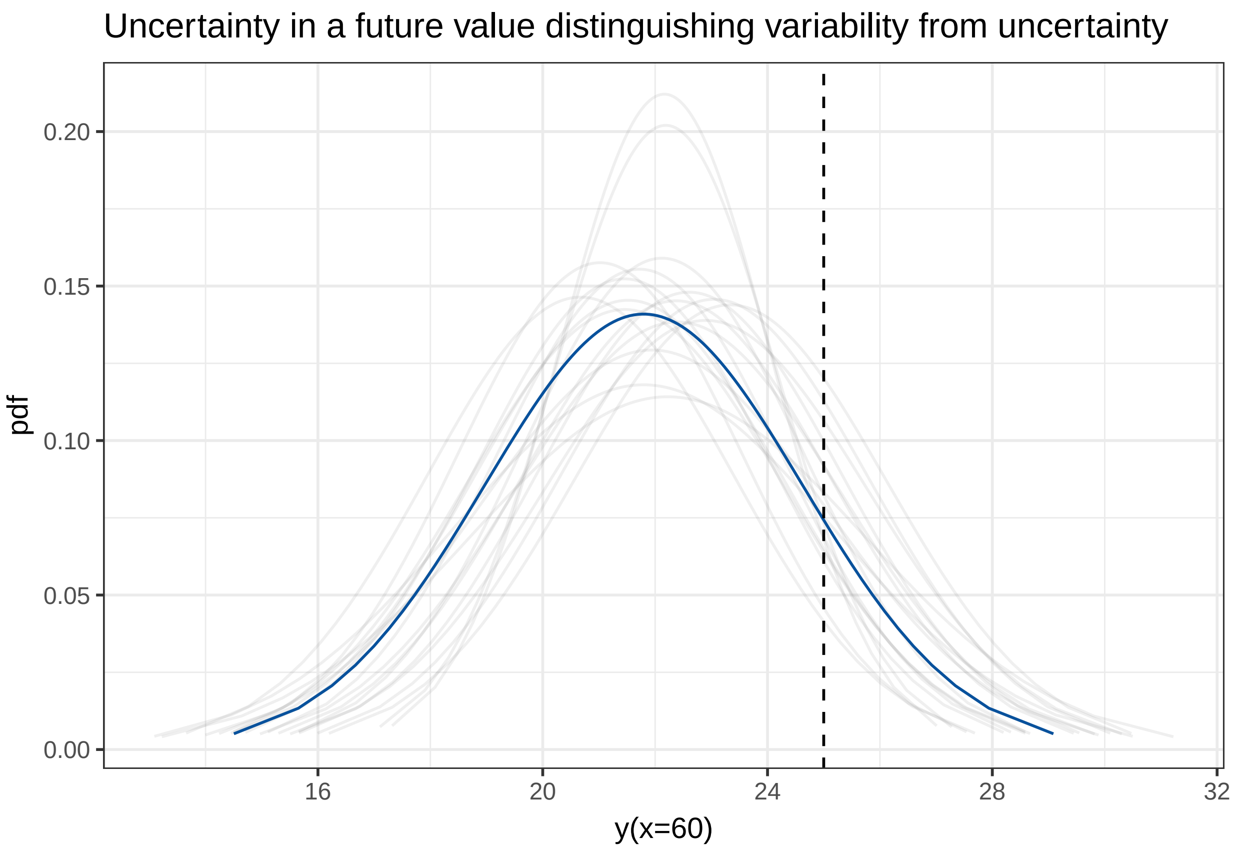
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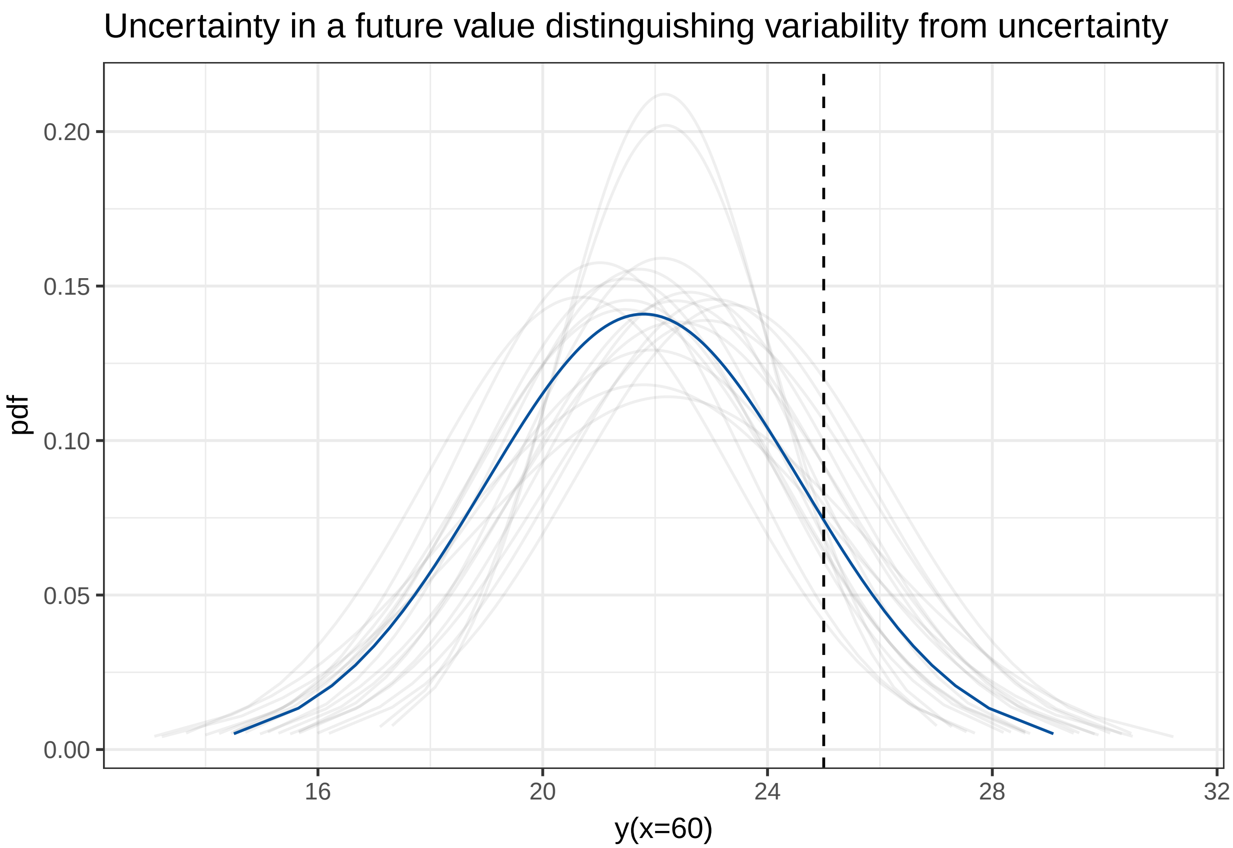
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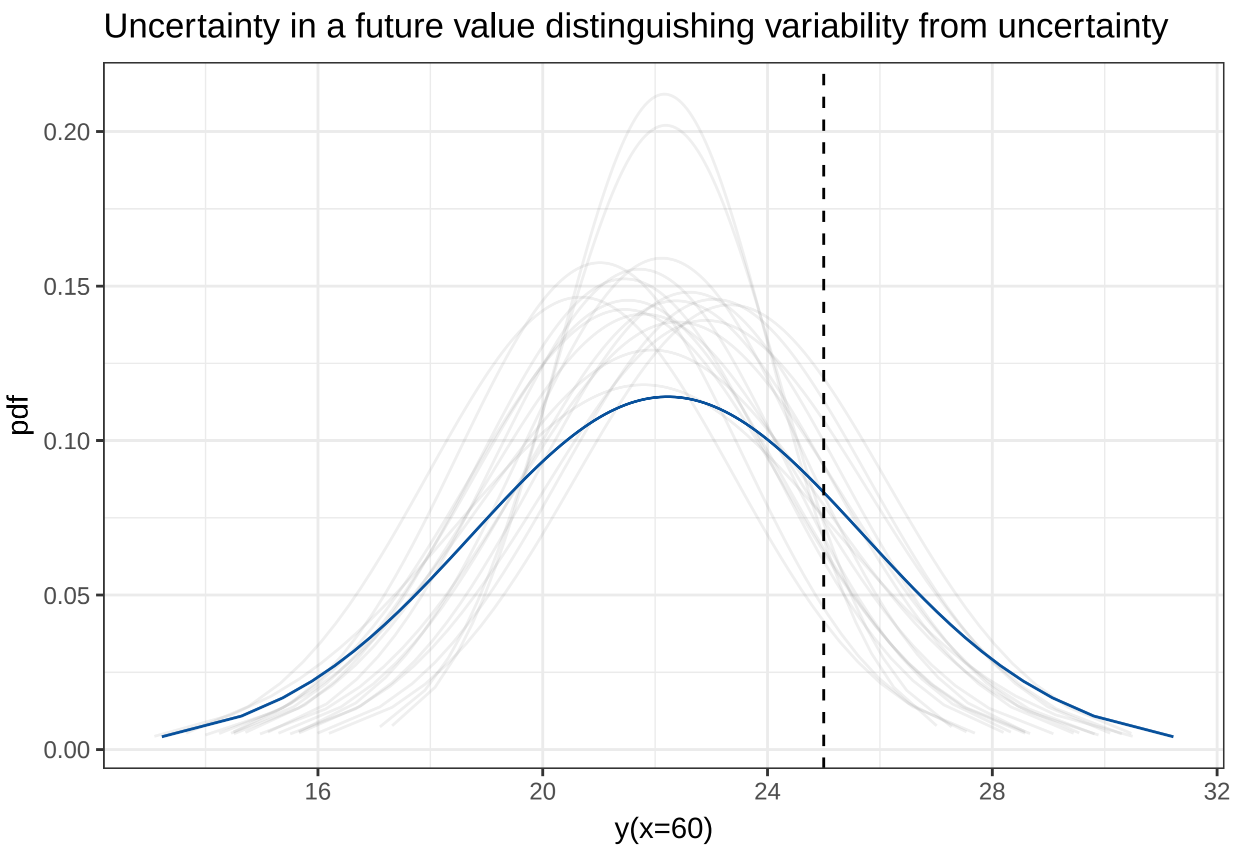

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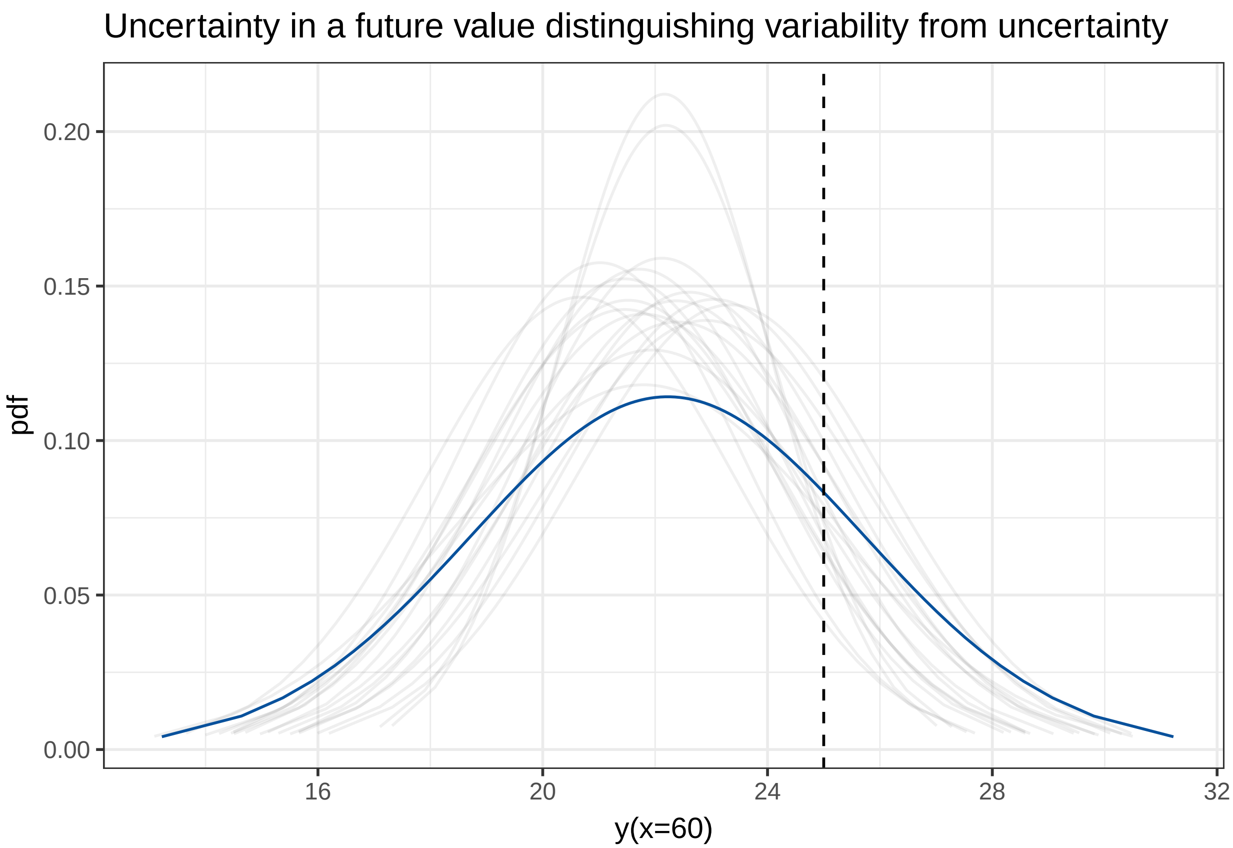
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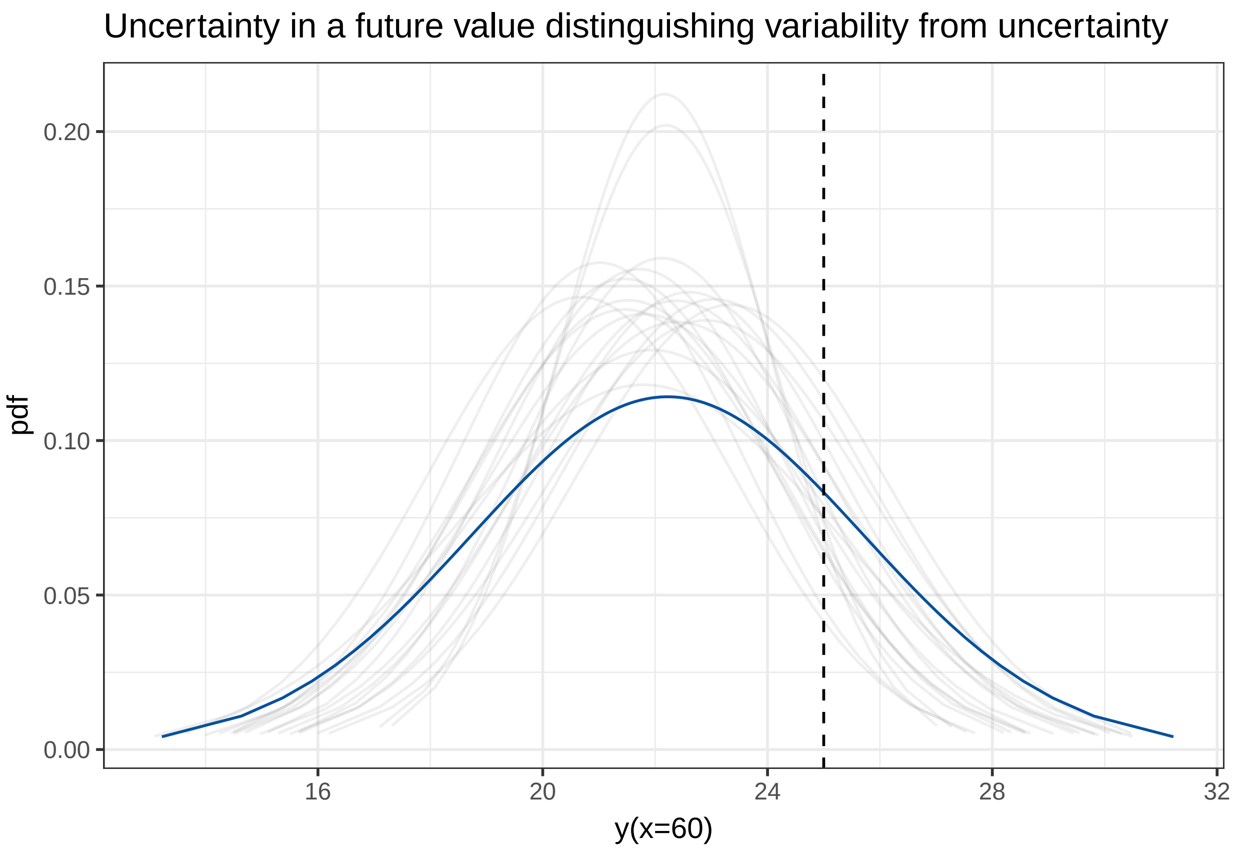

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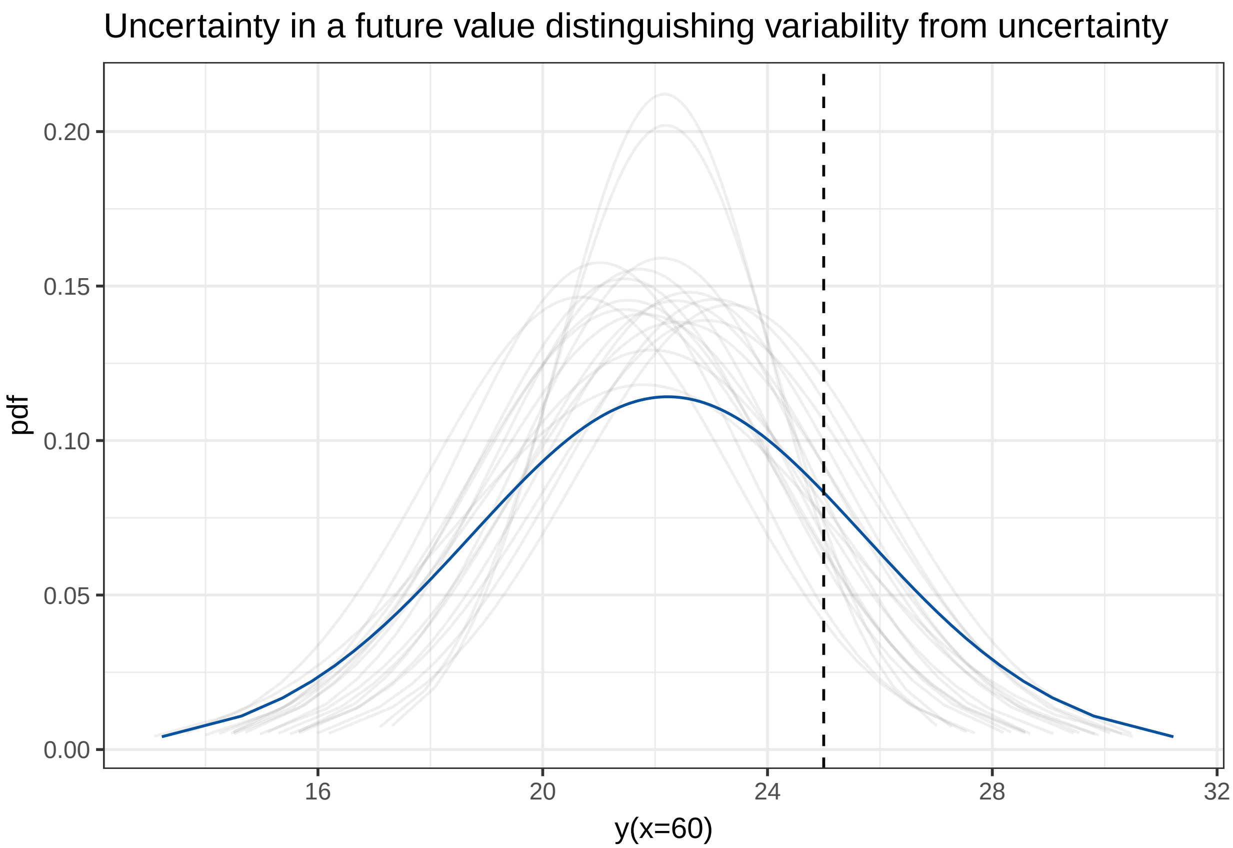
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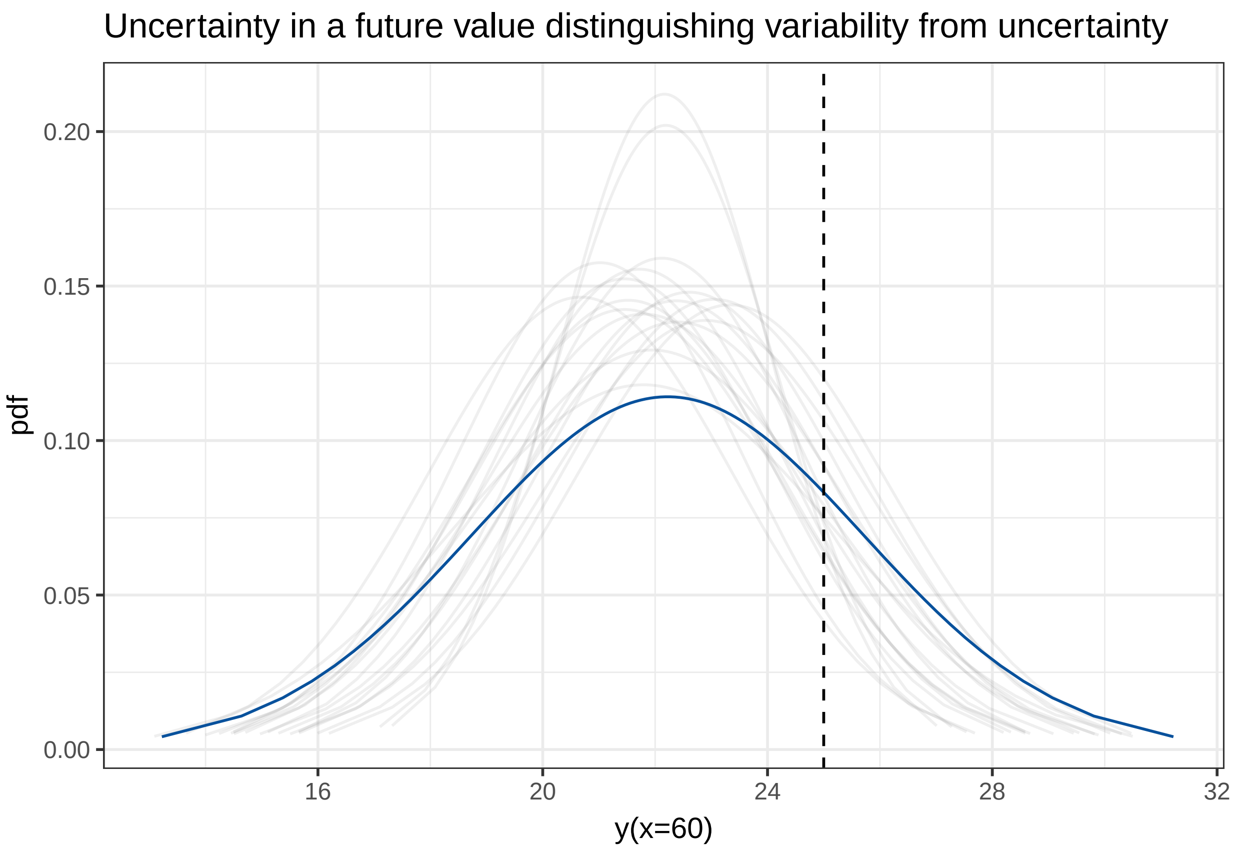
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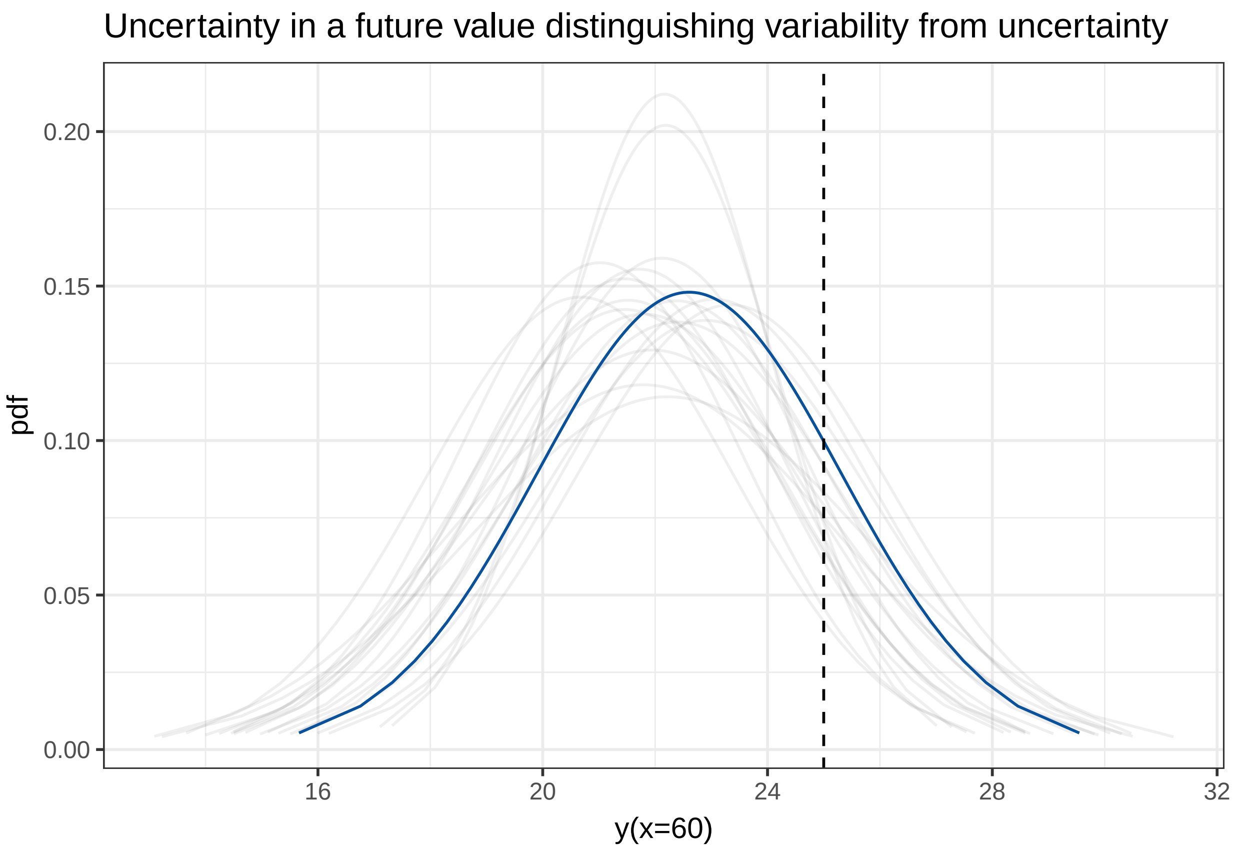
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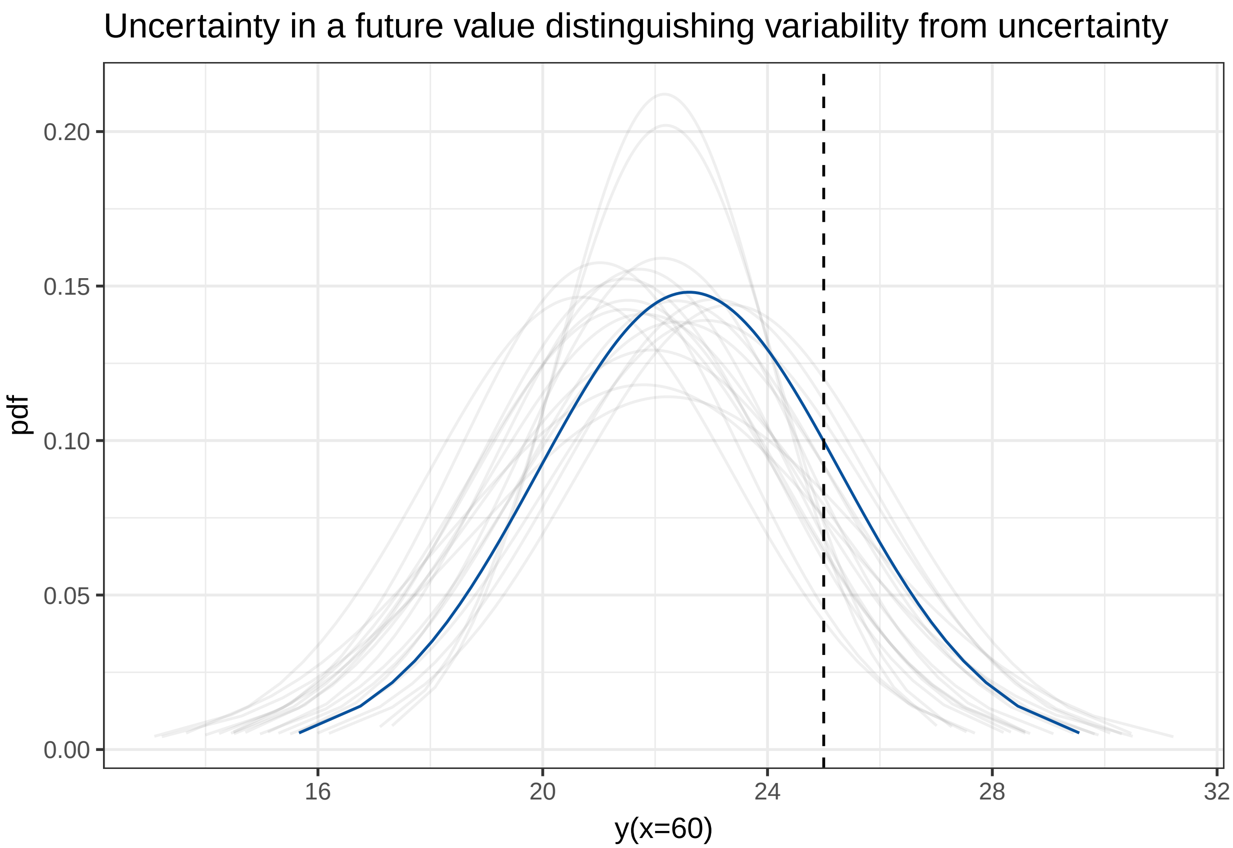
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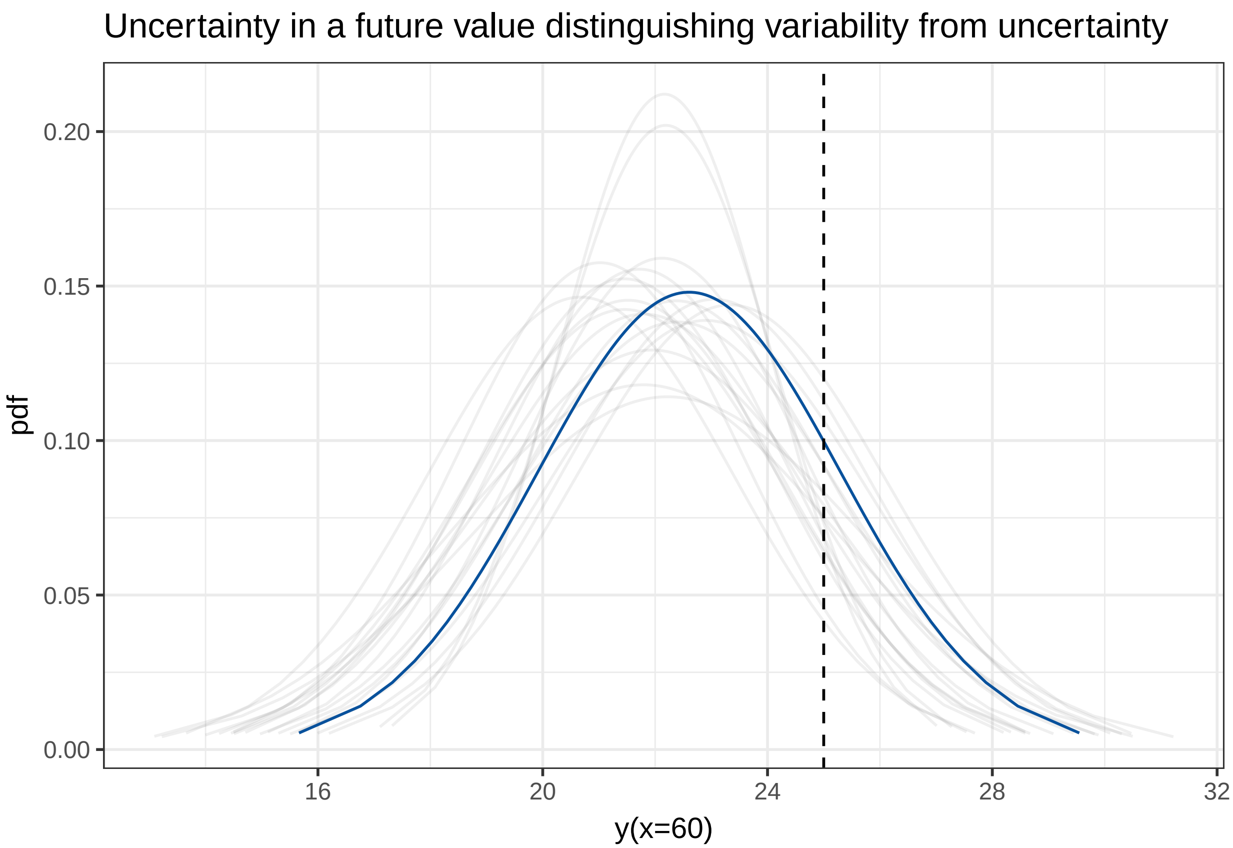
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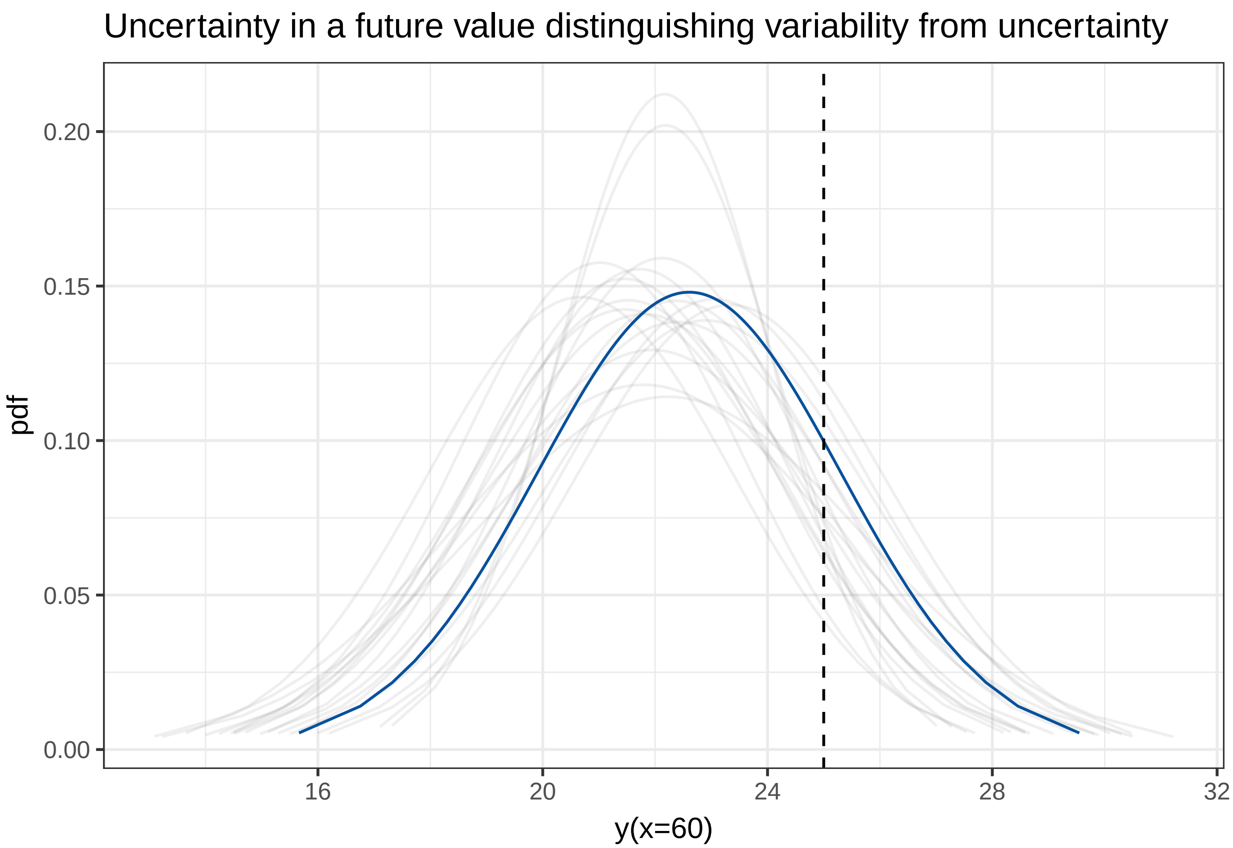

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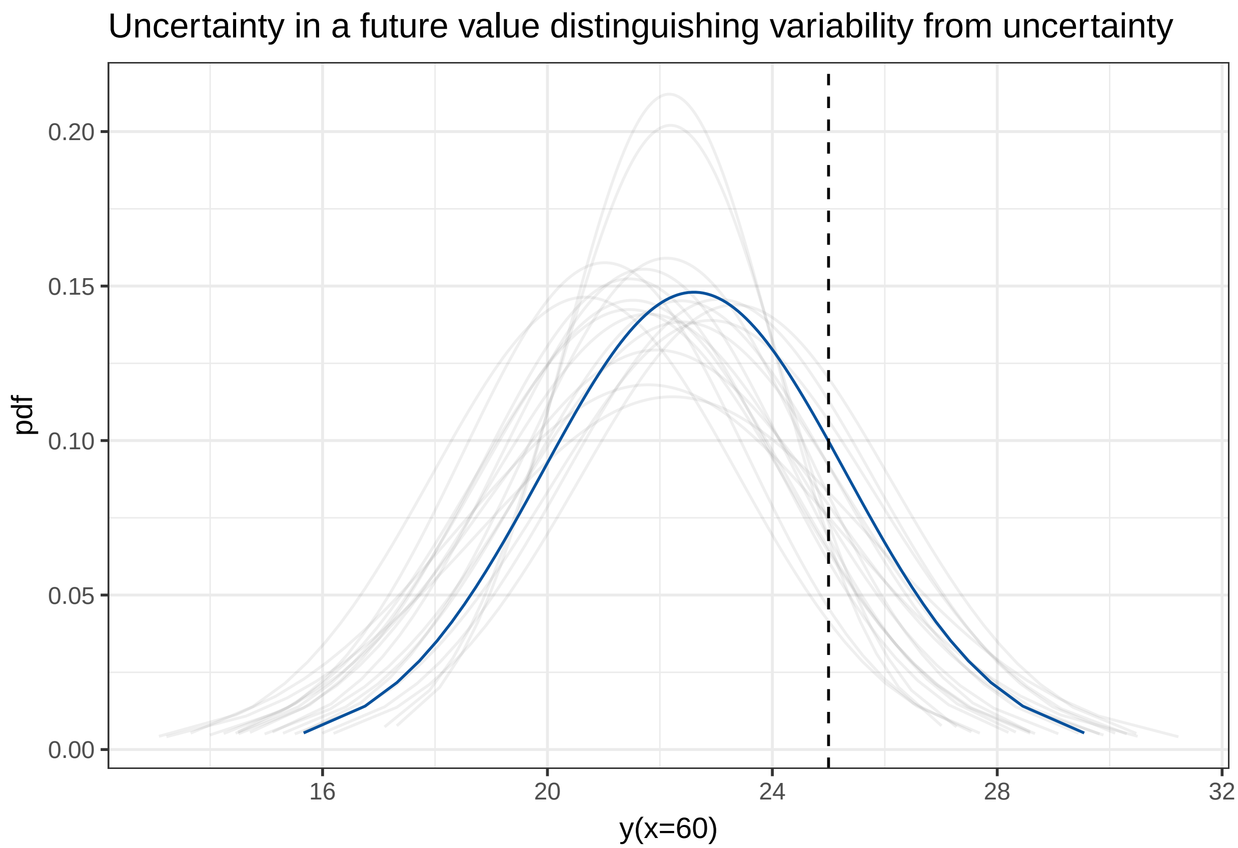
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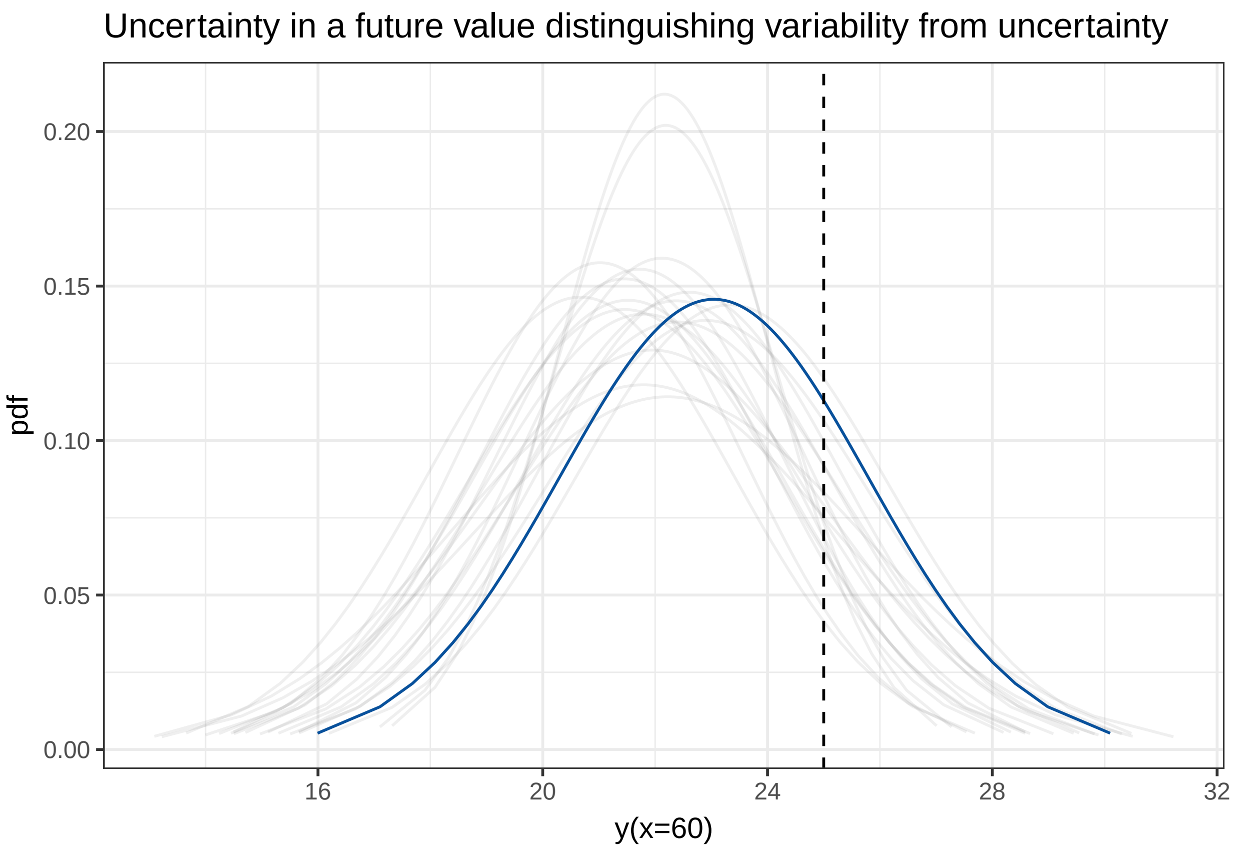
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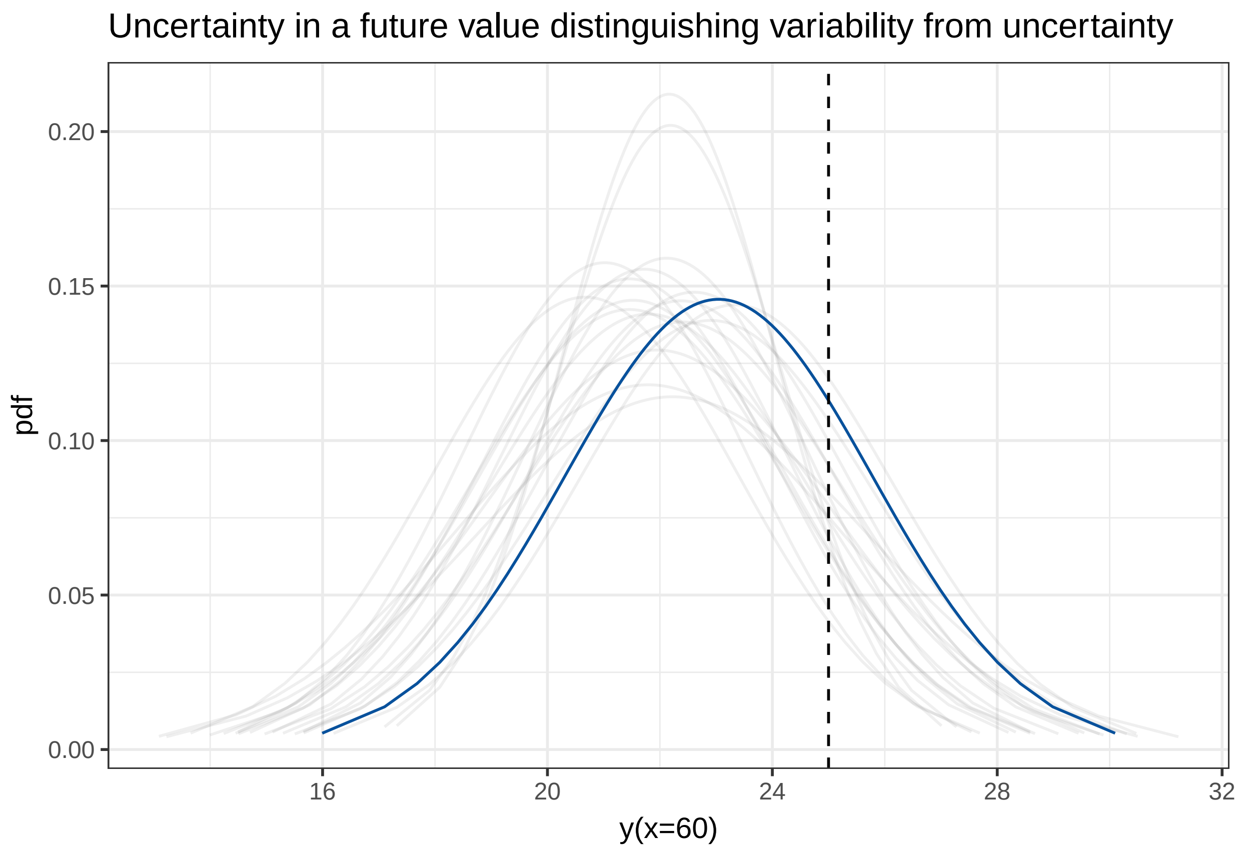
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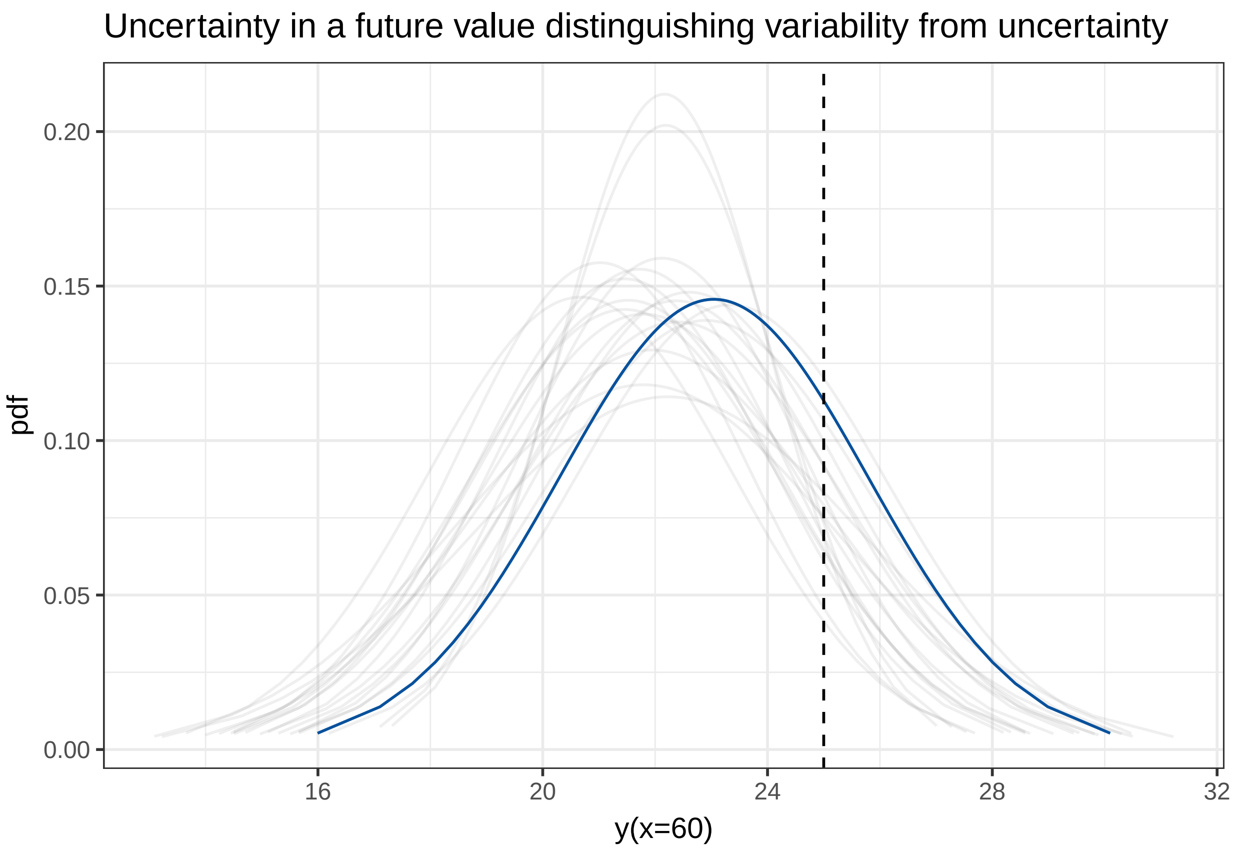
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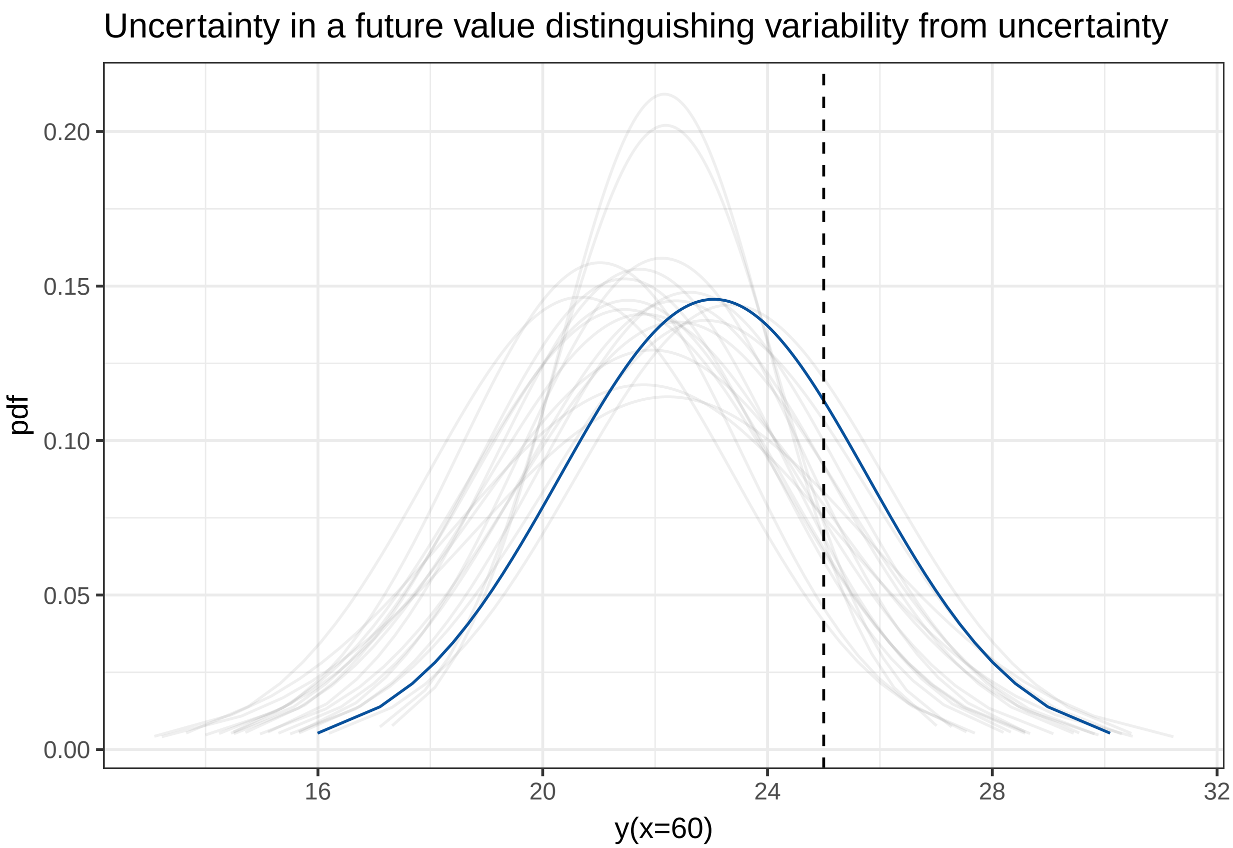

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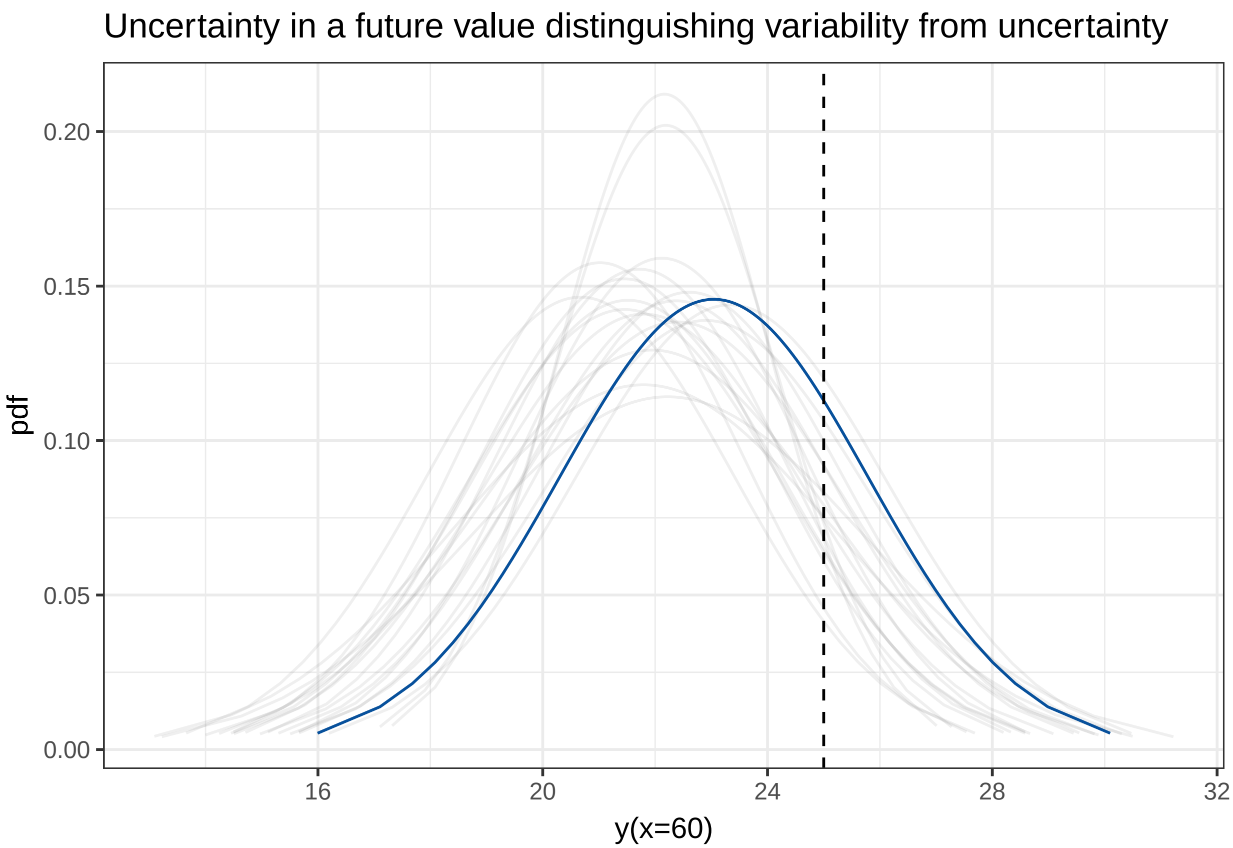

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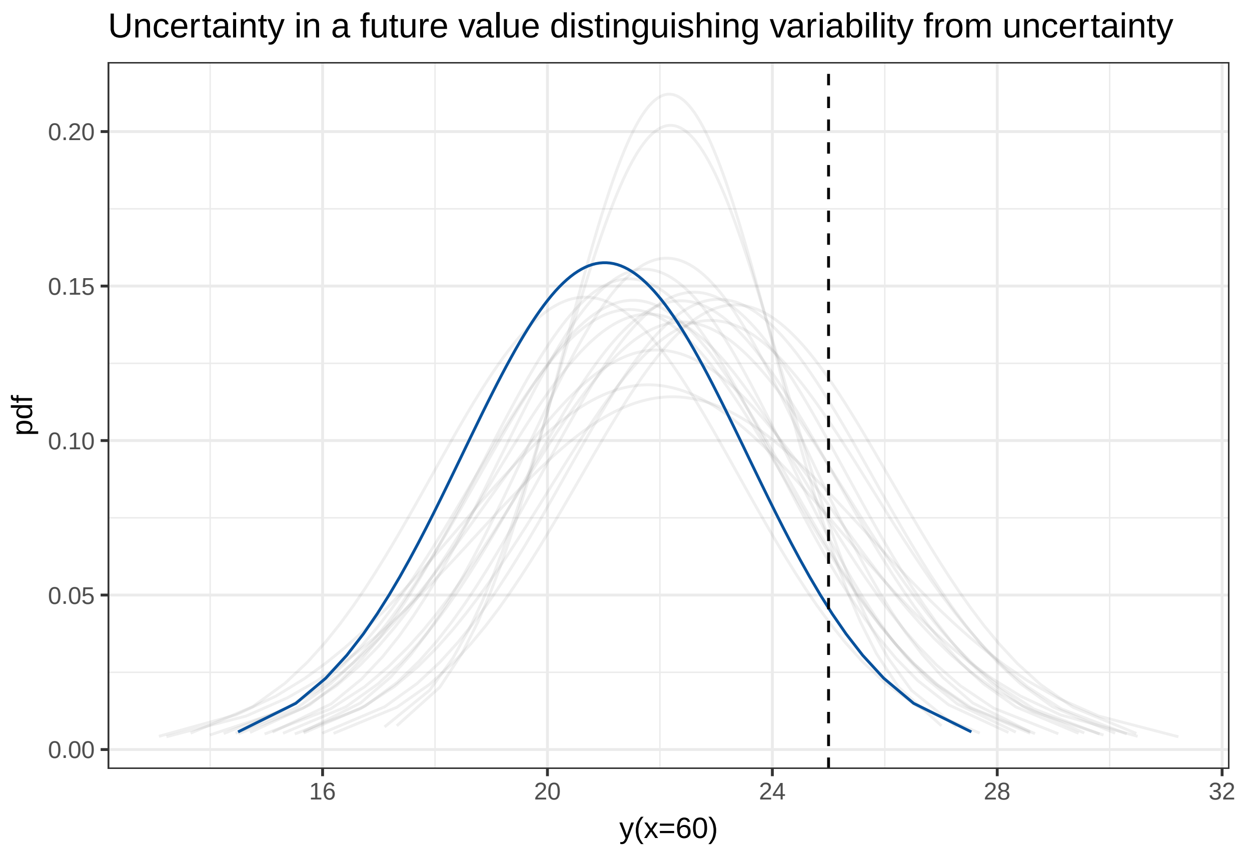

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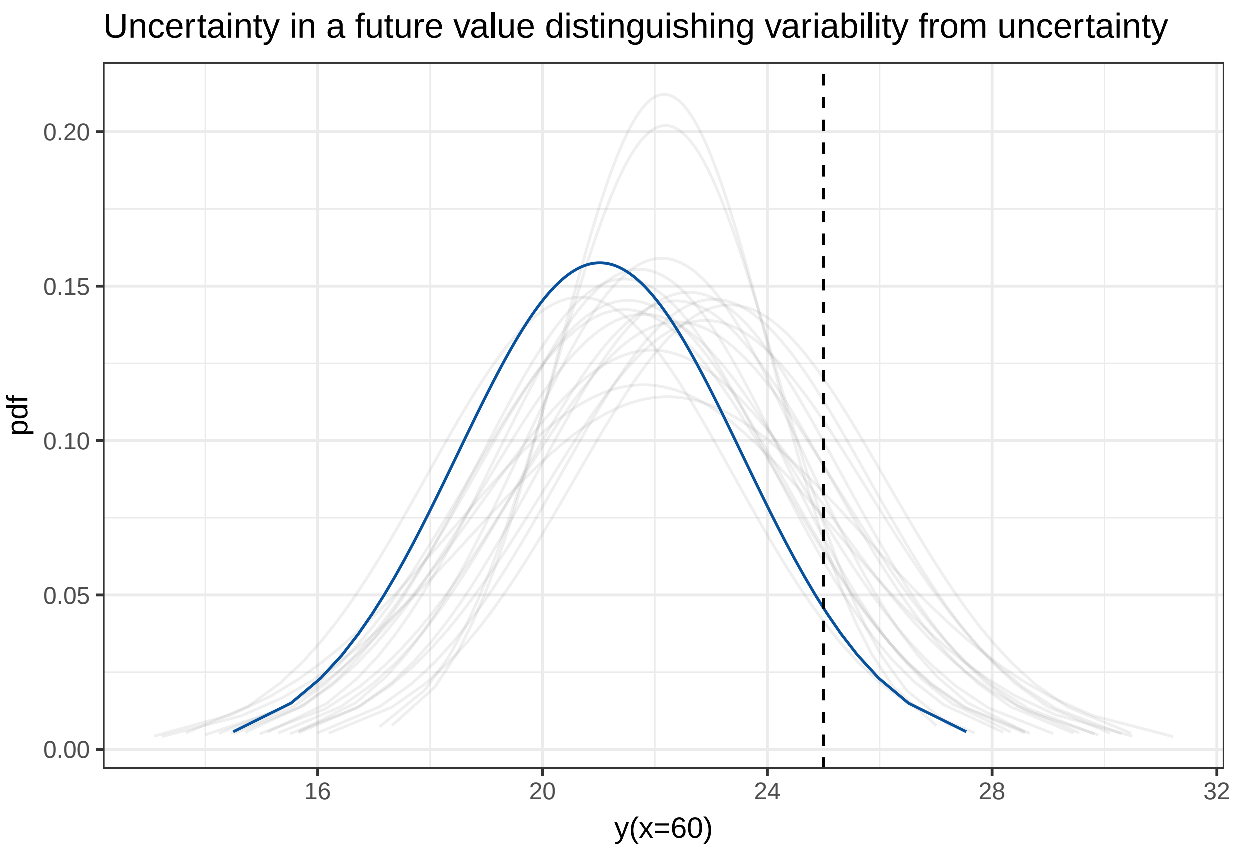
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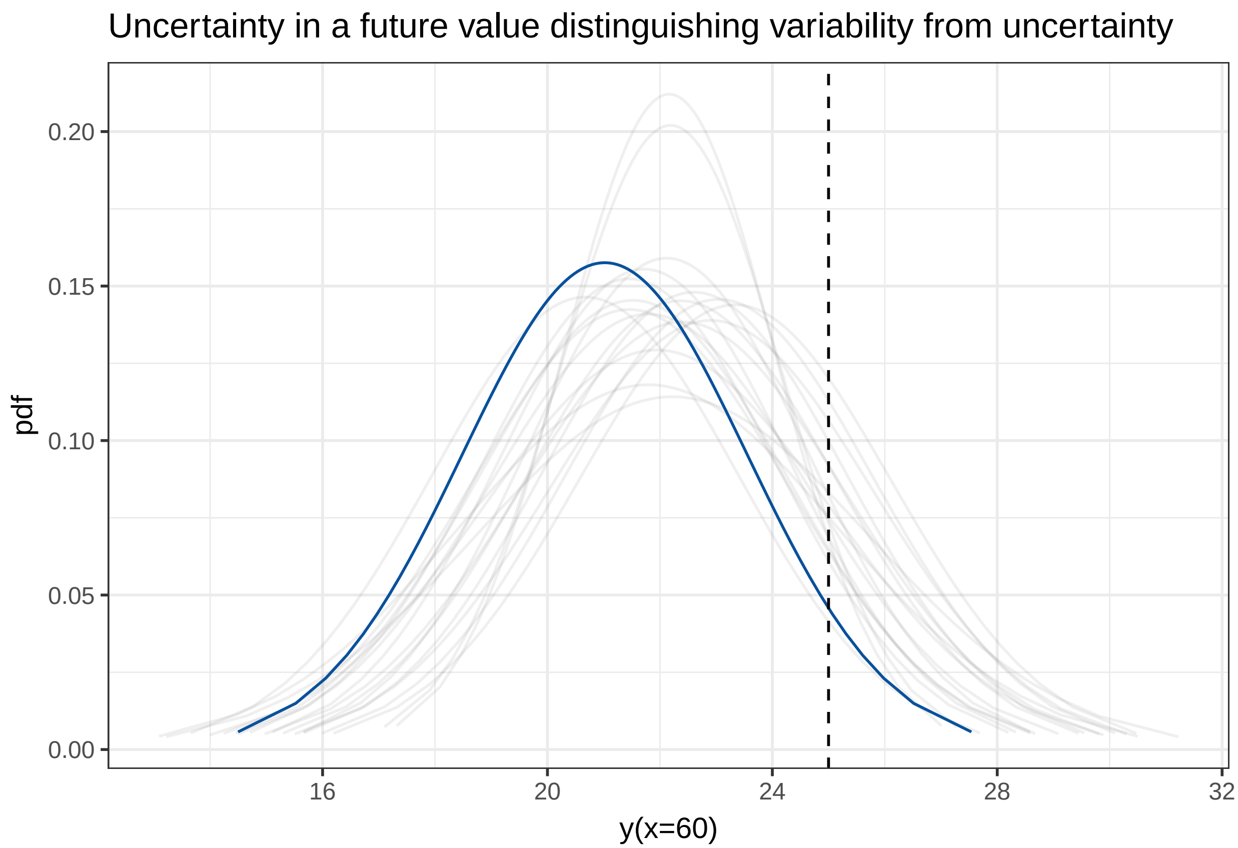
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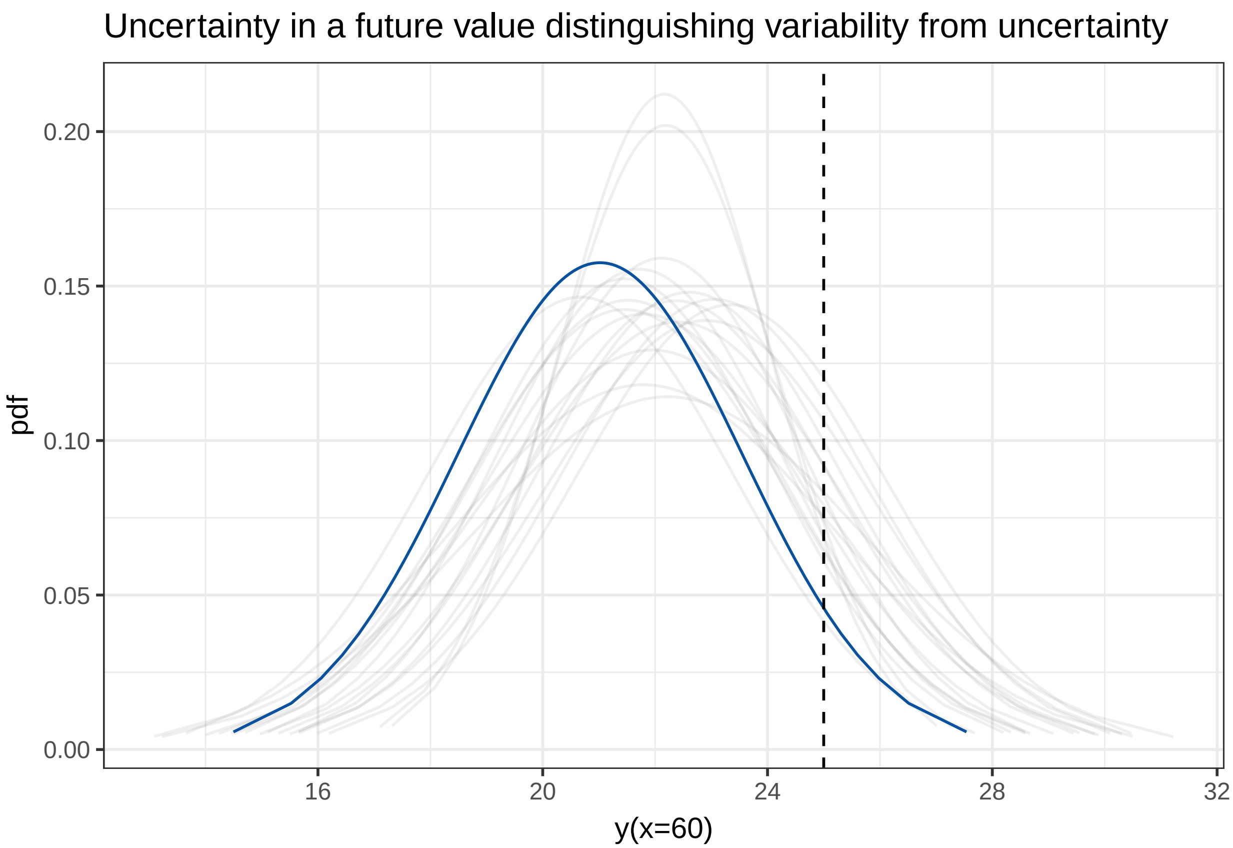
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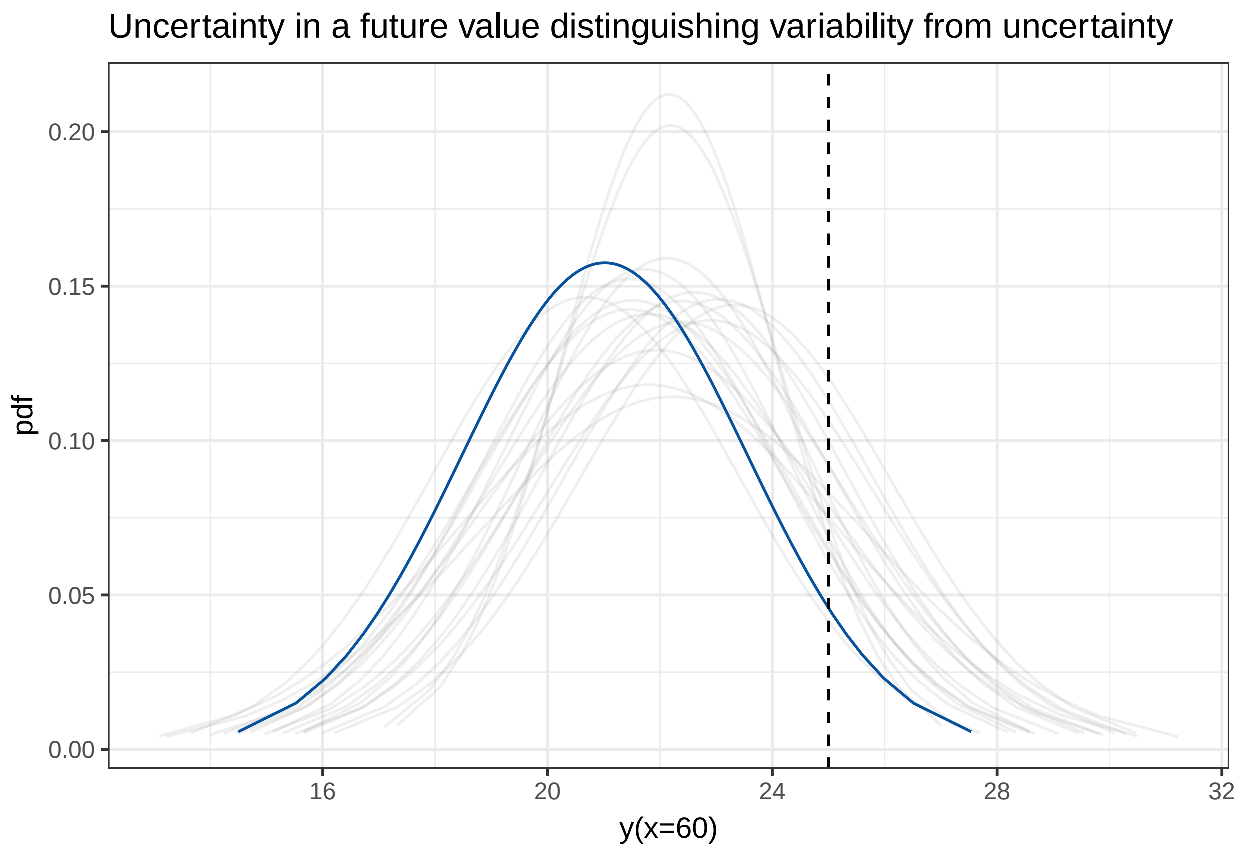

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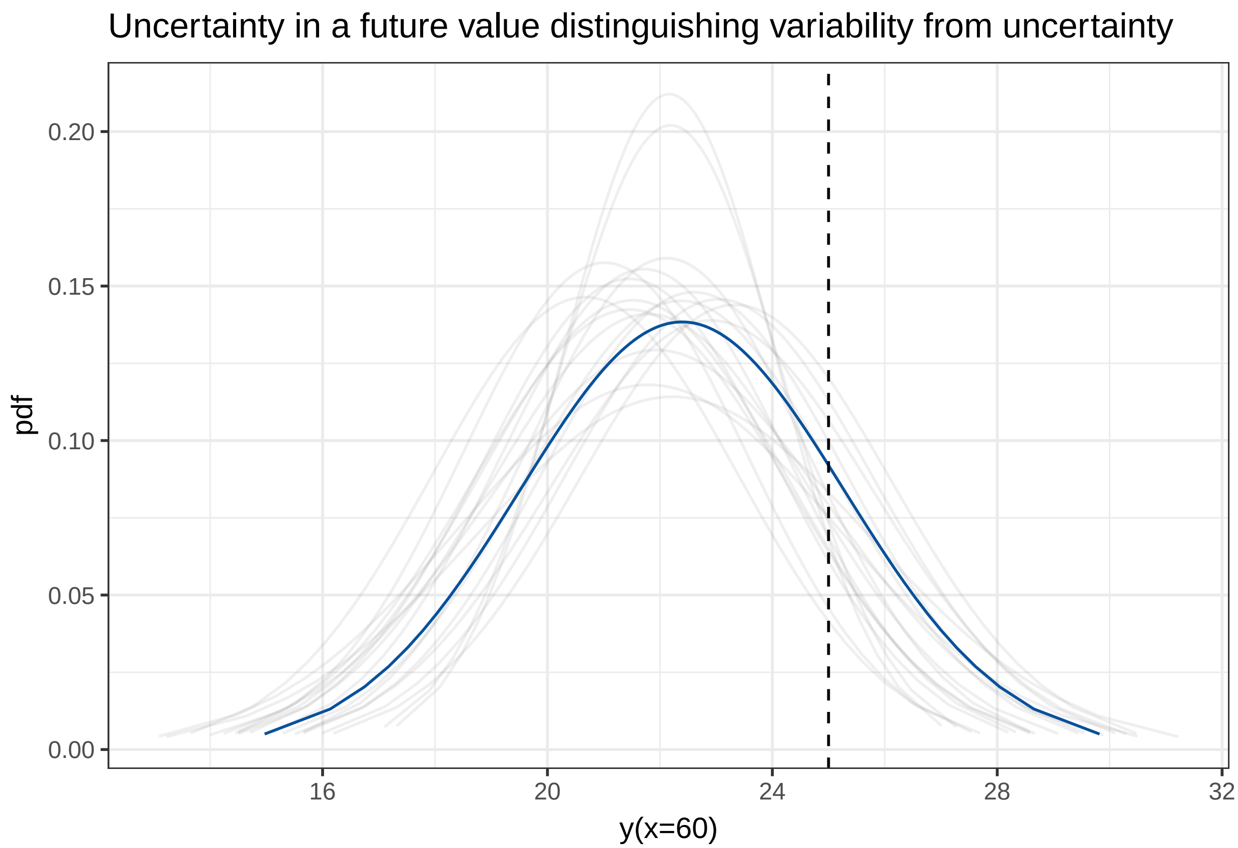
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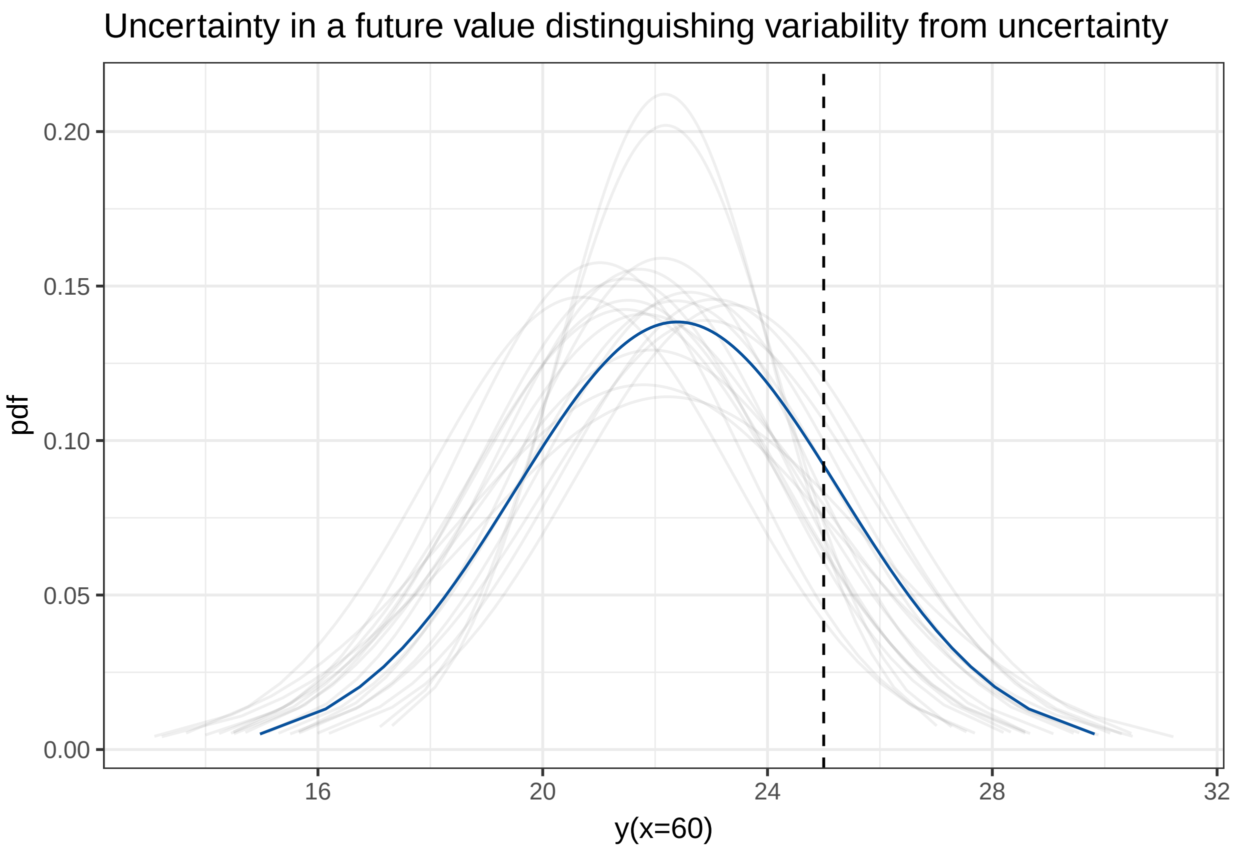
y(x=60)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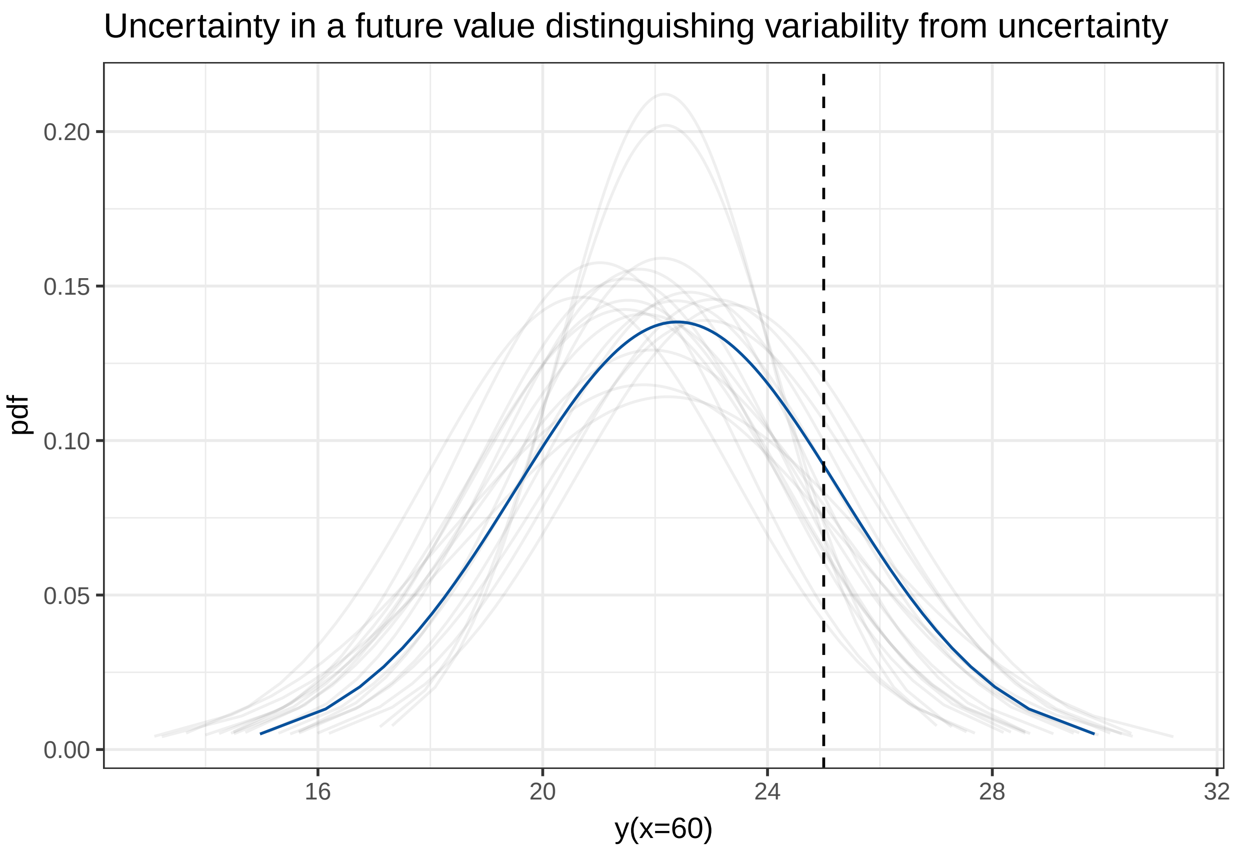
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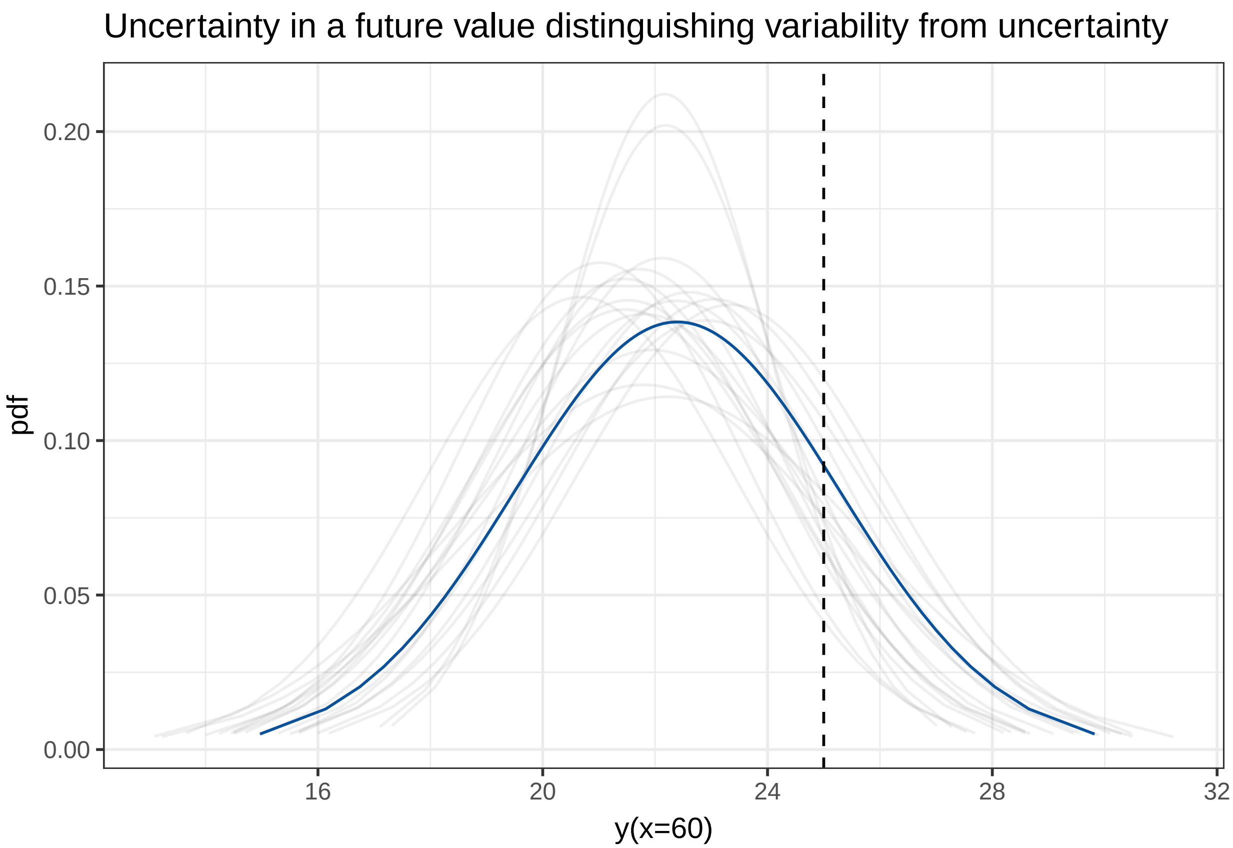

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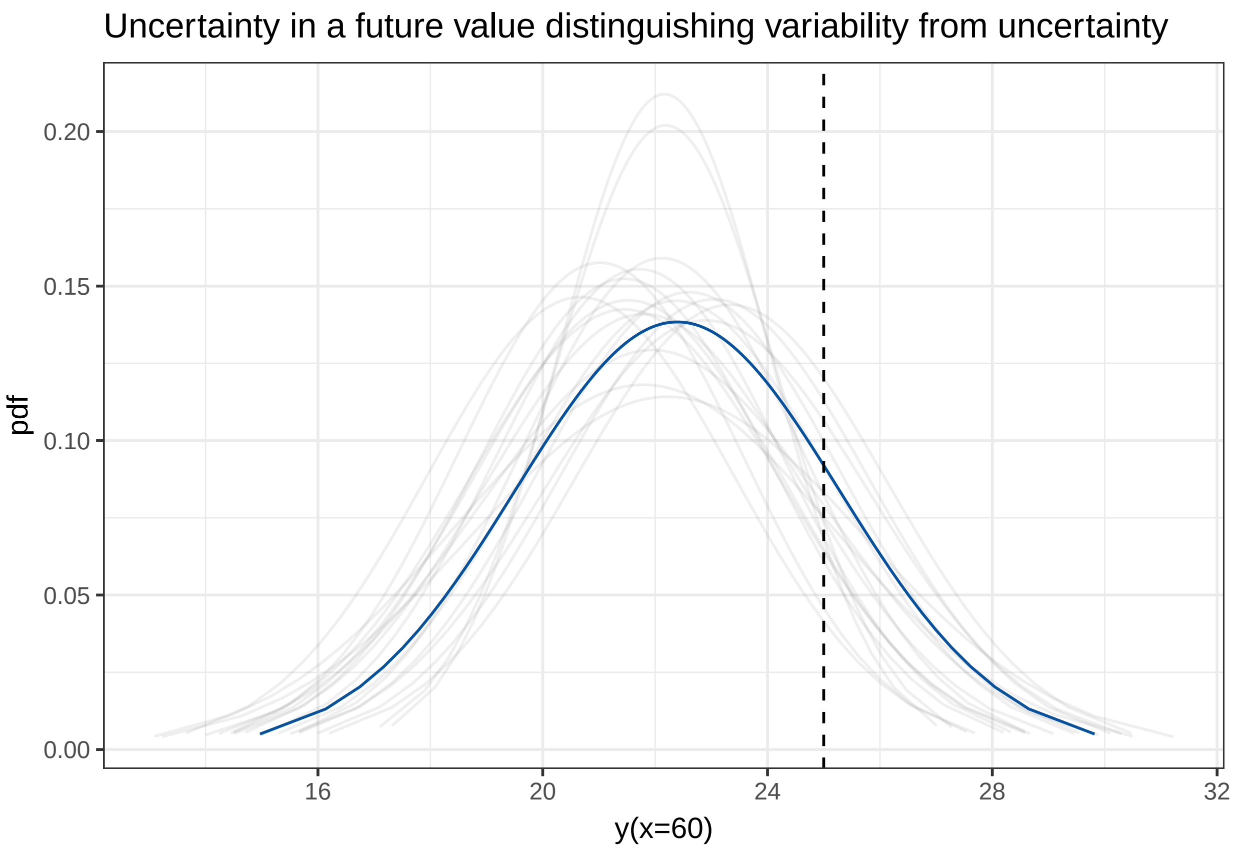
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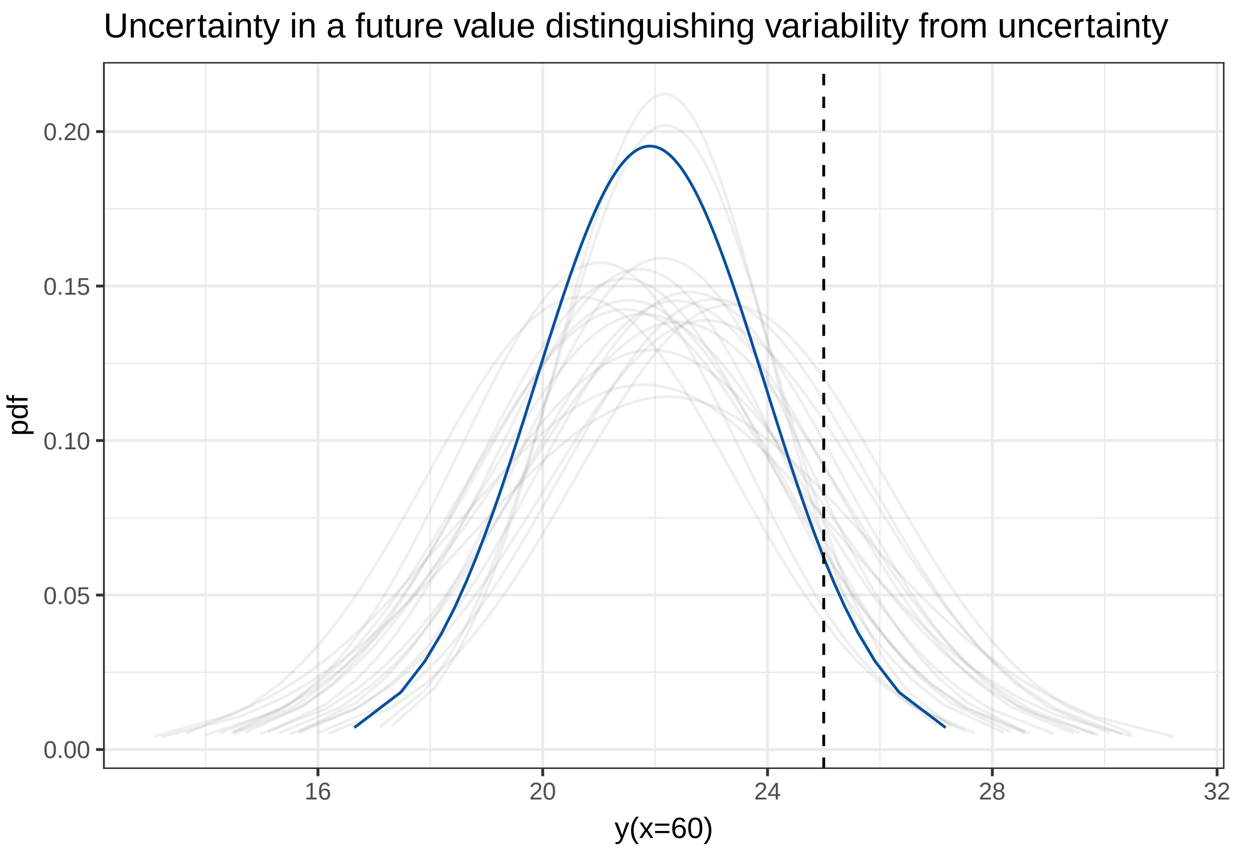

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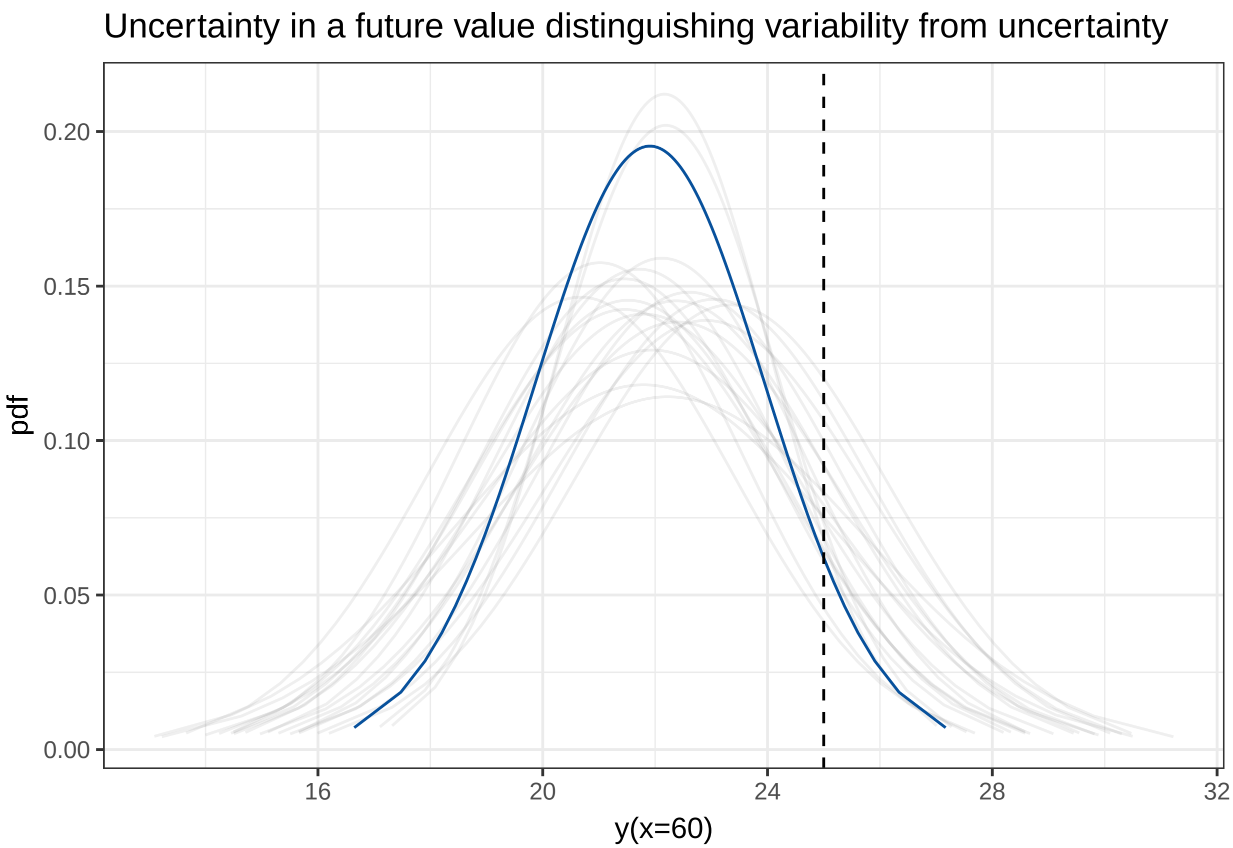

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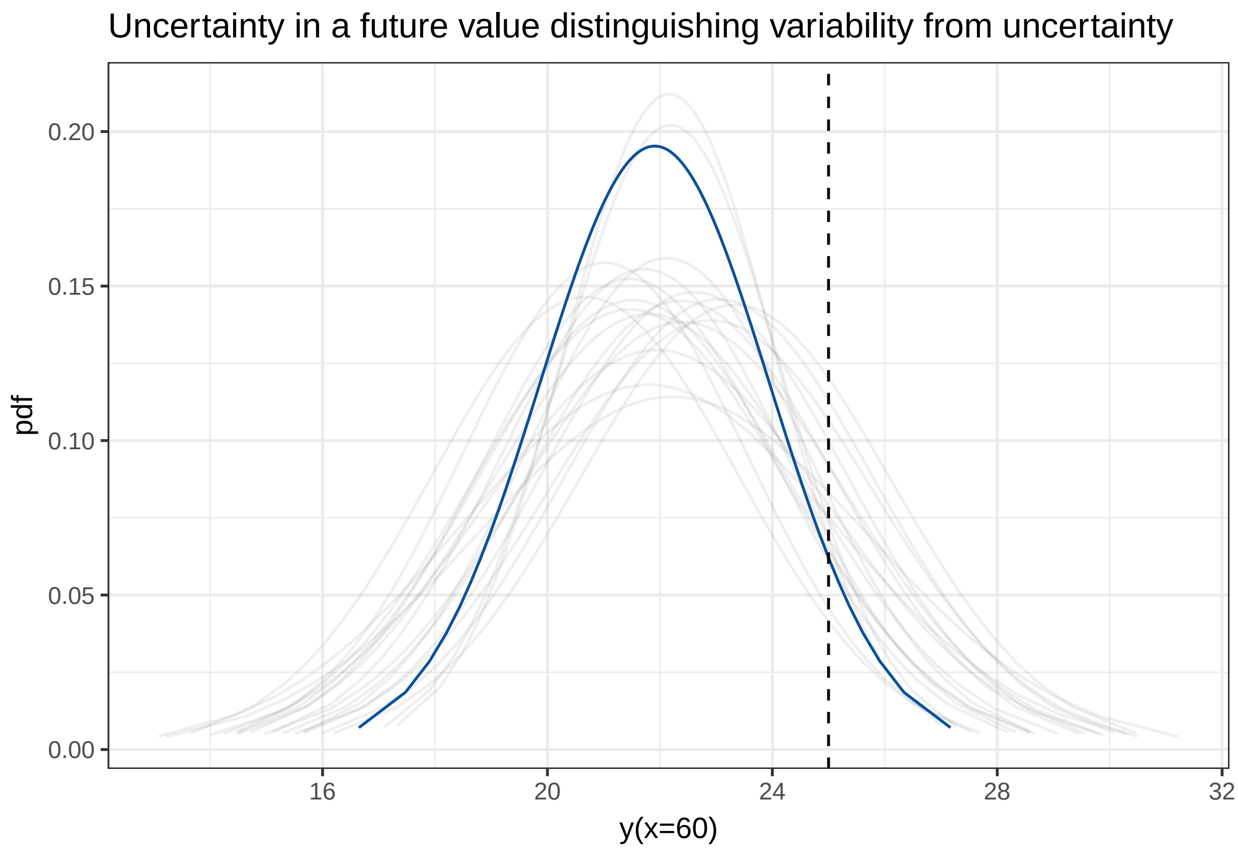

Uncertainty in a future value distinguishing variability from uncertainty
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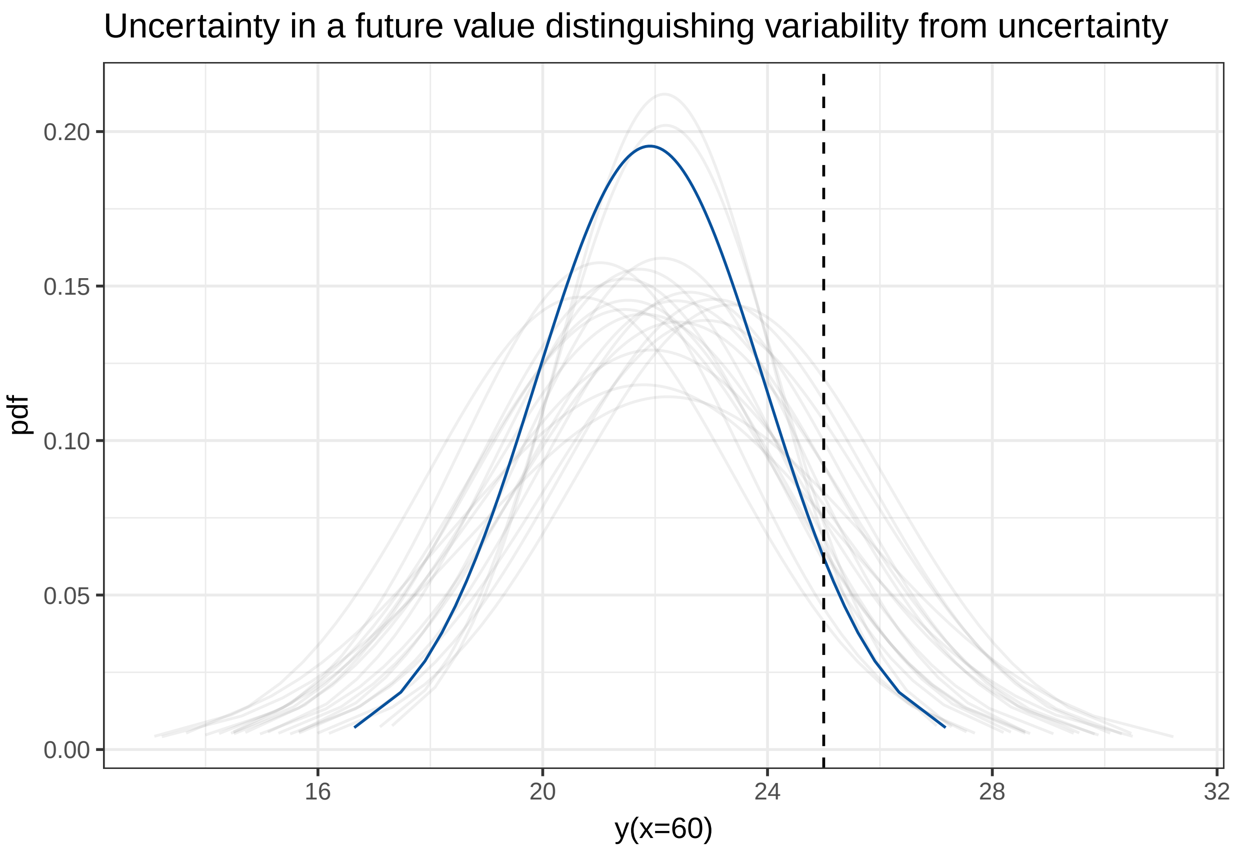


Specify a Bayesian model with a squared term

Model with squared term

$$Y = a + b \cdot X + c \cdot X^2 + e$$

$$e \sim N(0, \sigma)$$

```
mod_jags_sq <- function(){
    # Priors:
    a ~ dnorm(0, 0.001) # intercept
    b ~ dnorm(0, 0.001) # linear term
    c ~ dnorm(0, 0.001) # squared term
    sigma ~ dunif(0, 100) # standard deviation
    tau <- 1 / (sigma * sigma) # sigma^2 doesn't work in JAGS

    # Likelihood:
    for (i in 1:n){
        y[i] ~ dnorm(mu[i], tau) # tau is precision (1 / variance)
        mu[i] <- a + b * (x[i]-50)/50 + c * (x[i]-50)/50 * (x[i]-50)/50
    }

}
```

```r
# select initial values for the MCMC sampling
init_values_sq <- function(){
    list(a = rnorm(1), b = rnorm(1), c = rnorm(1), sigma = abs(rnorm(1,10,2)))
}

# parameters to save
params_sq <- c("a", "b", "c", "sigma")

# run MCMC sampling using Gibbs sampling (may take some time, but not long)
mcmc_jags_sq <- jags(data = data_jags, inits = init_values_sq, parameters.to.save = params_sq, model.fil
               n.chains = 3, n.iter = 12000, n.burnin = 2000, n.thin = 10)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 20
##    Unobserved stochastic nodes: 4
##    Total graph size: 212
##
## Initializing model
```

```r
mod_mcmc_sq <- as.mcmc(mcmc_jags_sq)

# study summary of output
mcmc_jags_sq
```

```
## Inference for Bugs model at "C:/Users/ekol-usa/AppData/Local/Temp/Rtmp40grAX/model2aa04d153bed.txt",
##  3 chains, each with 12000 iterations (first 2000 discarded), n.thin = 10
##  n.sims = 3000 iterations saved
##          mu.vect sd.vect   2.5%    25%    50%    75%   97.5%  Rhat n.eff
## a         21.488   0.813 19.853 20.963 21.493 22.009  23.117 1.001  3000
## b          4.722   1.102  2.524  4.010  4.726  5.435   6.906 1.006   870
## c         -2.642   1.970 -6.511 -3.949 -2.617 -1.358   1.353 1.001  3000
## sigma      2.547   0.485  1.813  2.209  2.471  2.808   3.666 1.001  3000
## deviance  92.441   3.316 88.340 89.979 91.652 94.074 100.841 1.002  2400
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 5.5 and DIC = 97.9
## DIC is an estimate of expected predictive error (lower deviance is better).
```

```r
# Study the convergence of the samples of the parameters
#plot(mod_mcmc_sq)
```

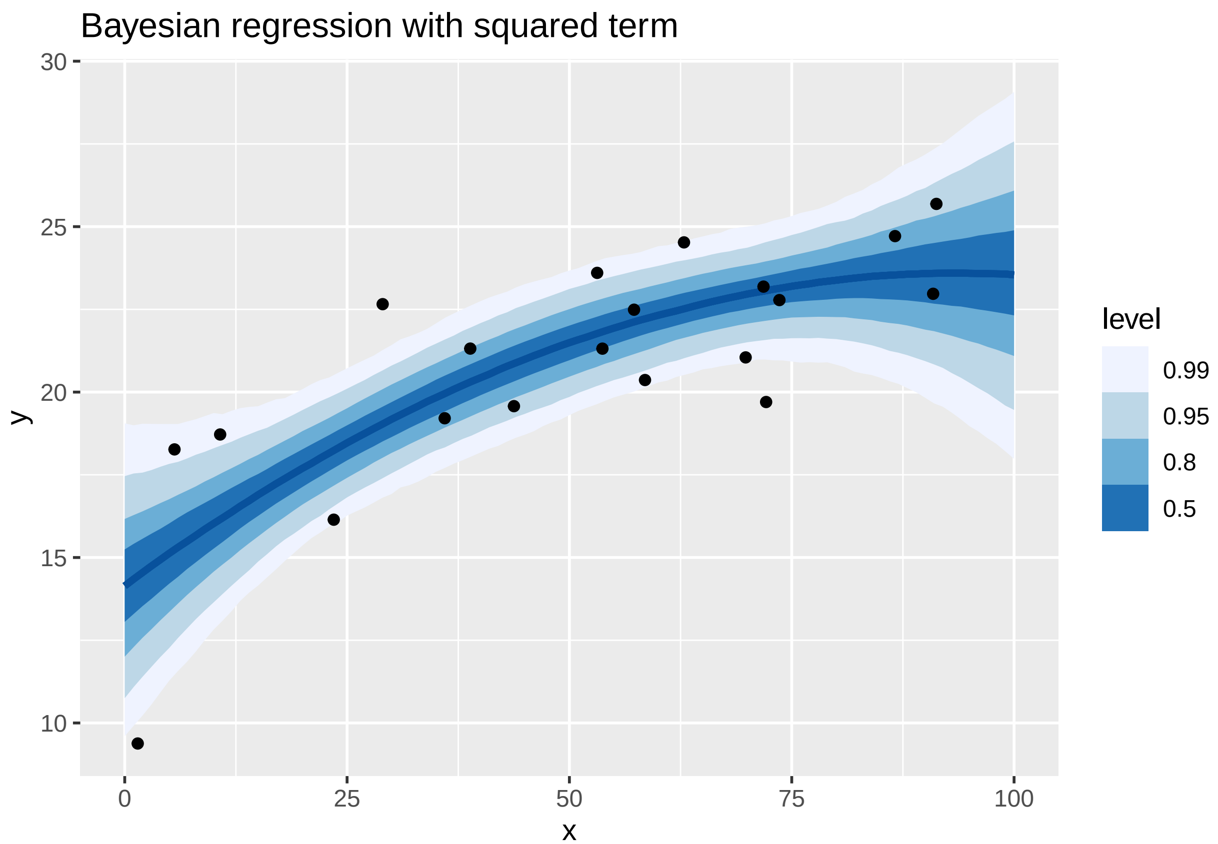
Uncertainty about the model

```r
# save posterior from three chains into one sample
mcmc_sample_sq <- as.mcmc(rbind(mod_mcmc_sq[[1]], mod_mcmc_sq[[2]], mod_mcmc_sq[[3]]))

# make predictions for different values on x
x_new = seq(0,100,by=1)

pred_sample2_sq <- do.call('rbind',lapply(1:nrow(mcmc_sample_sq),function(i){
data.frame(y=mcmc_sample_sq[i,"a"] + (x_new-50)/50 * mcmc_sample_sq[i,"b"] + (x_new-50)/50 * (x_new-50)/
}))

ggplot(pred_sample2_sq,aes(x=x,y=y)) +
    stat_lineribbon(aes(y = y), .width = c(.99, .95, .8, .5), color = "#08519C") +
  scale_fill_brewer() +
  geom_point(data=df,aes(x=x,y=y)) +
  ggtitle('Bayesian regression with squared term')
```

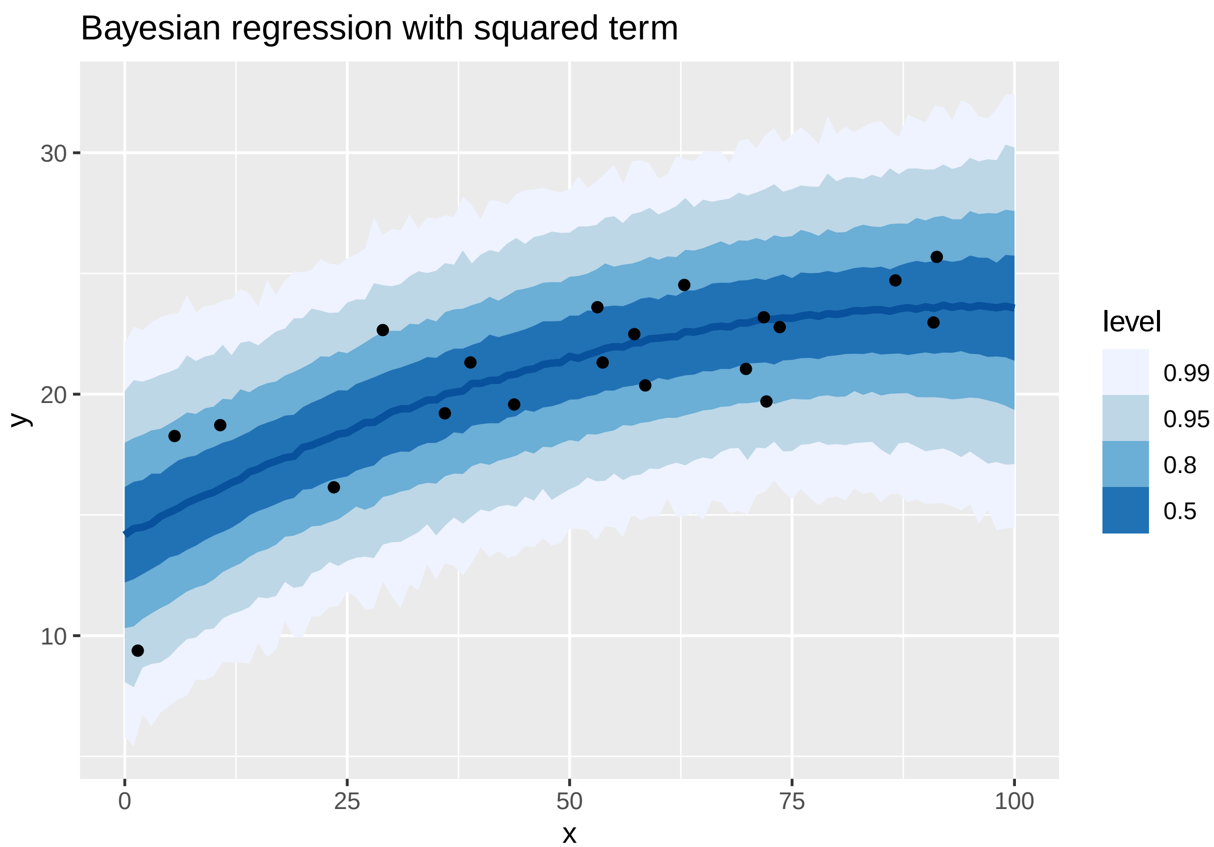


Uncertainty about the future data

```r
pred_sample3_sq <- do.call('rbind',lapply(1:nrow(mcmc_sample_sq),function(i){
data.frame(y=mcmc_sample_sq[i,"a"] + (x_new-50)/50 * mcmc_sample_sq[i,"b"] + (x_new-50)/50 * (x_new-50)/
}))

ggplot(pred_sample3_sq,aes(x=x,y=y)) +
```

```
    stat_lineribbon(aes(y = y), .width = c(.99, .95, .8, .5), color = "#08519C") +
  scale_fill_brewer() +
  geom_point(data=df,aes(x=x,y=y)) +
  ggtitle('Bayesian regression with squared term')
```

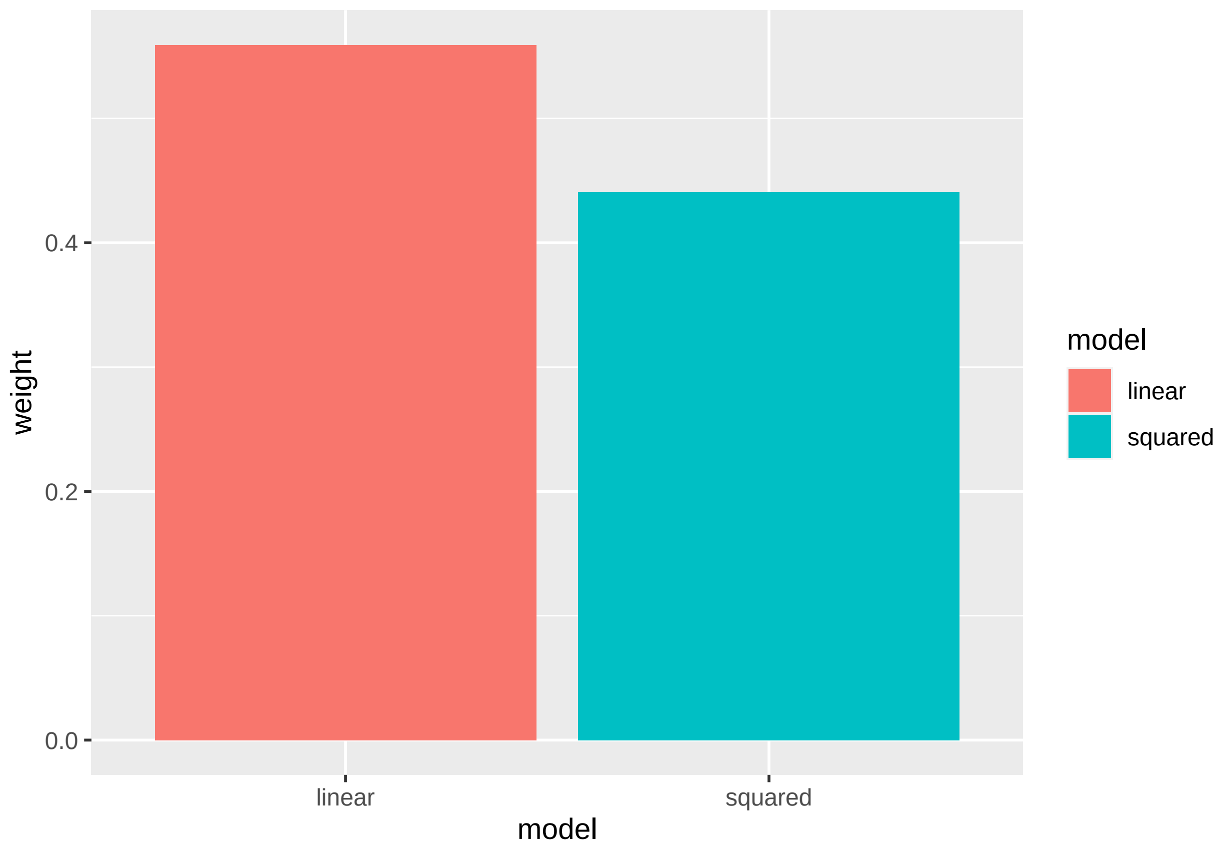


Bayesian model selection and model averaging

There are plenty of nice ways to compare alternative Bayesian models. Here we use the DIC-values (an estimate of the prediction error considering uncertainty in parameters) to weight the two Bayesian models when doing the MC-simulation.

Estimated model weights

```
model_dics <- c(mcmc_jags$BUGSoutput$DIC, mcmc_jags_sq$BUGSoutput$DIC)
w <- exp(-model_dics/2)
df_w <- data.frame(weight = w/sum(w), model = c('linear','squared'))
ggplot(df_w,aes(x=model,y=weight,fill = model)) +
  geom_bar(stat='identity')
```

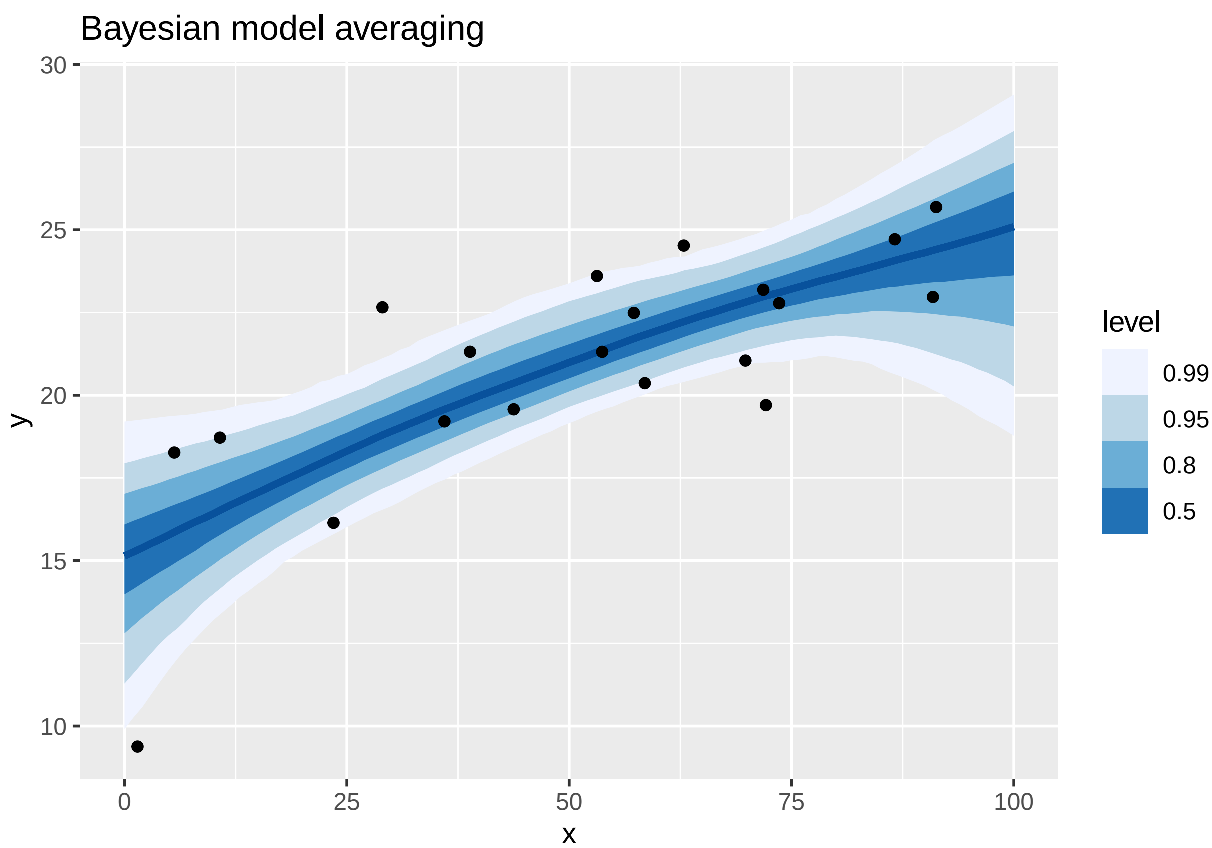


Uncertainty in predictions for the averaged model

```
niter <- min(nrow(mcmc_sample),nrow(mcmc_sample_sq))
iter <- sample.int(2,niter,prob=df_w$weight,replace = TRUE)
pred_sample_ma <- do.call('rbind',lapply(1:niter,function(i){

if(iter[i]==1){
y=mcmc_sample[i,"a"] + (x_new-50)/50 * mcmc_sample[i,"b"]
}else{
y=mcmc_sample_sq[i,"a"] + (x_new-50)/50 * mcmc_sample_sq[i,"b"] + (x_new-50)/50 * (x_new-50)/50 * mcmc_s
}
data.frame(y=y,x=x_new,iter=i)
}
))

ggplot(pred_sample_ma,aes(x=x,y=y)) +
    stat_lineribbon(aes(y = y), .width = c(.99, .95, .8, .5), color = "#08519C") +
  scale_fill_brewer() +
  geom_point(data=df,aes(x=x,y=y)) +
  ggtitle('Bayesian model averaging')
```

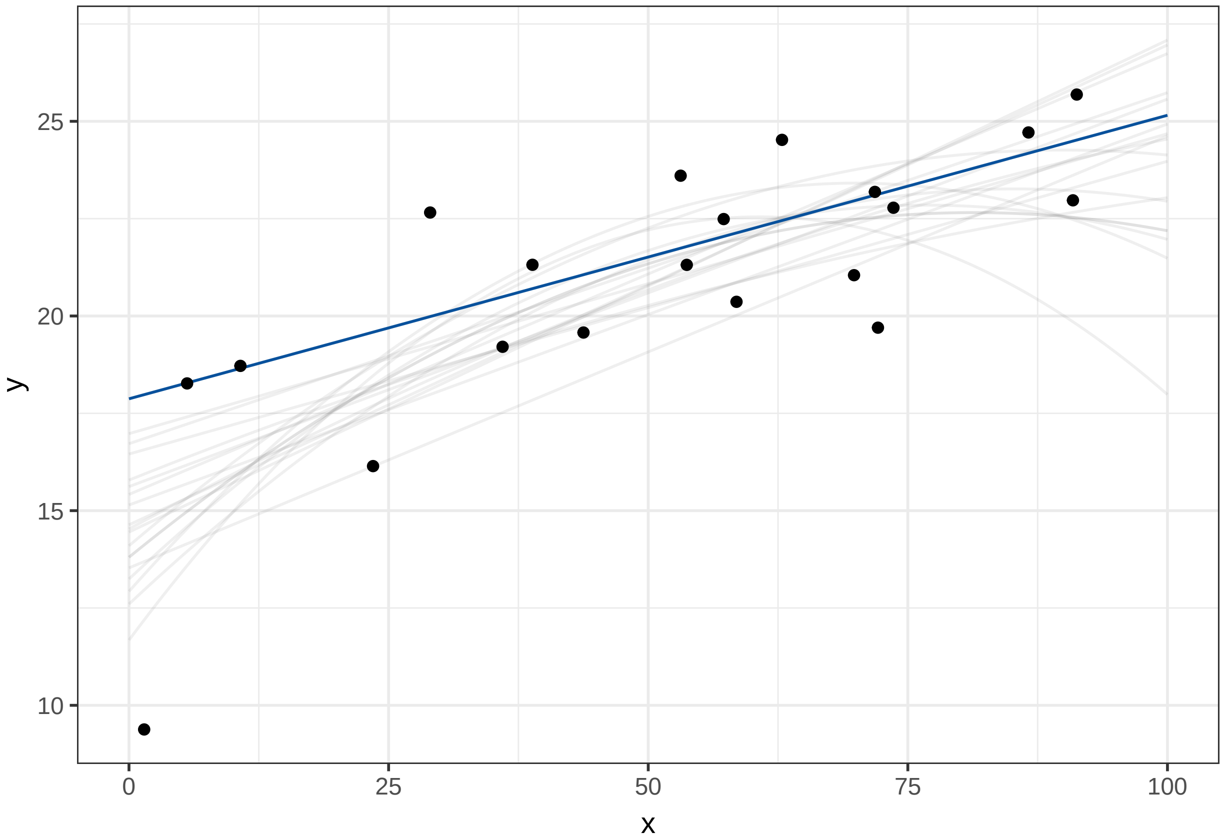


Uncertainty about the average model using animated plots

```
pred_sample_draws_av <- do.call('rbind',lapply(1:20,function(j){
  i <- sample.int(nrow(mcmc_sample),1)

  data.frame(pred_sample_ma[pred_sample_ma$iter == i,],draw = j)
}
))

 ggplot(pred_sample_draws_av,aes(x=x,y=y)) +
  geom_line(aes(group = draw), color = "#08519C") +
  geom_point(data = df) +
  theme_bw() +
  transition_states(draw, 0, 0.2) +
  shadow_mark(past = TRUE, future = TRUE, alpha = 1/8, color = "gray50")
```



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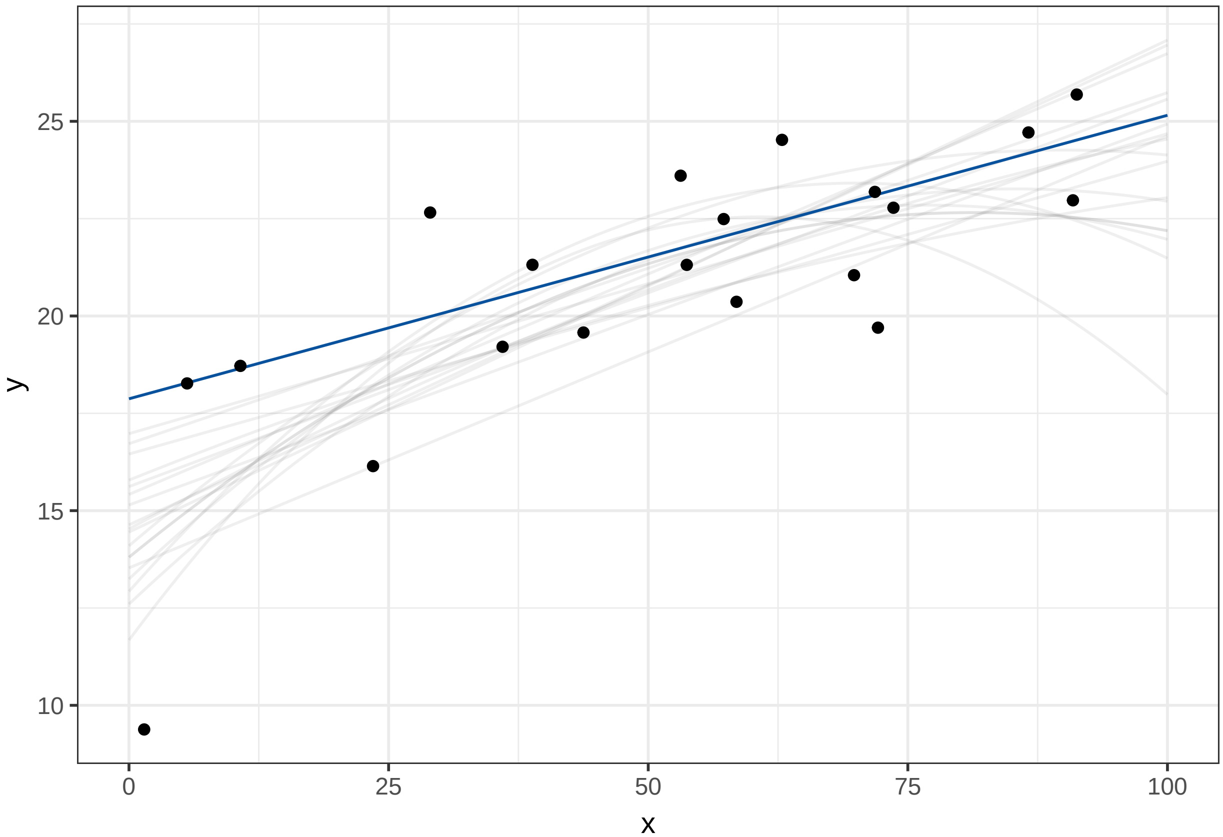

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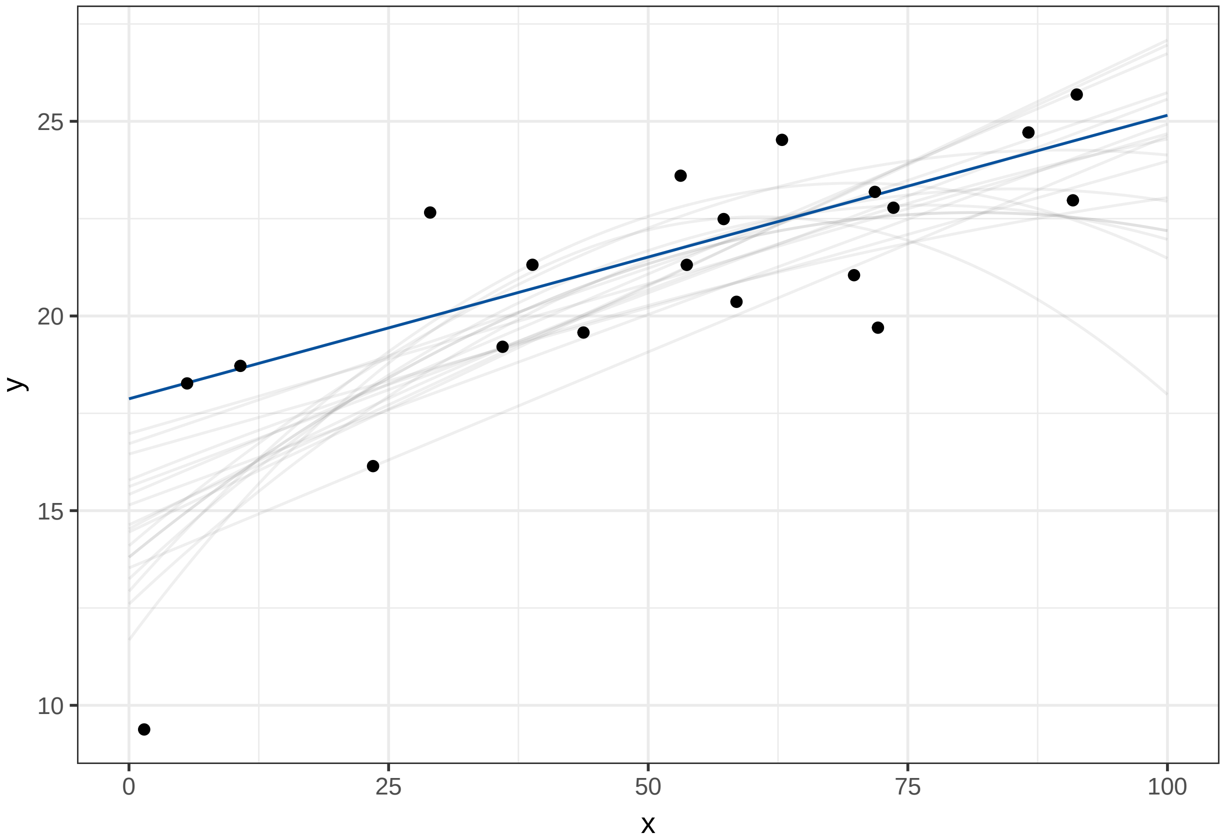

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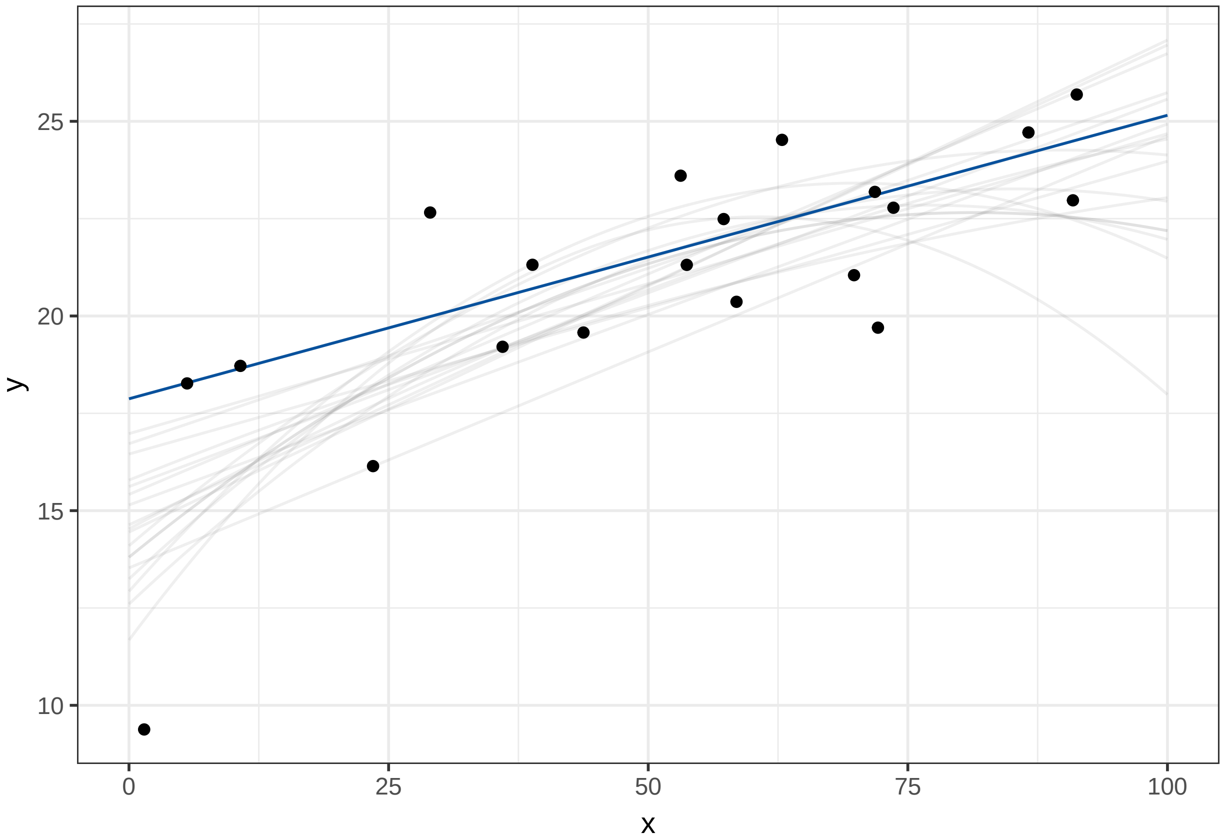

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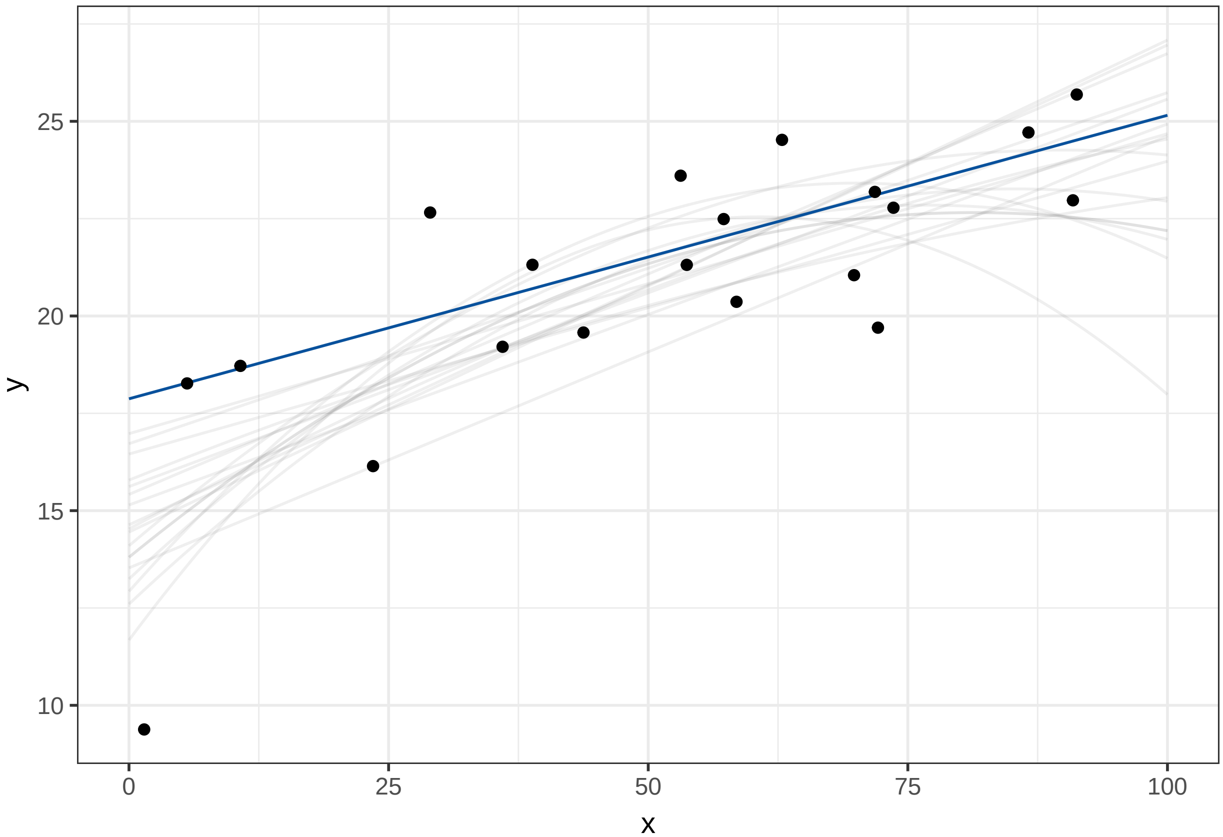

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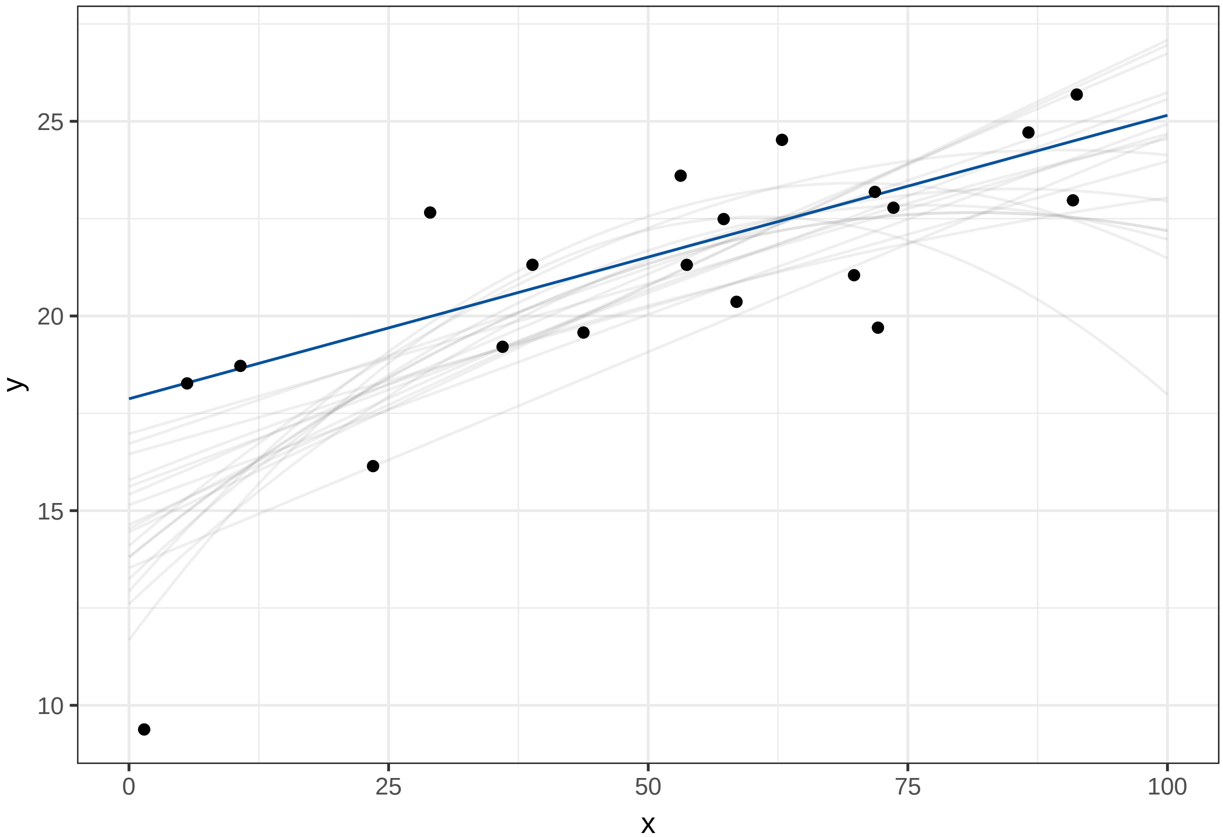

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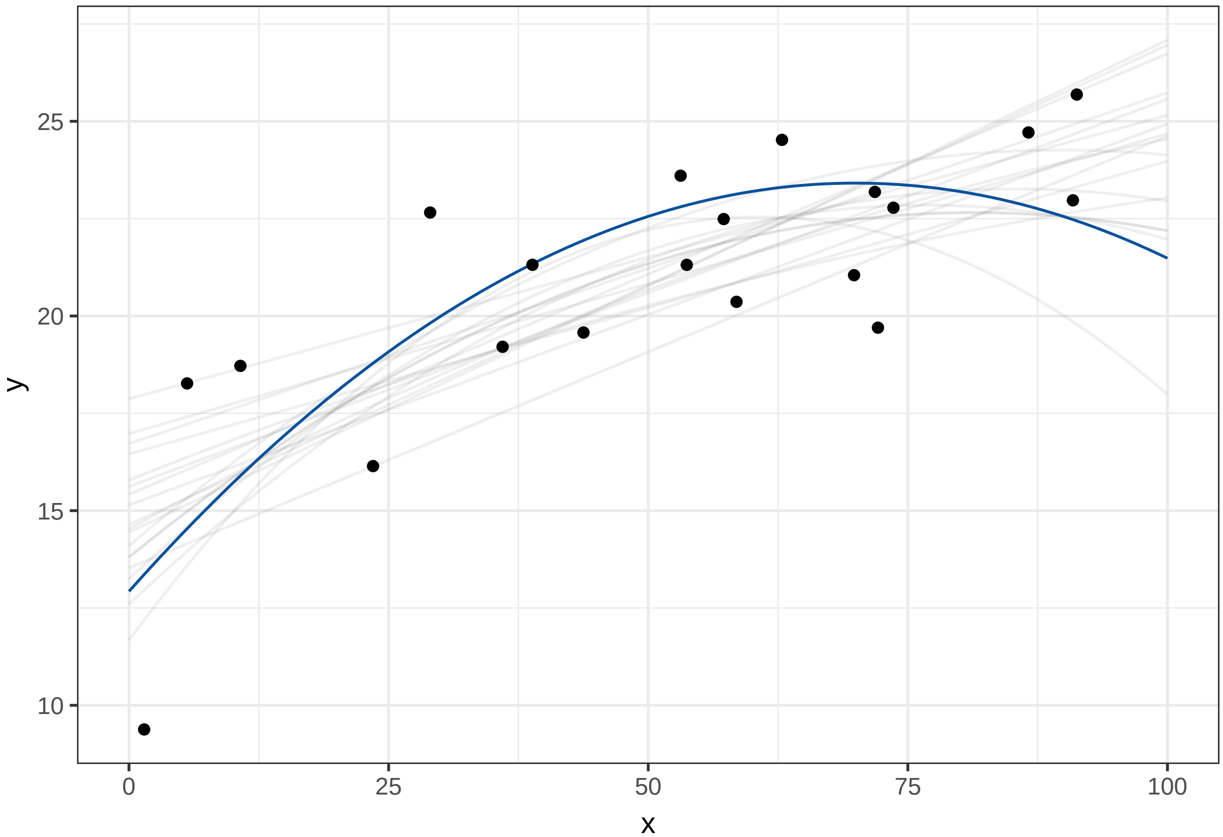

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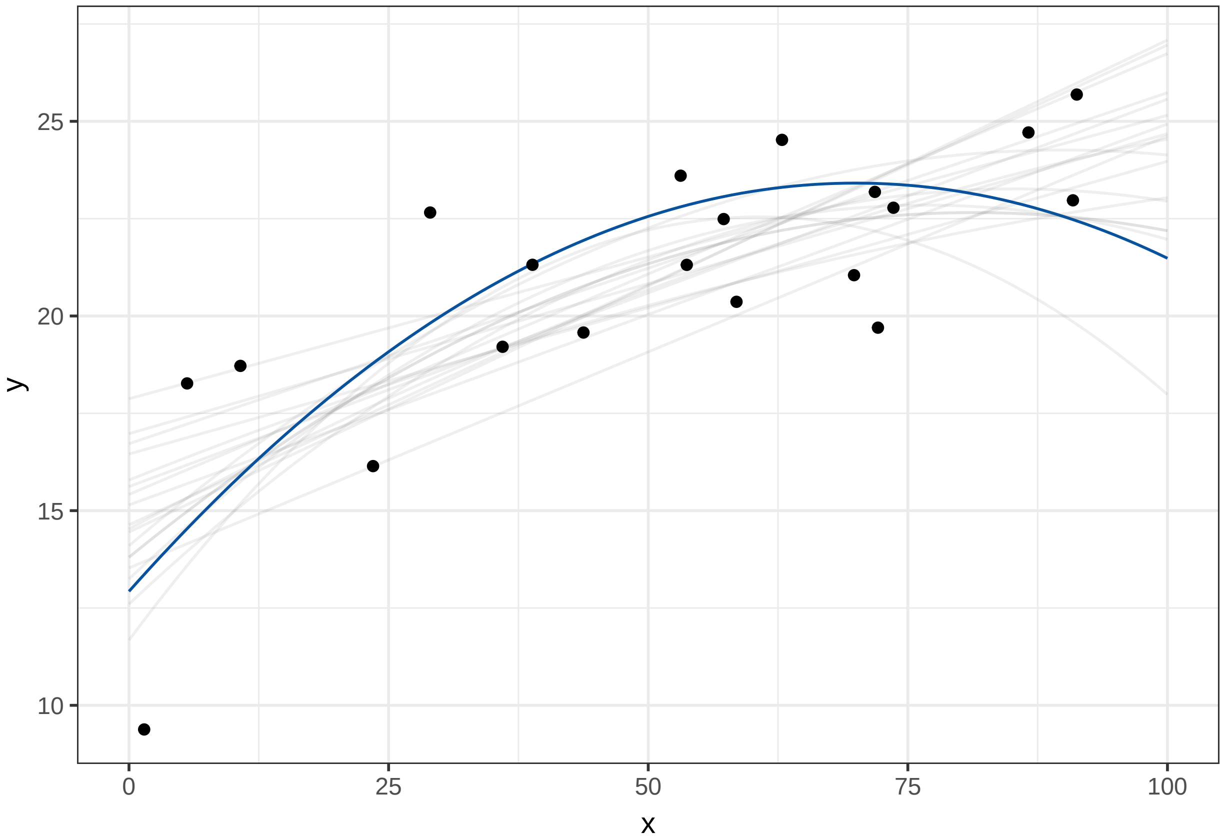

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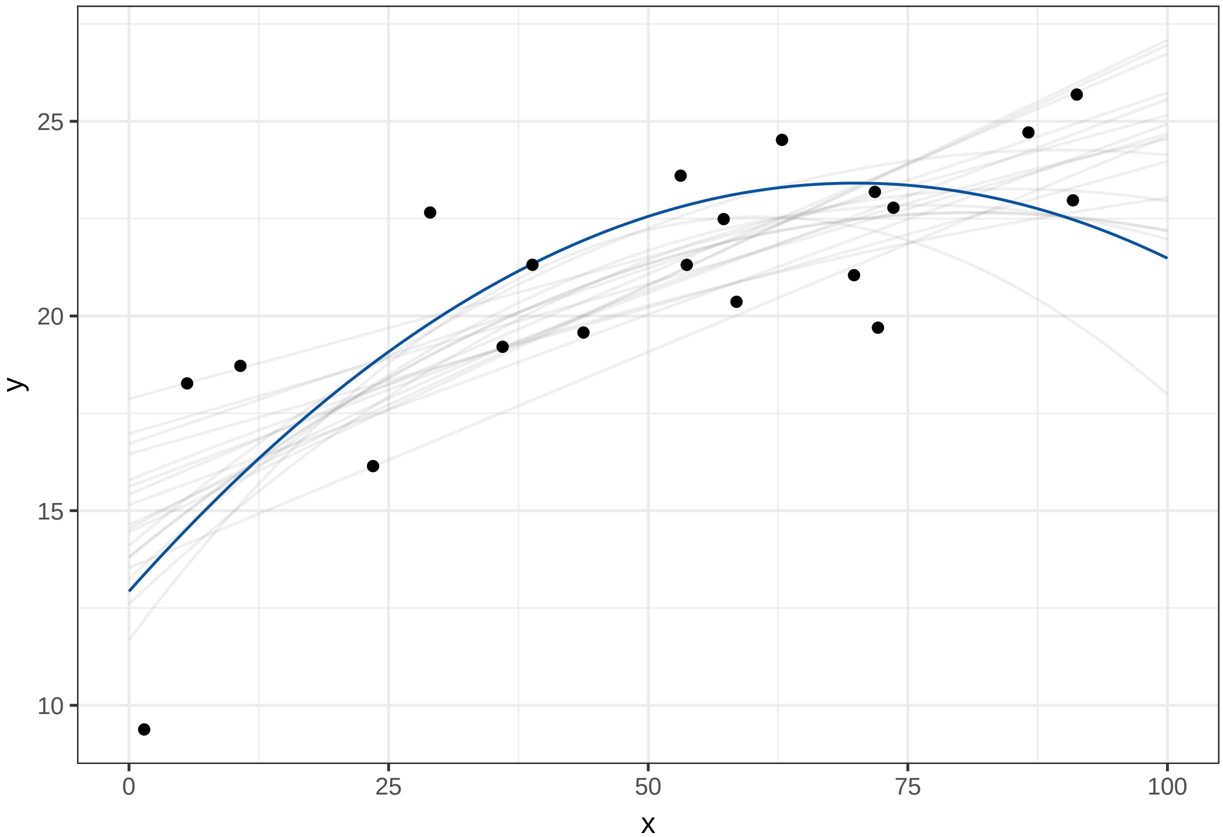

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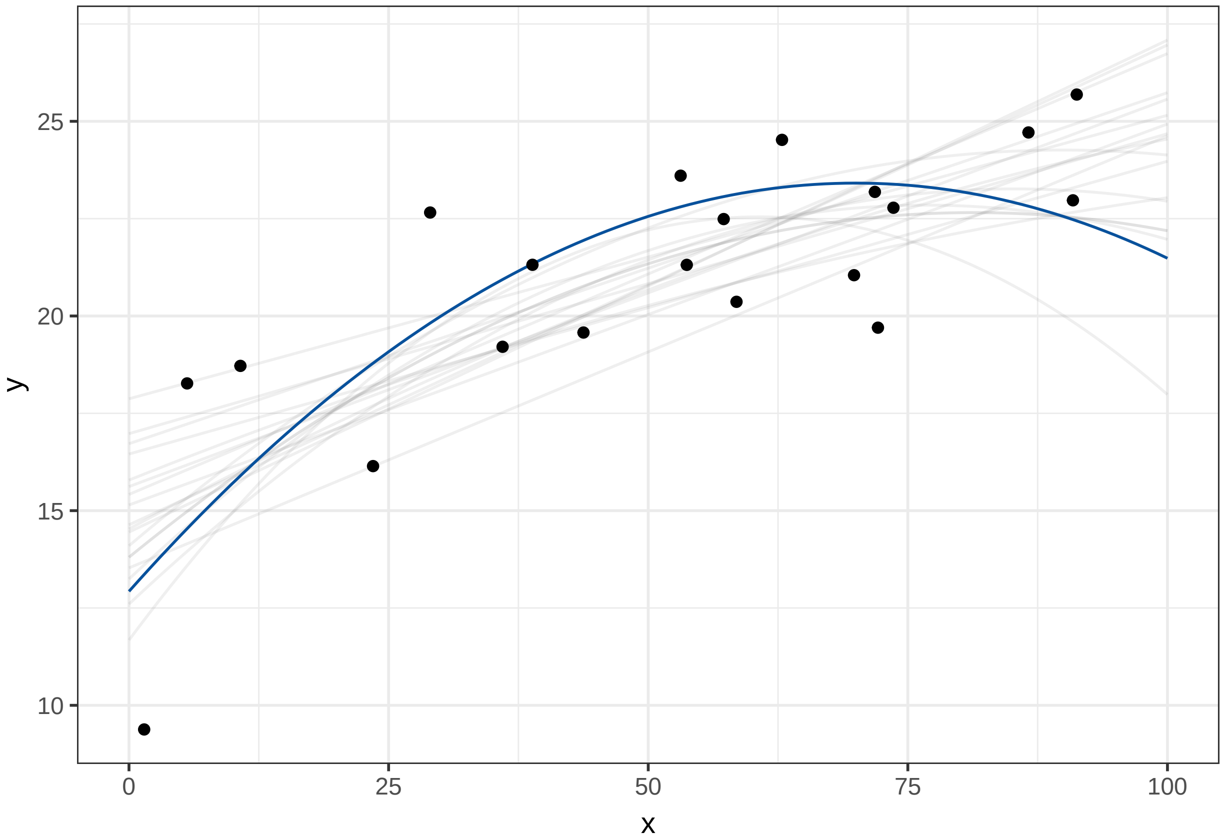

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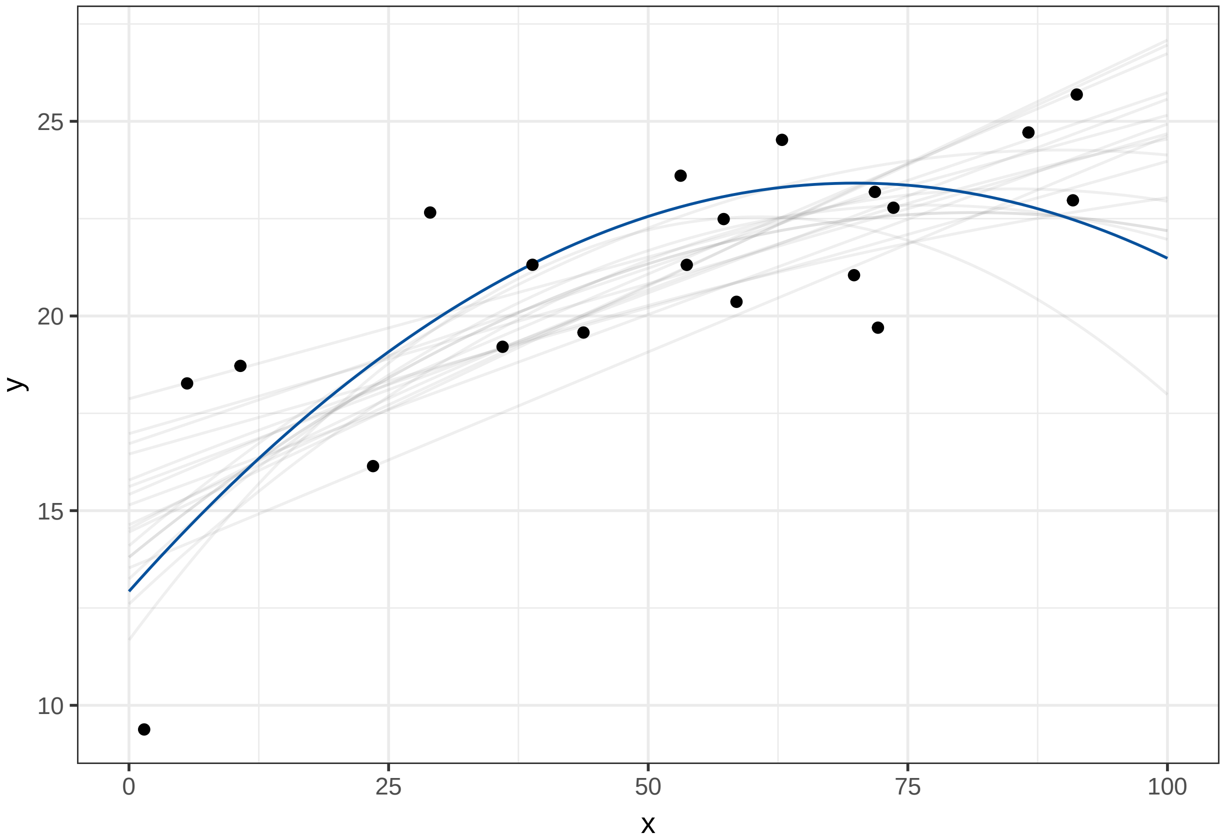

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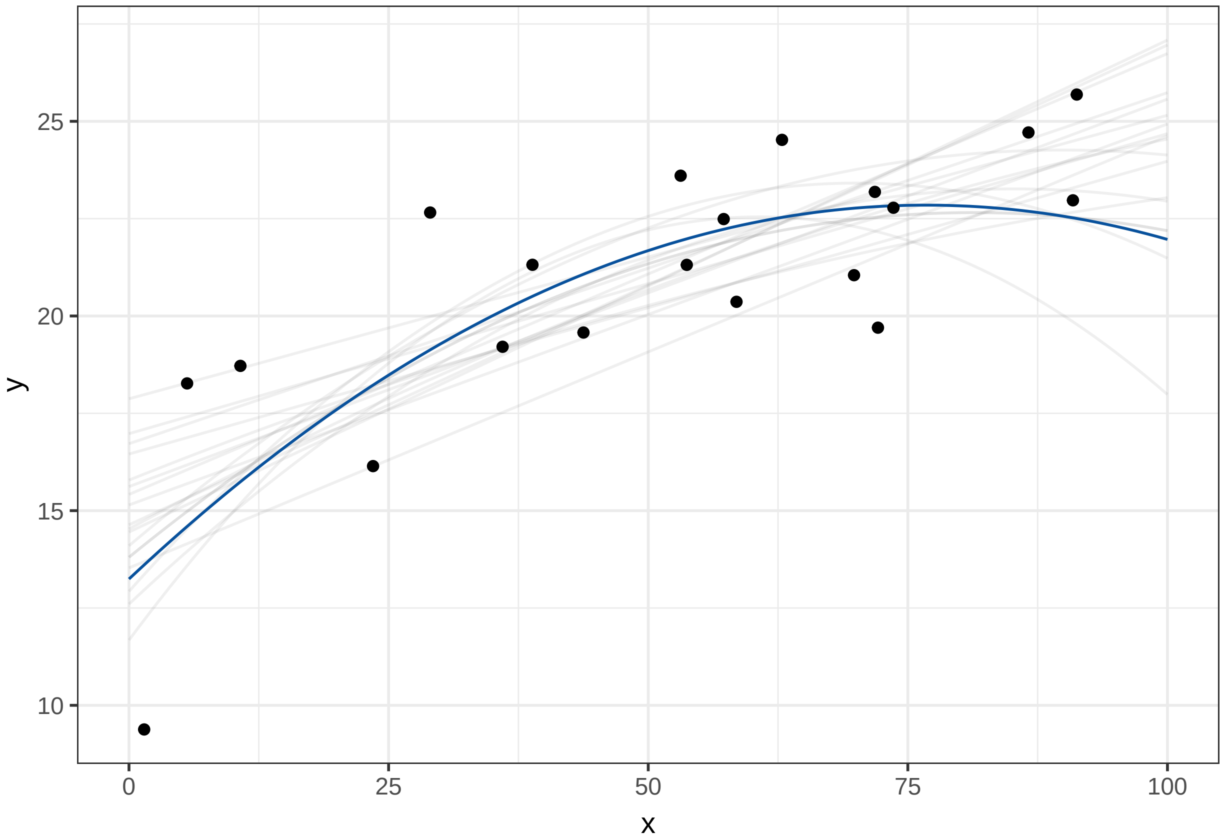

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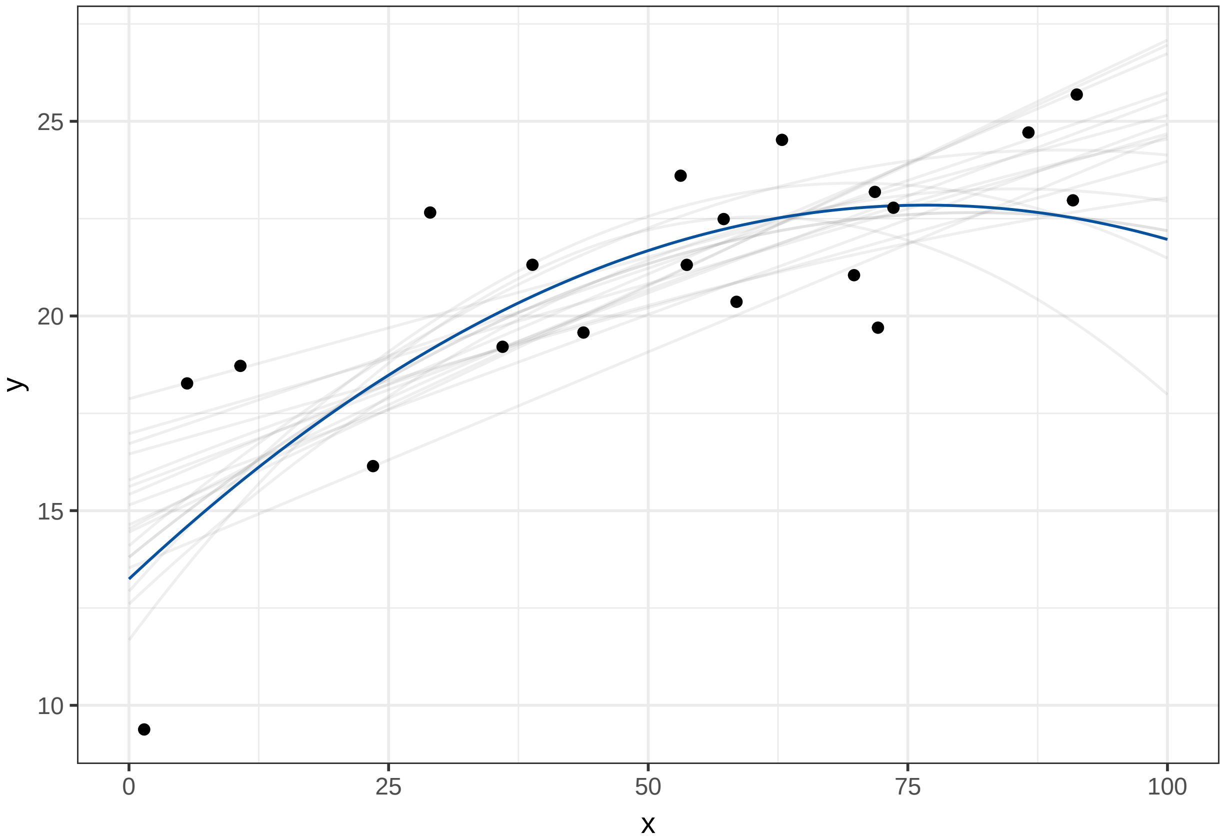

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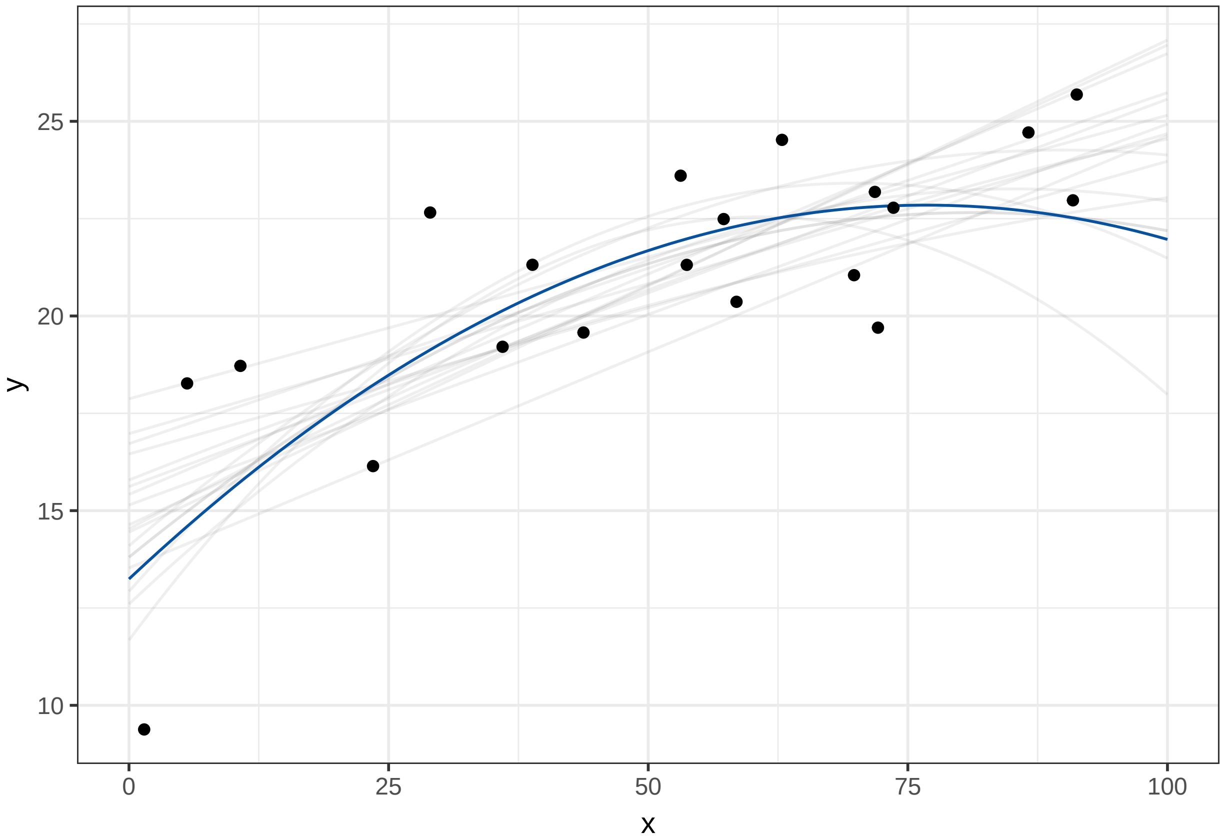

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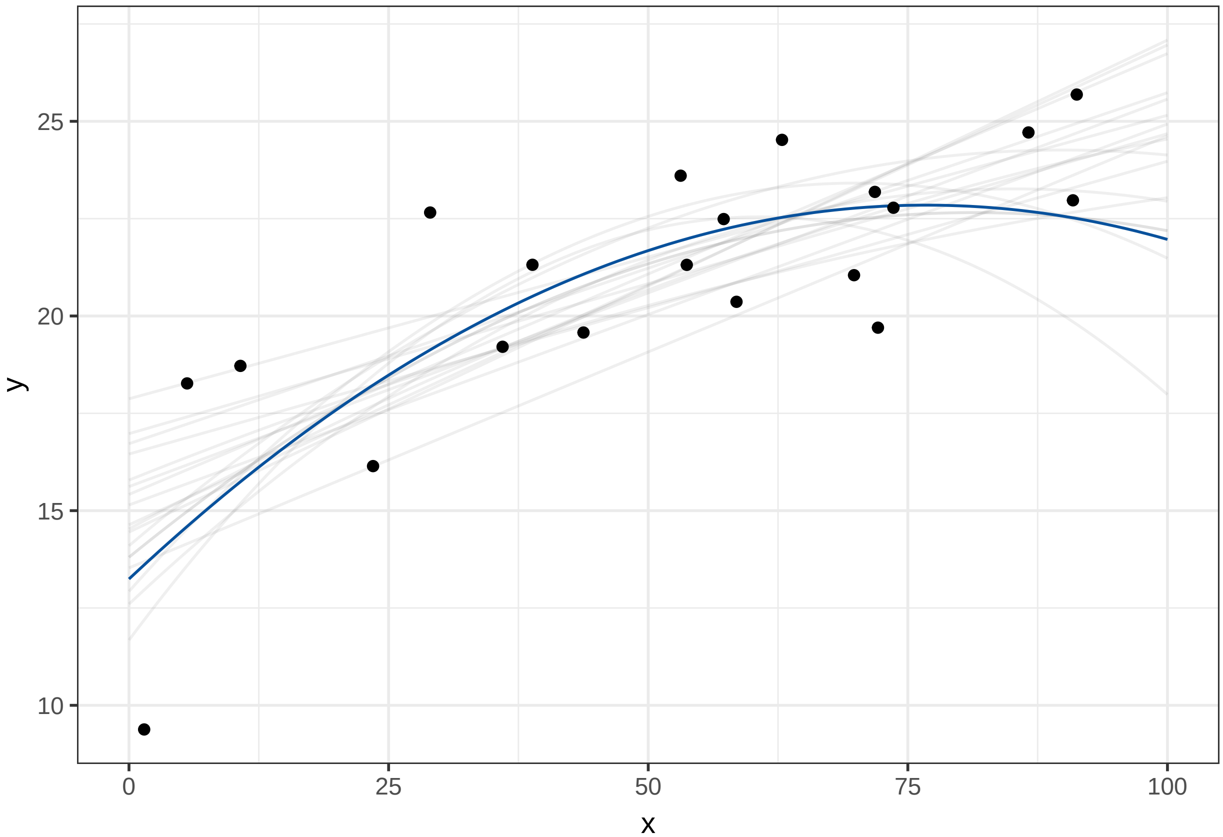

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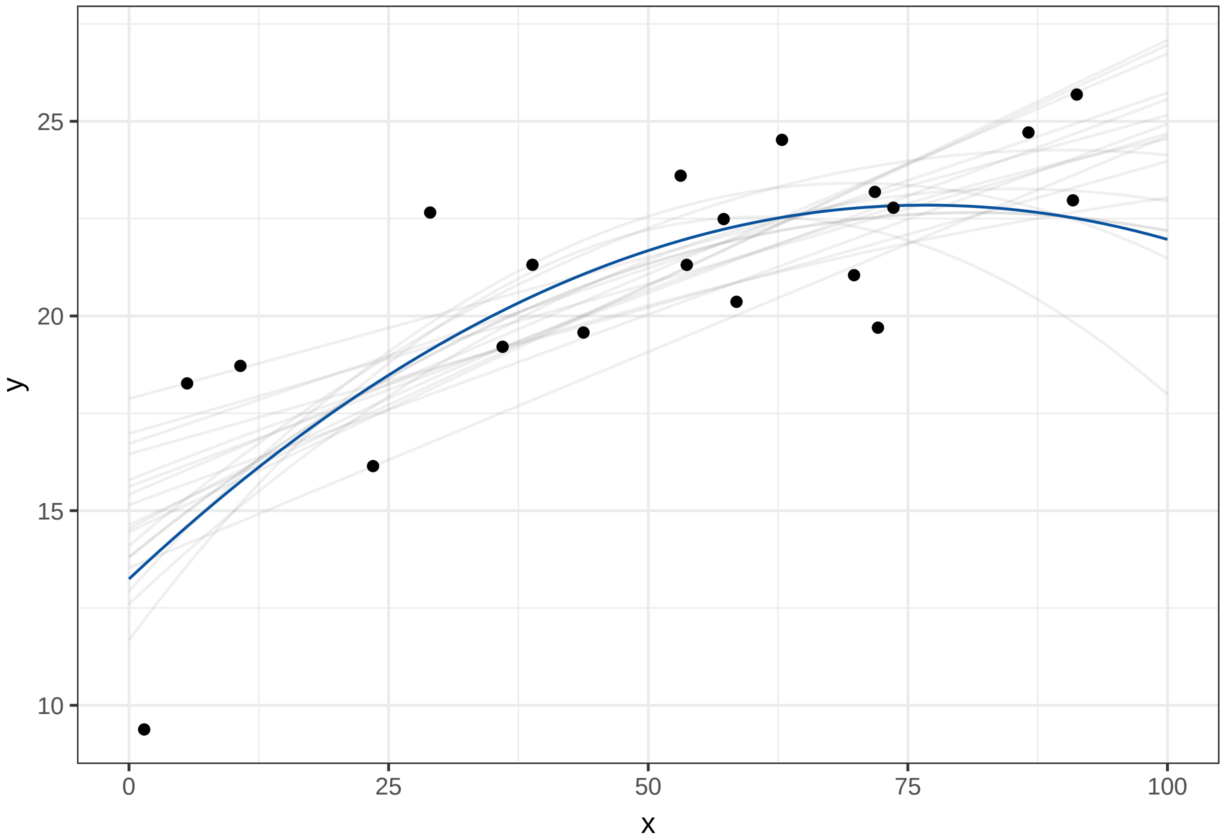

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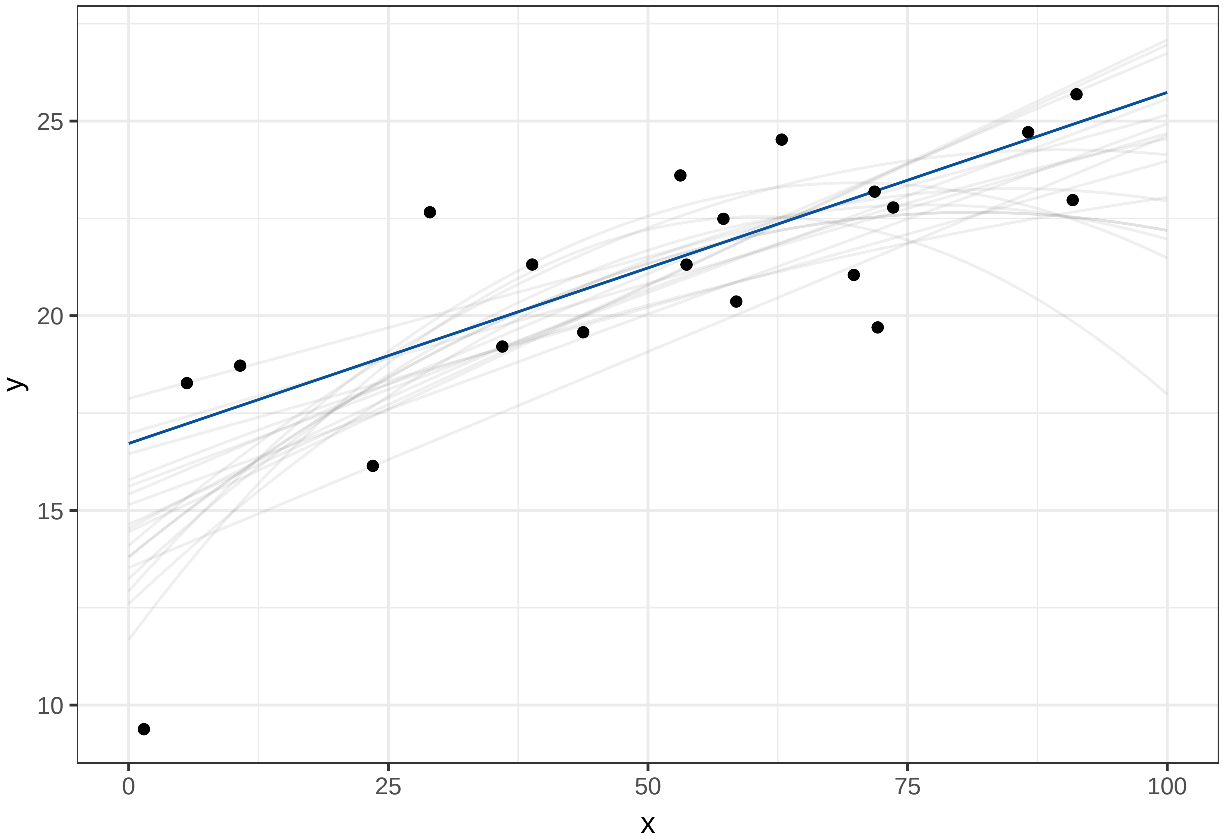

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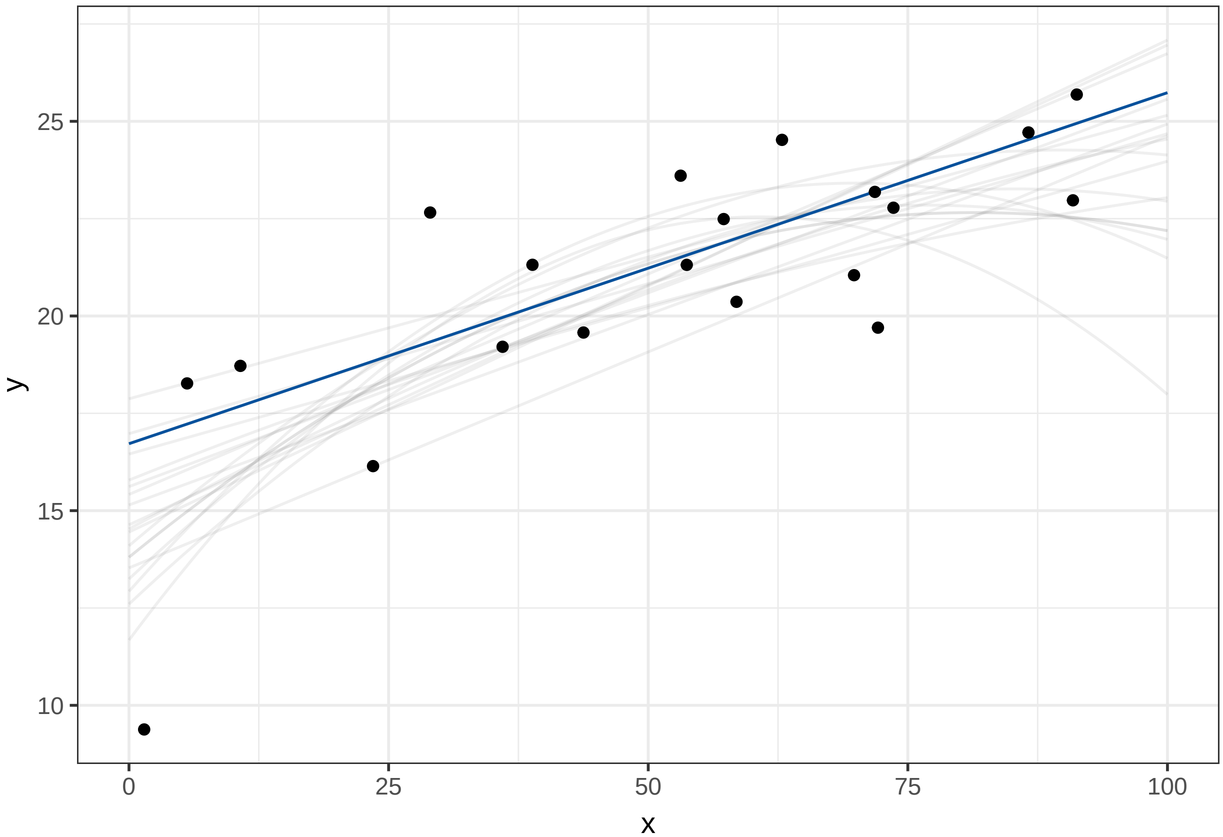

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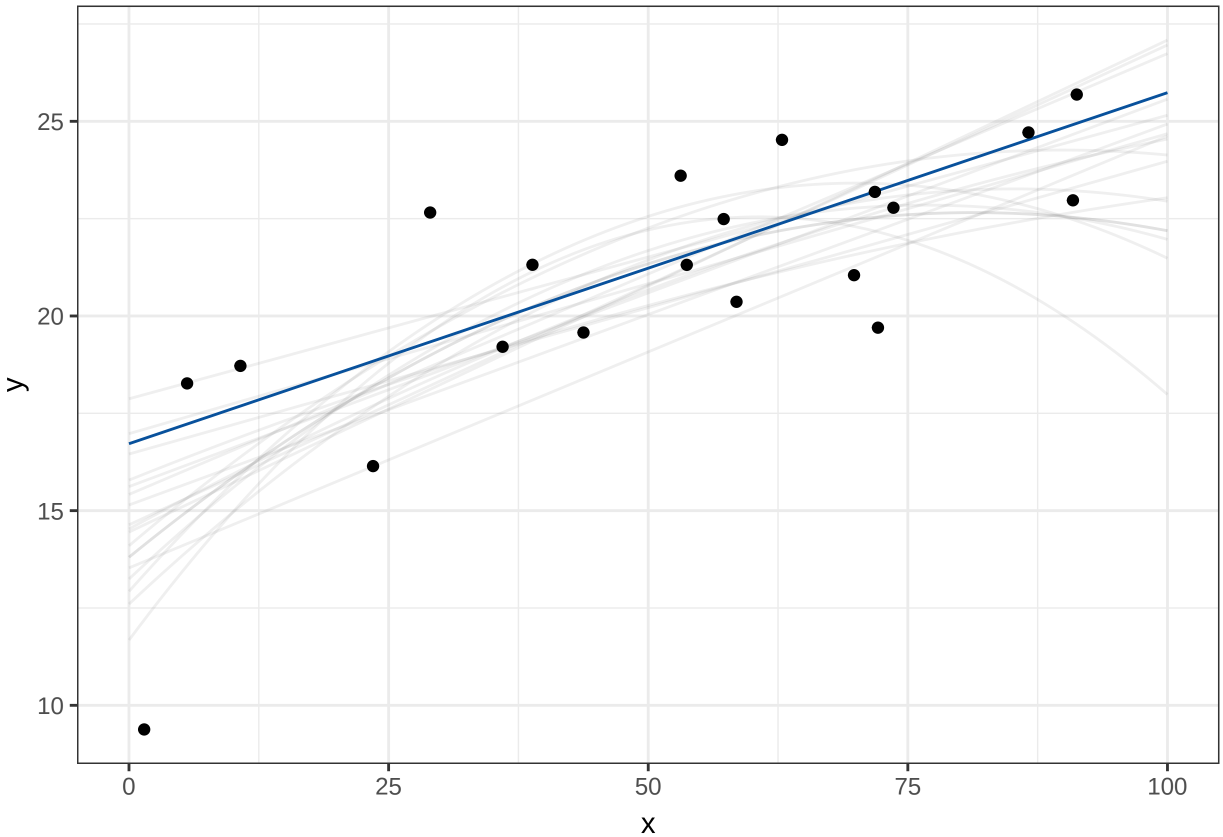
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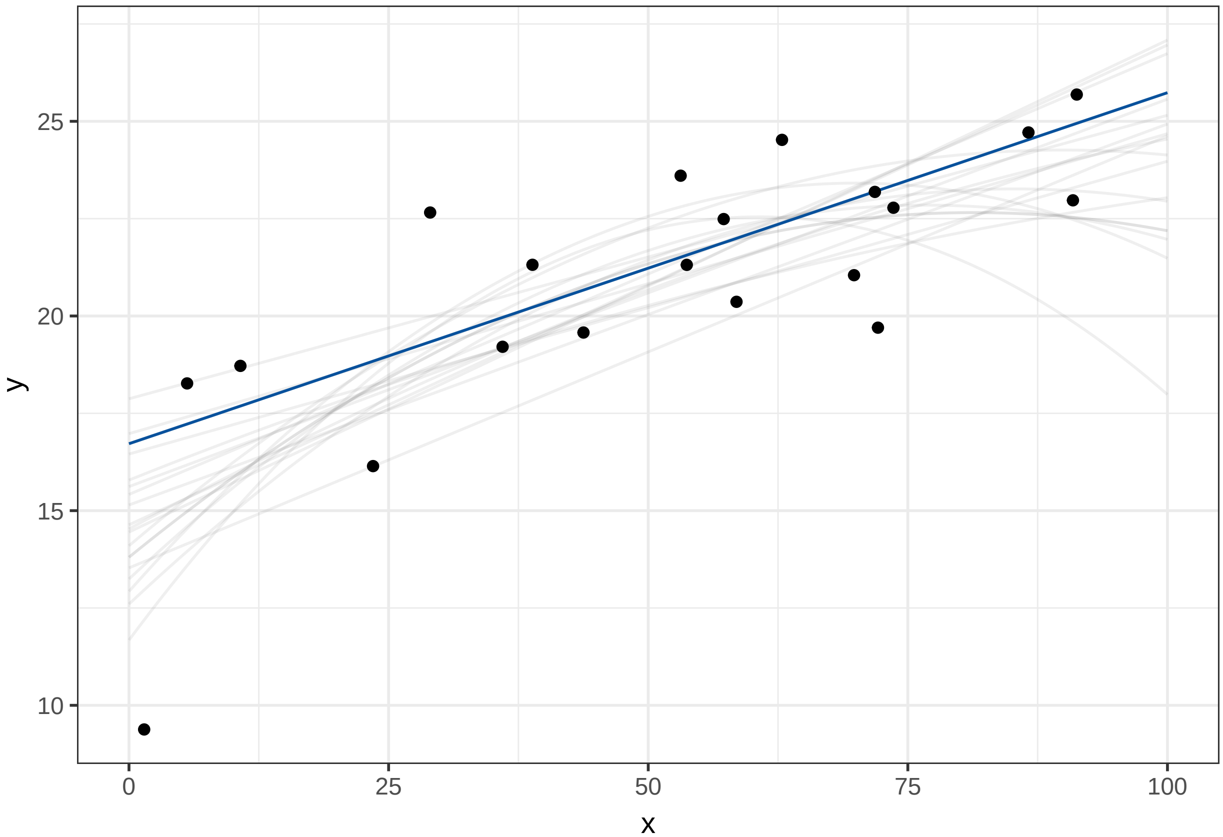
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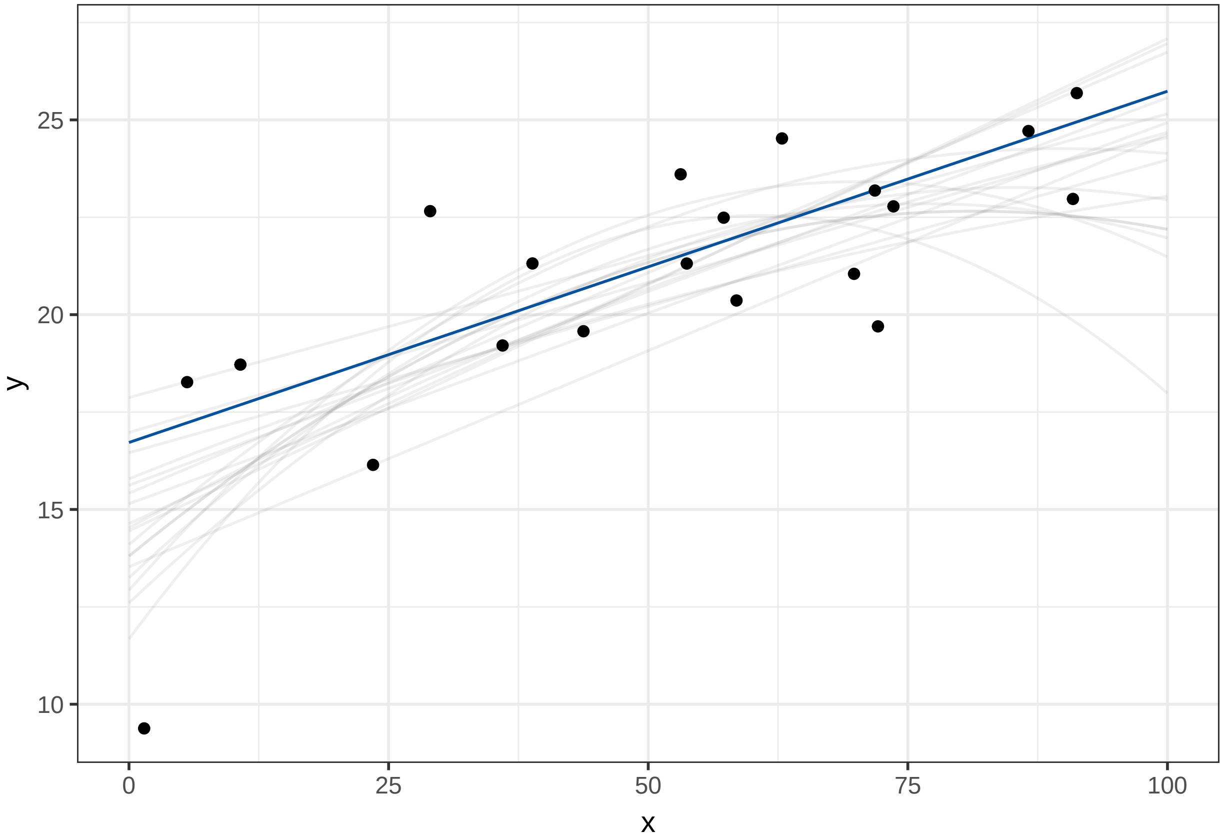

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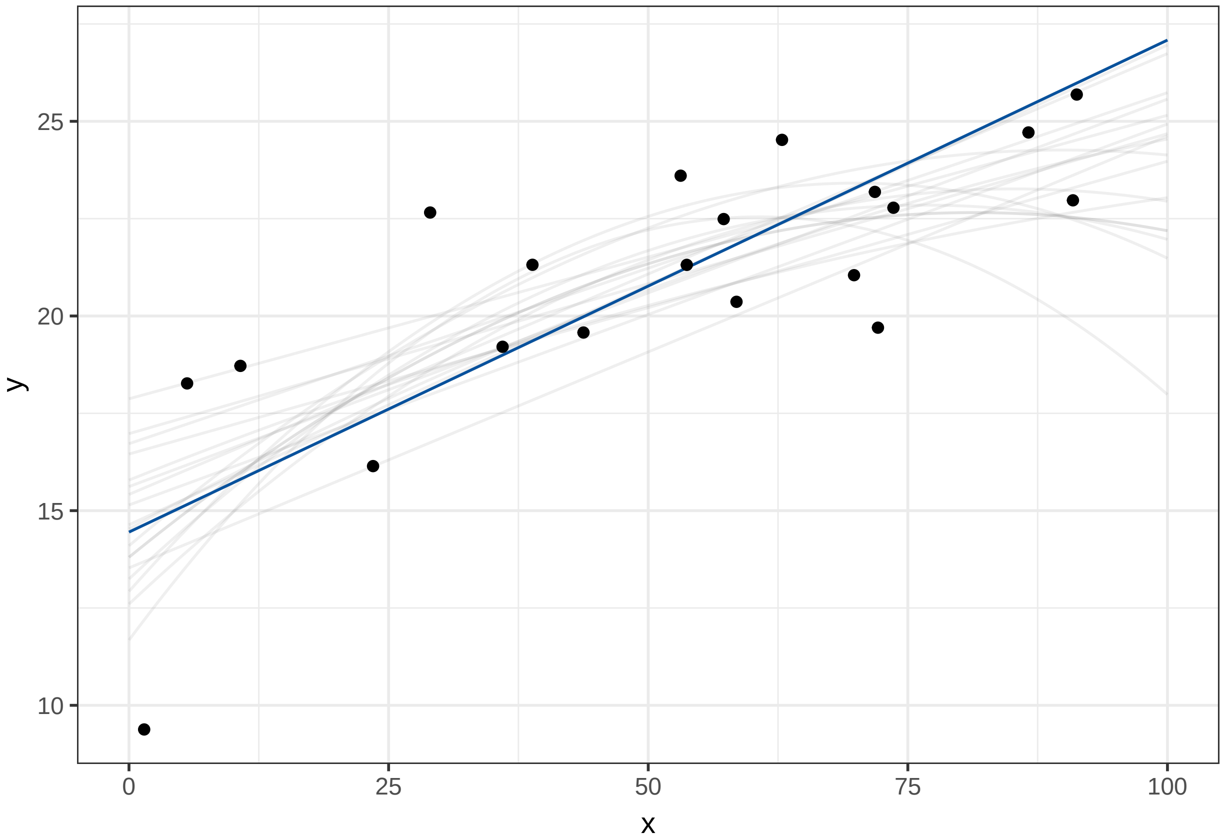

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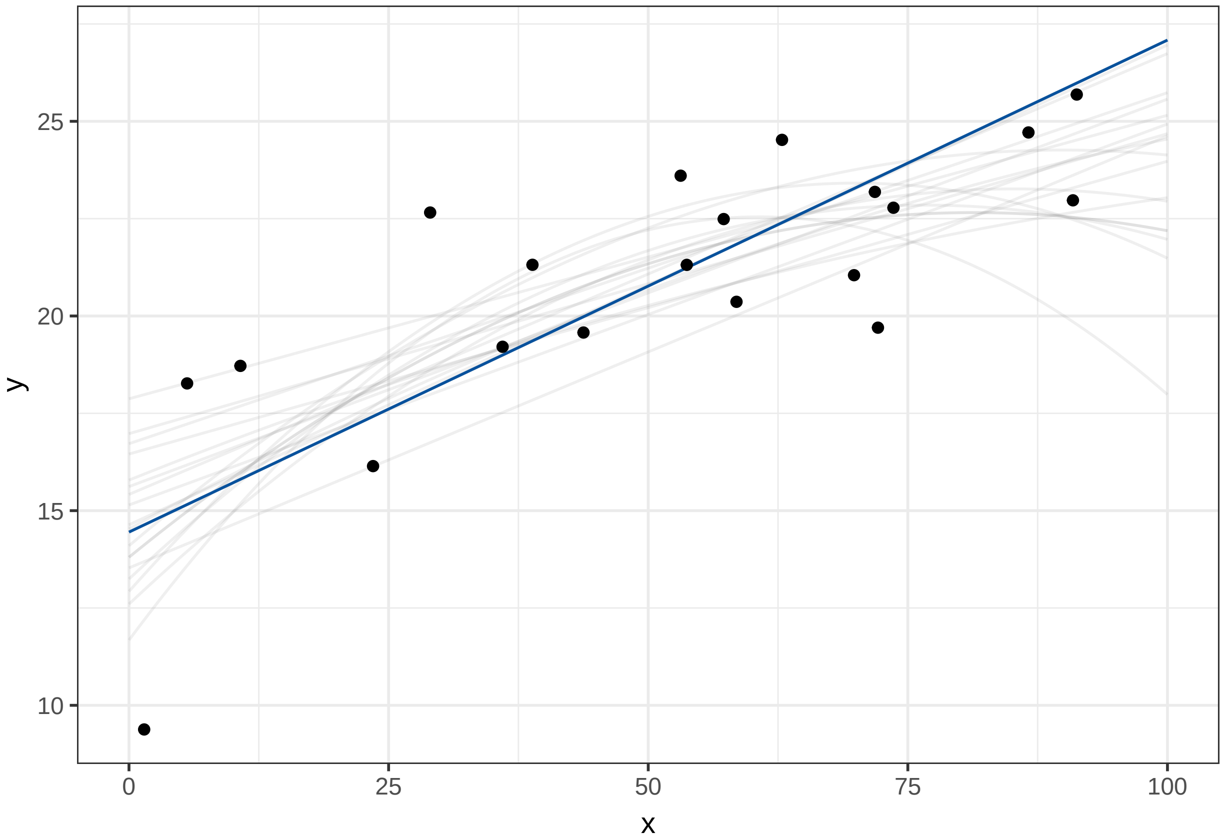

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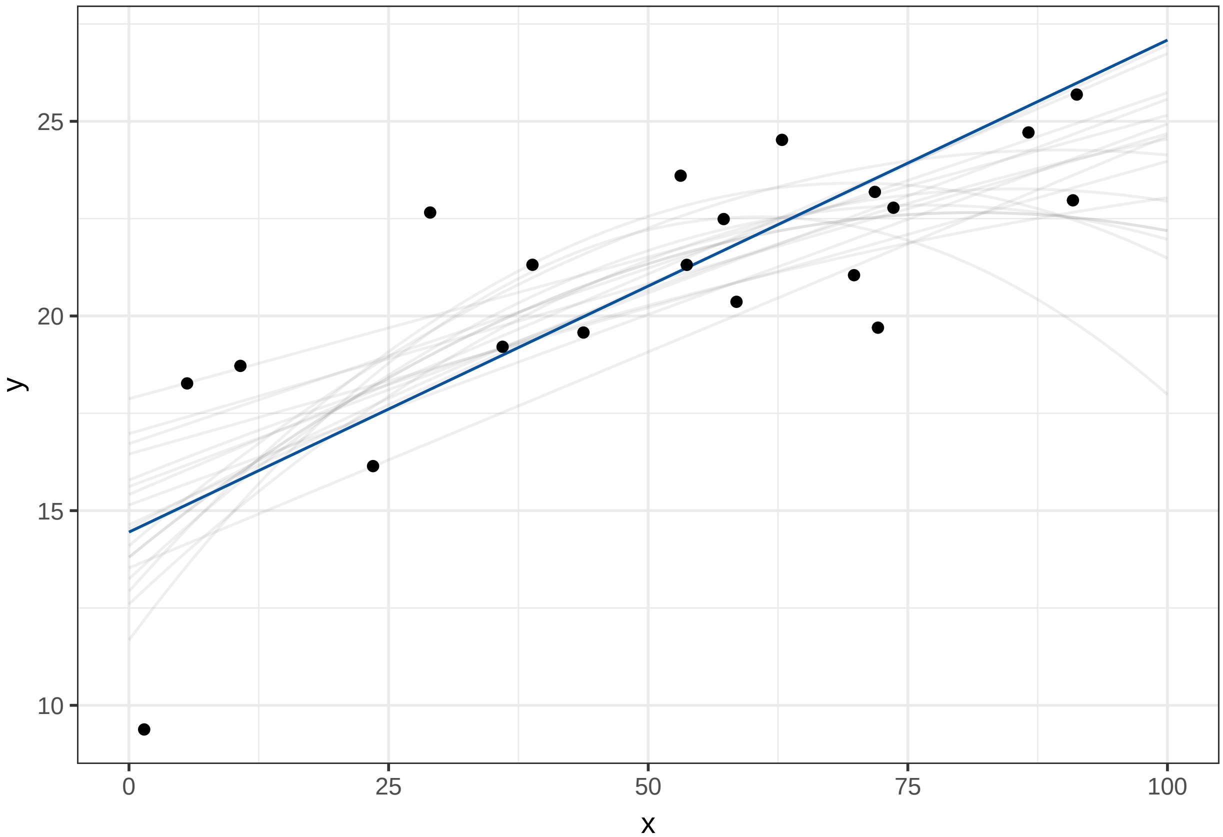

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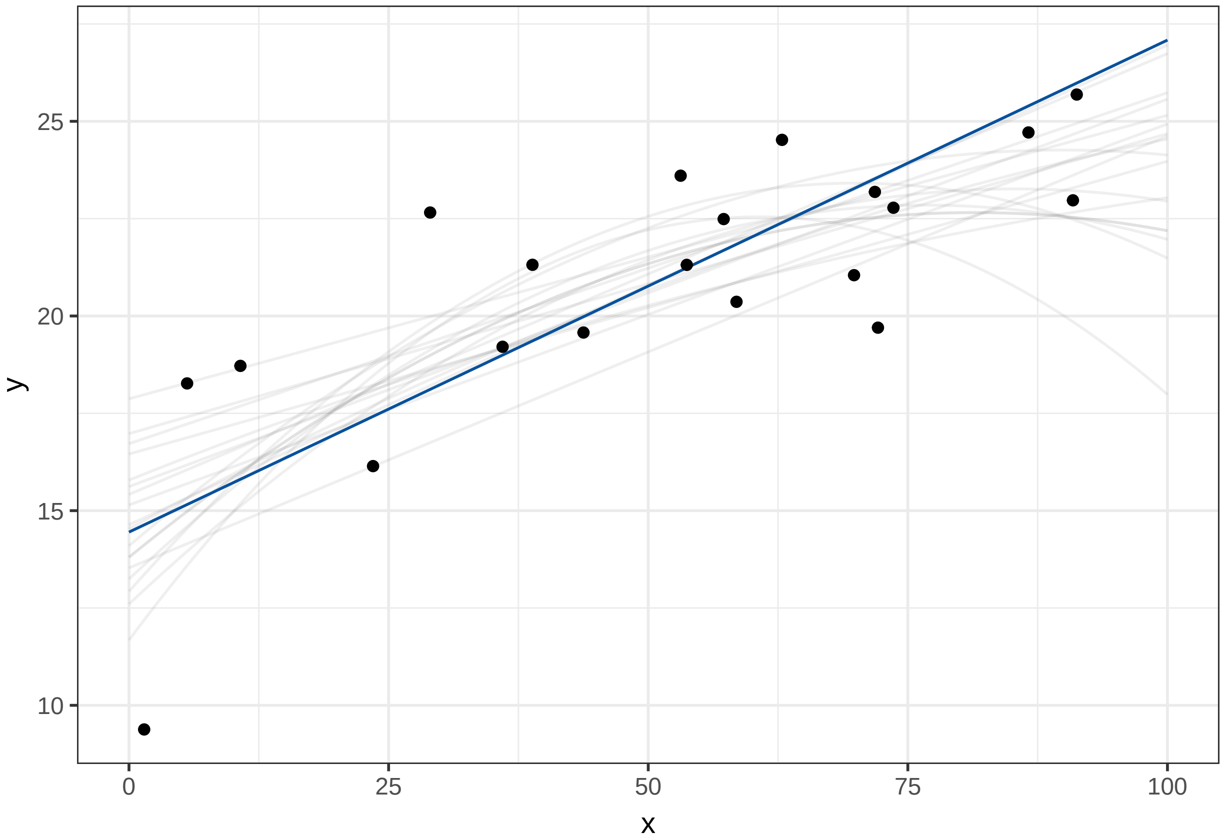

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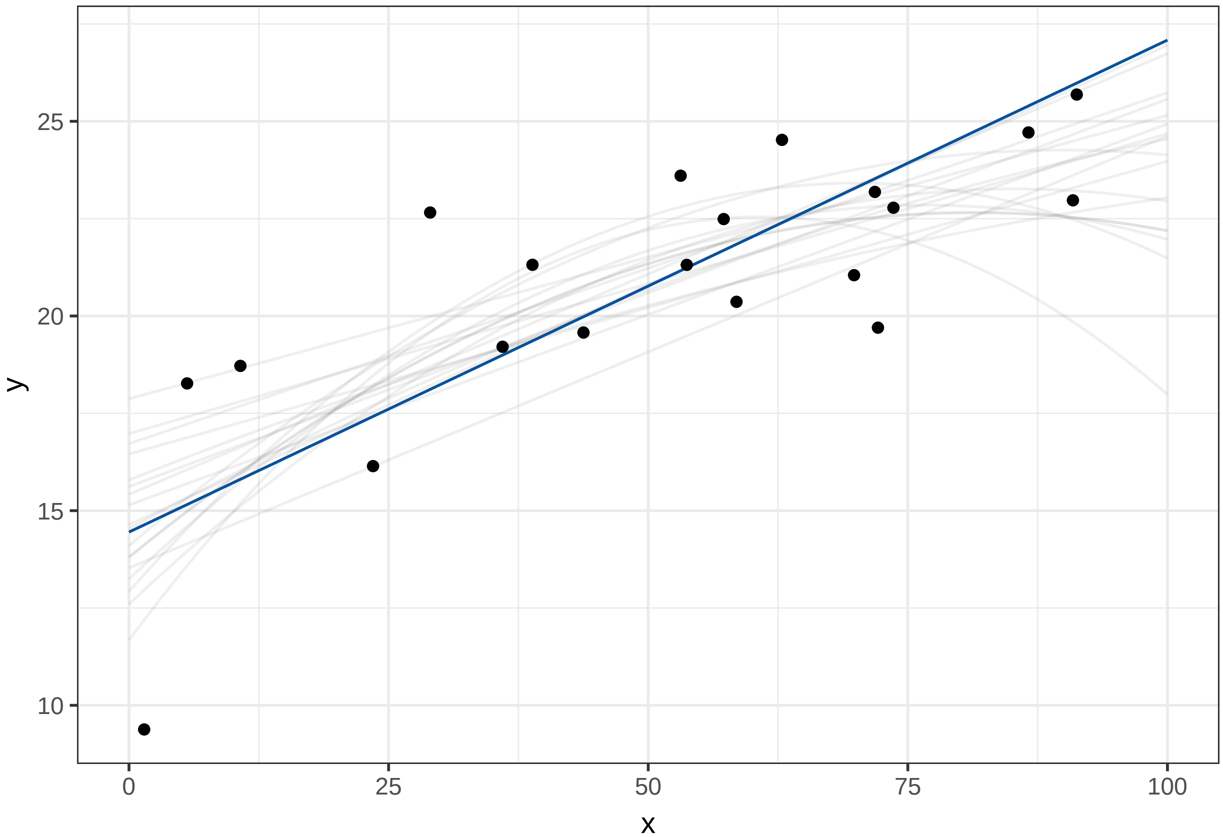

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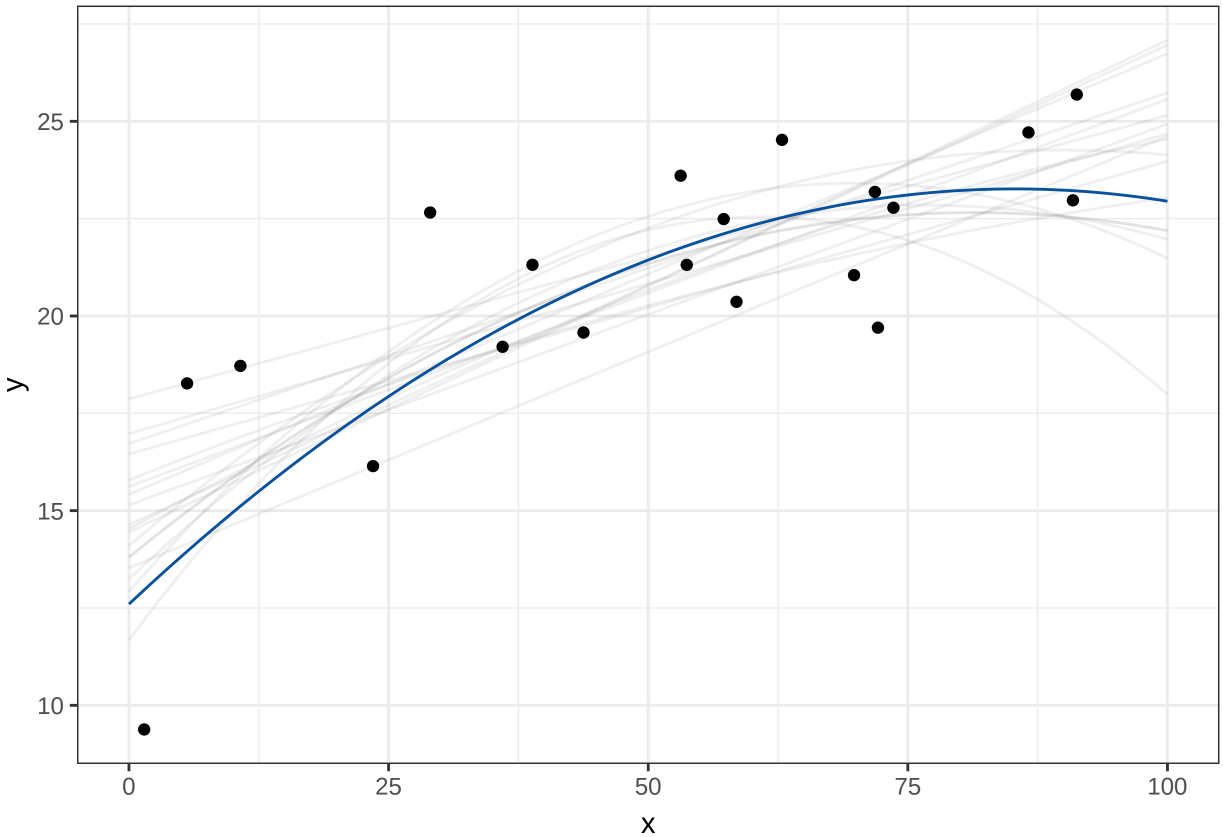

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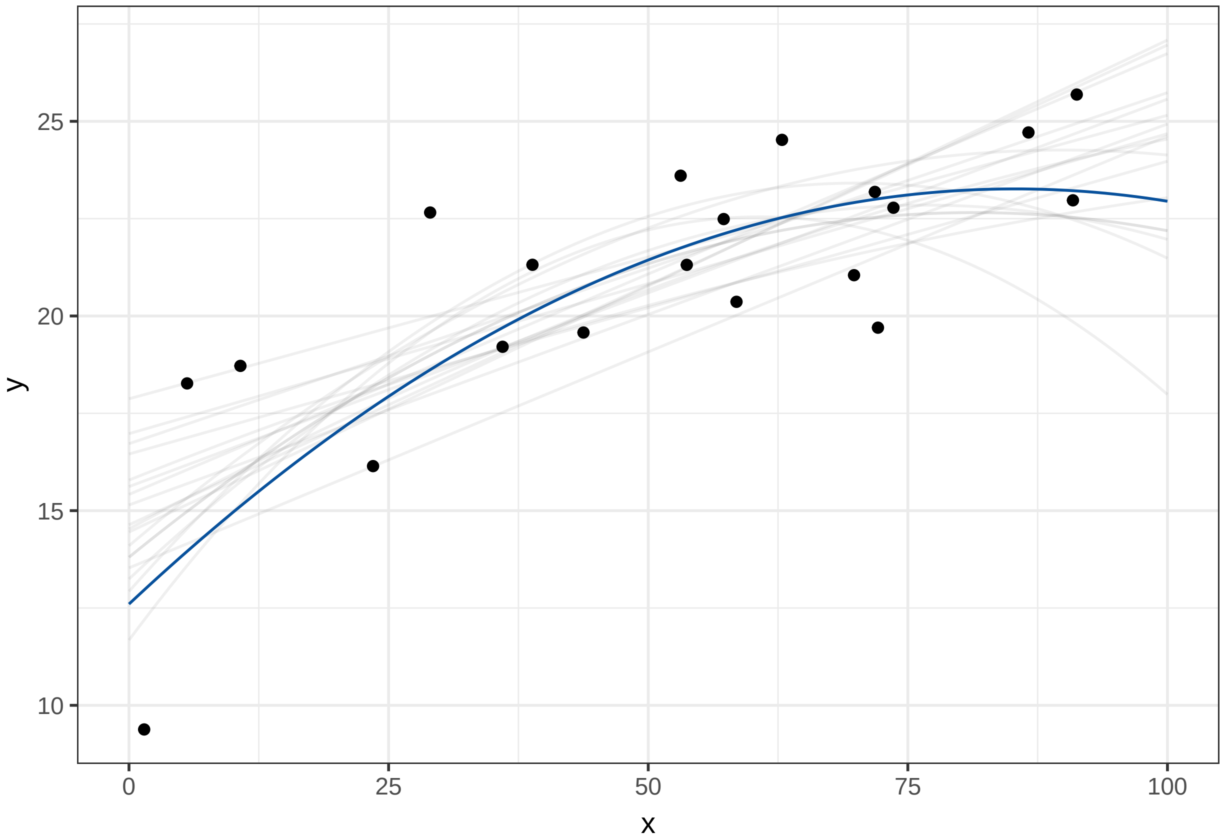

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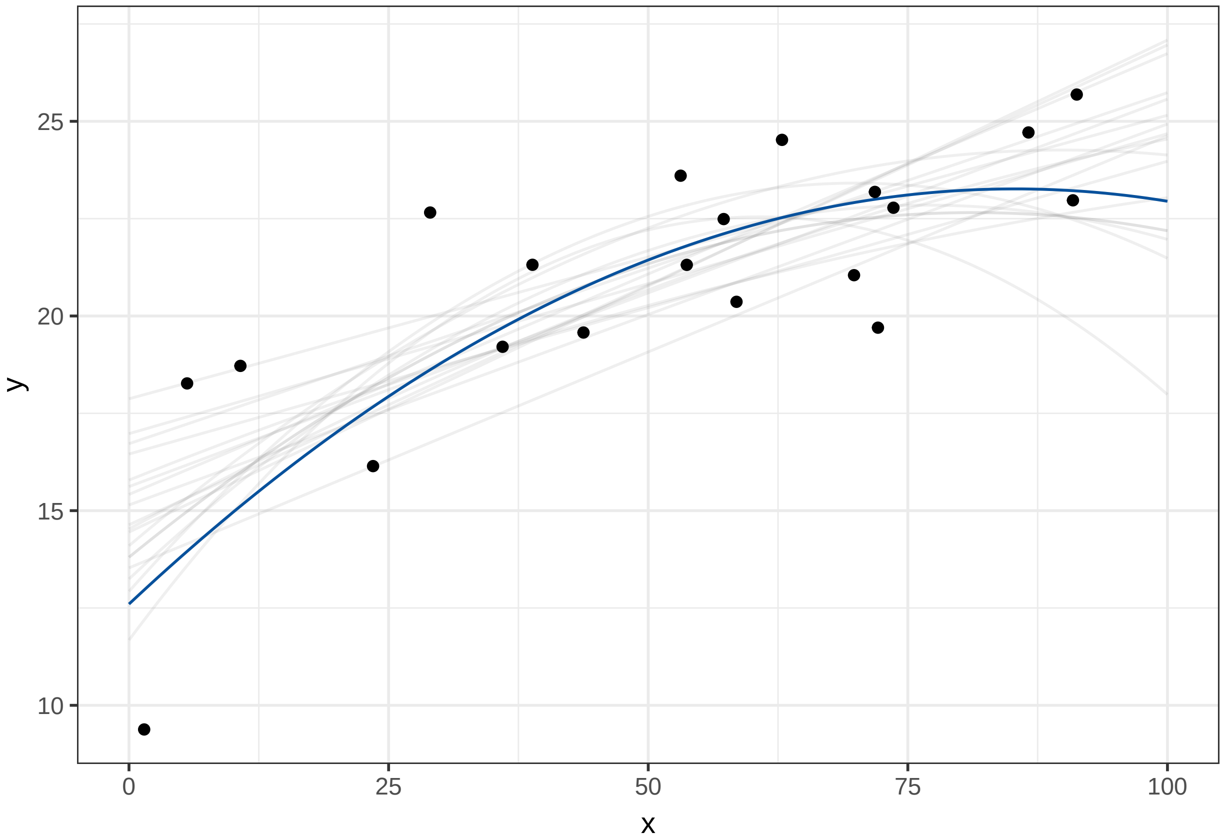

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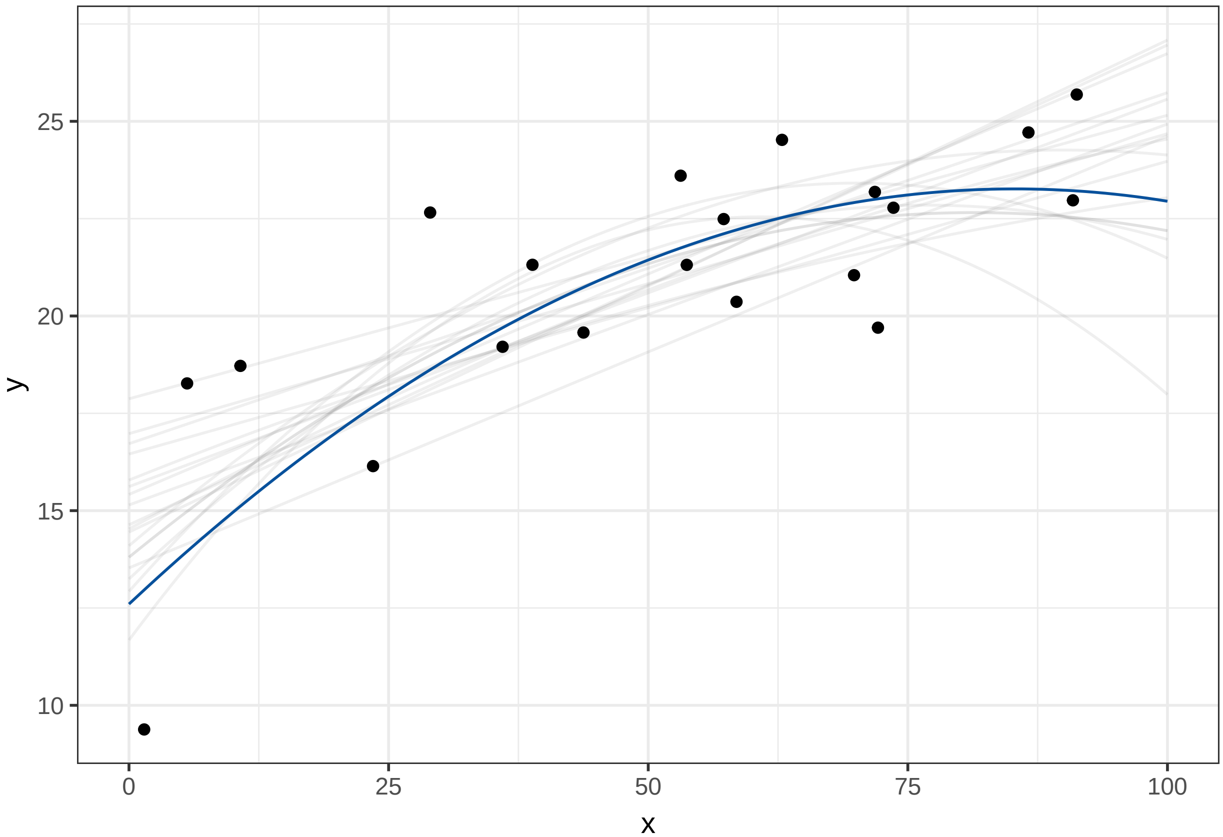

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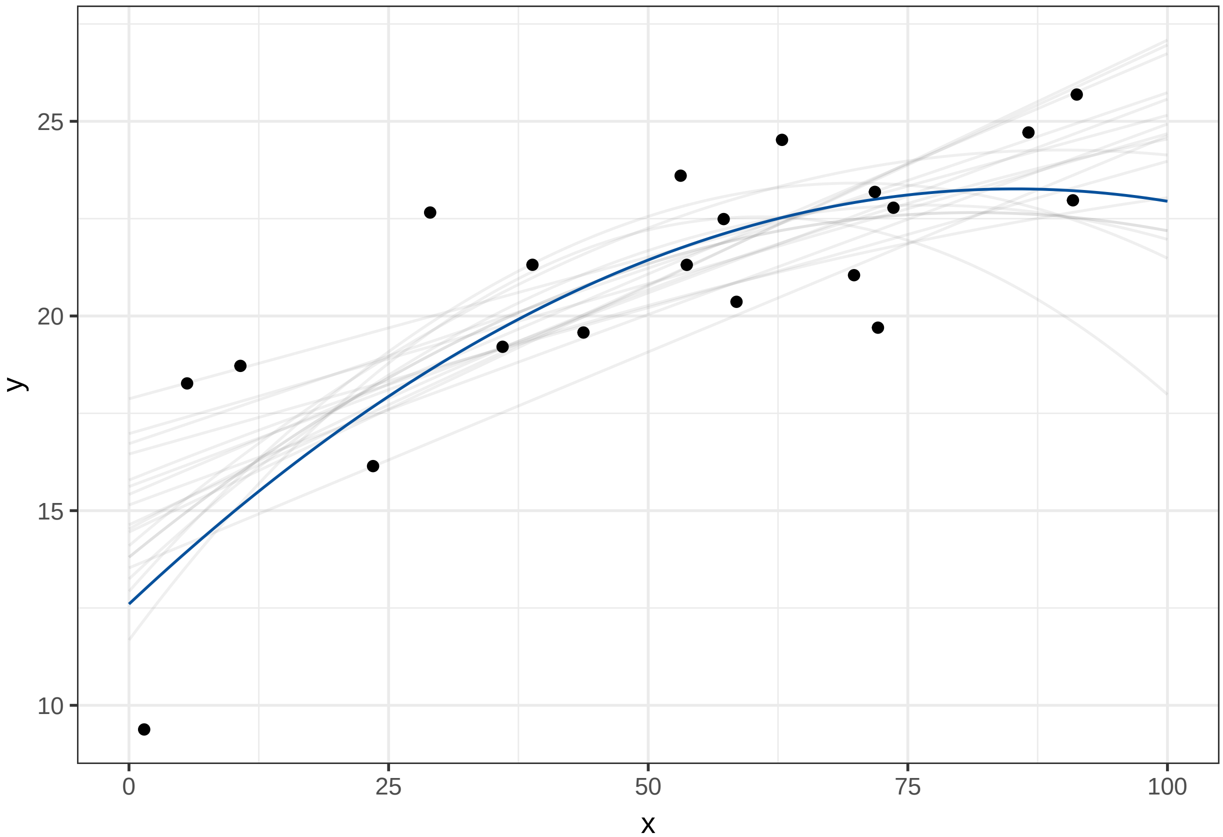
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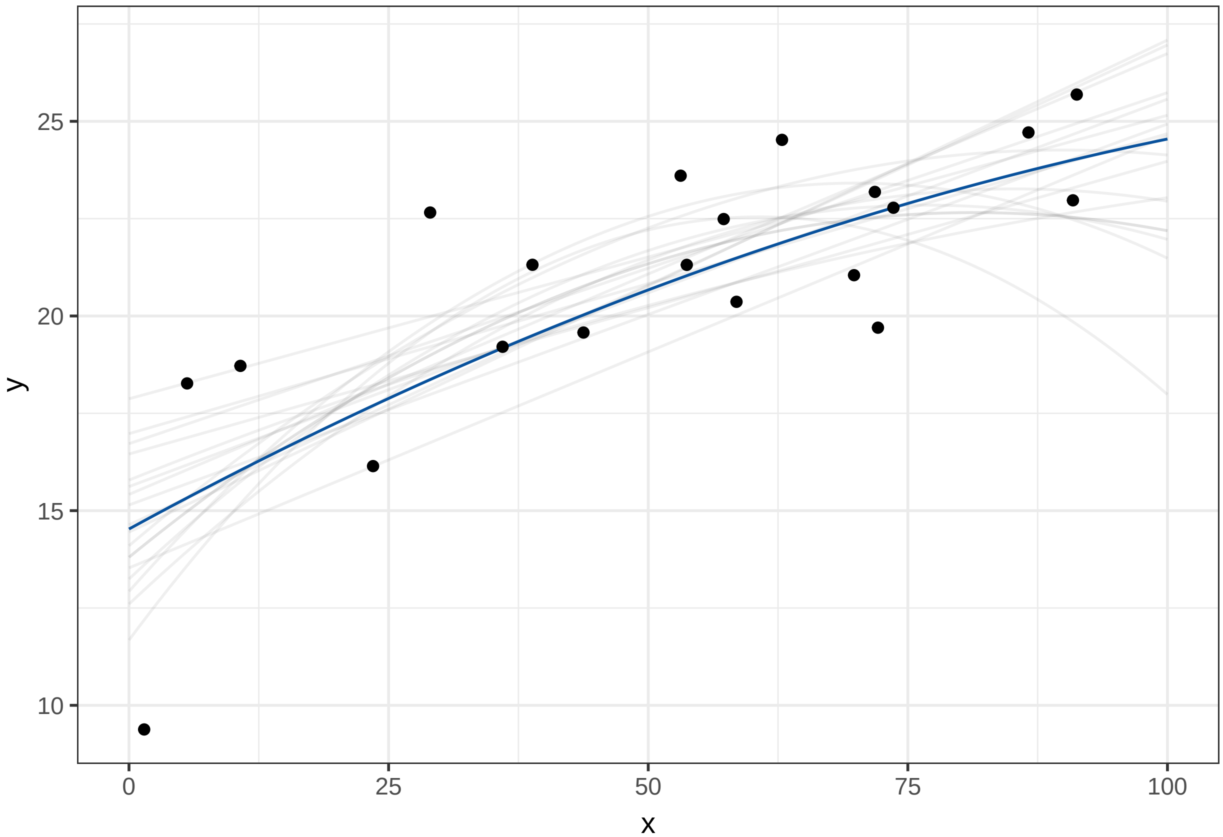

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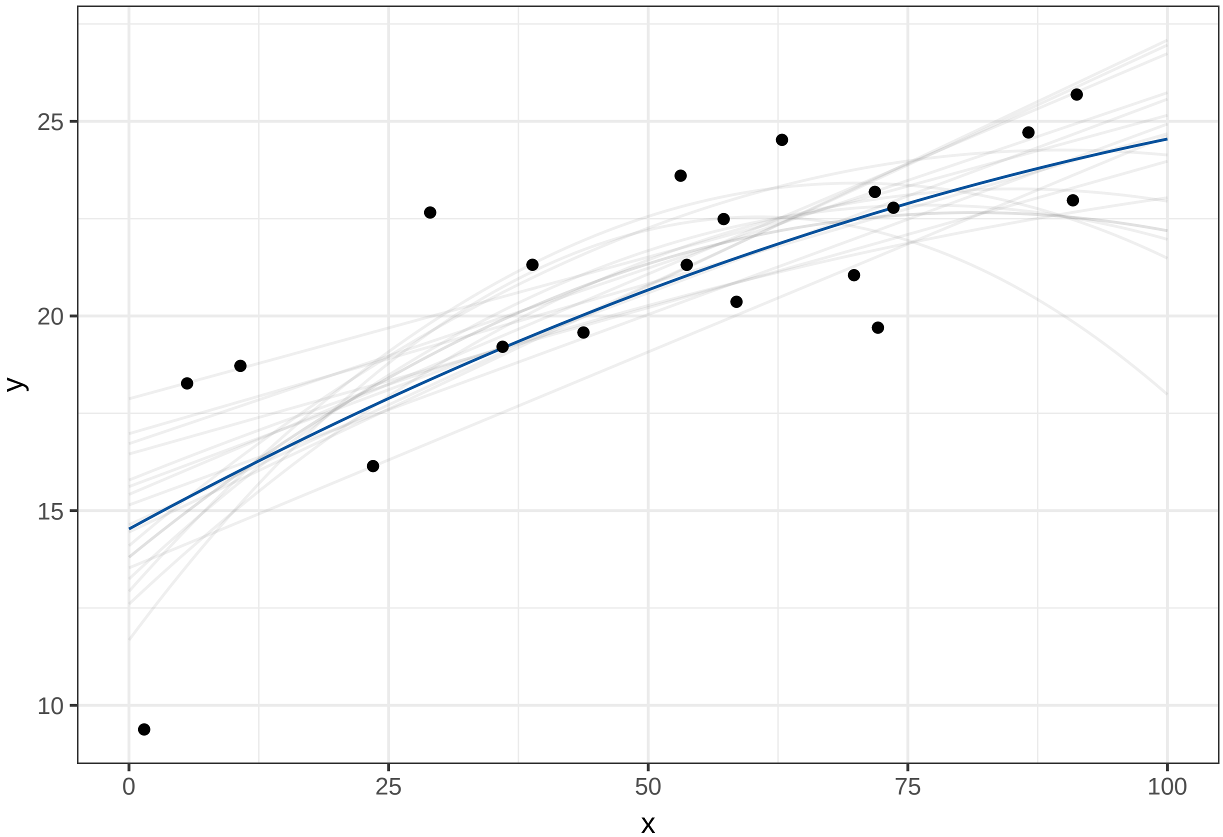
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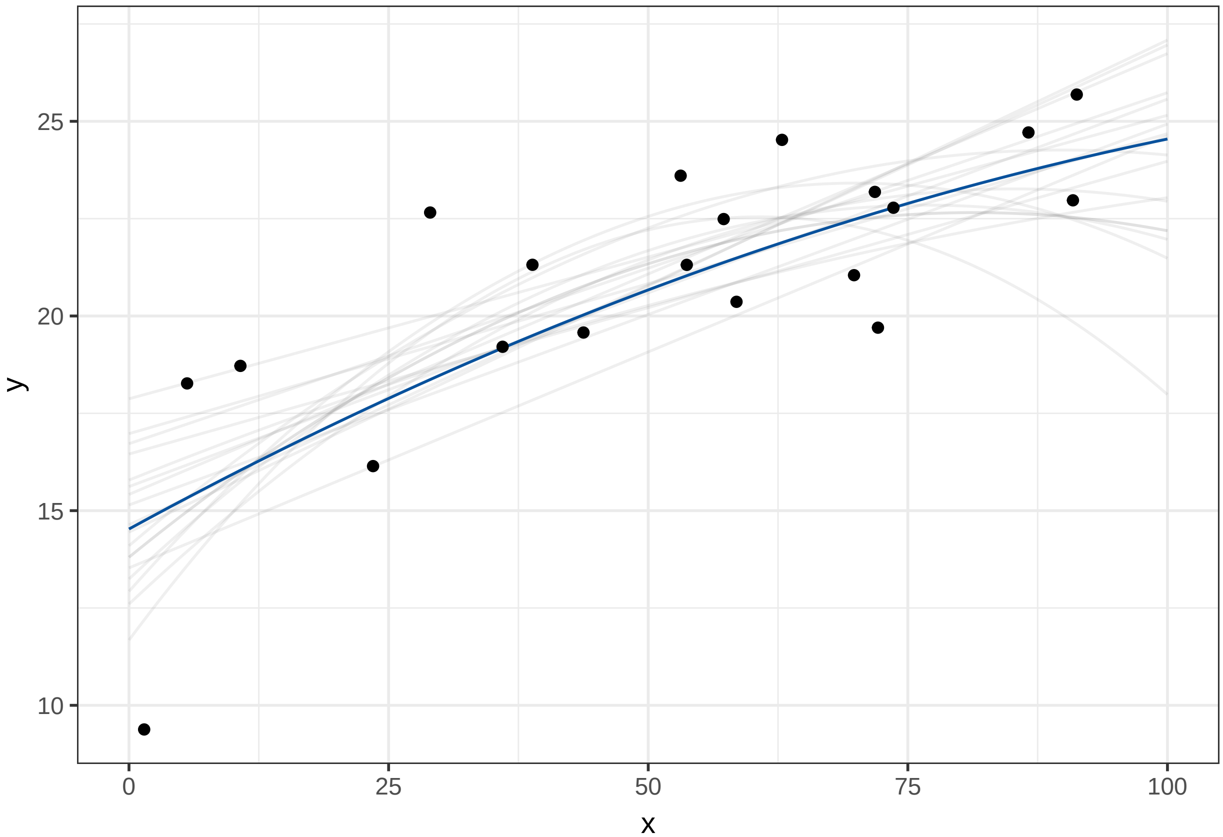

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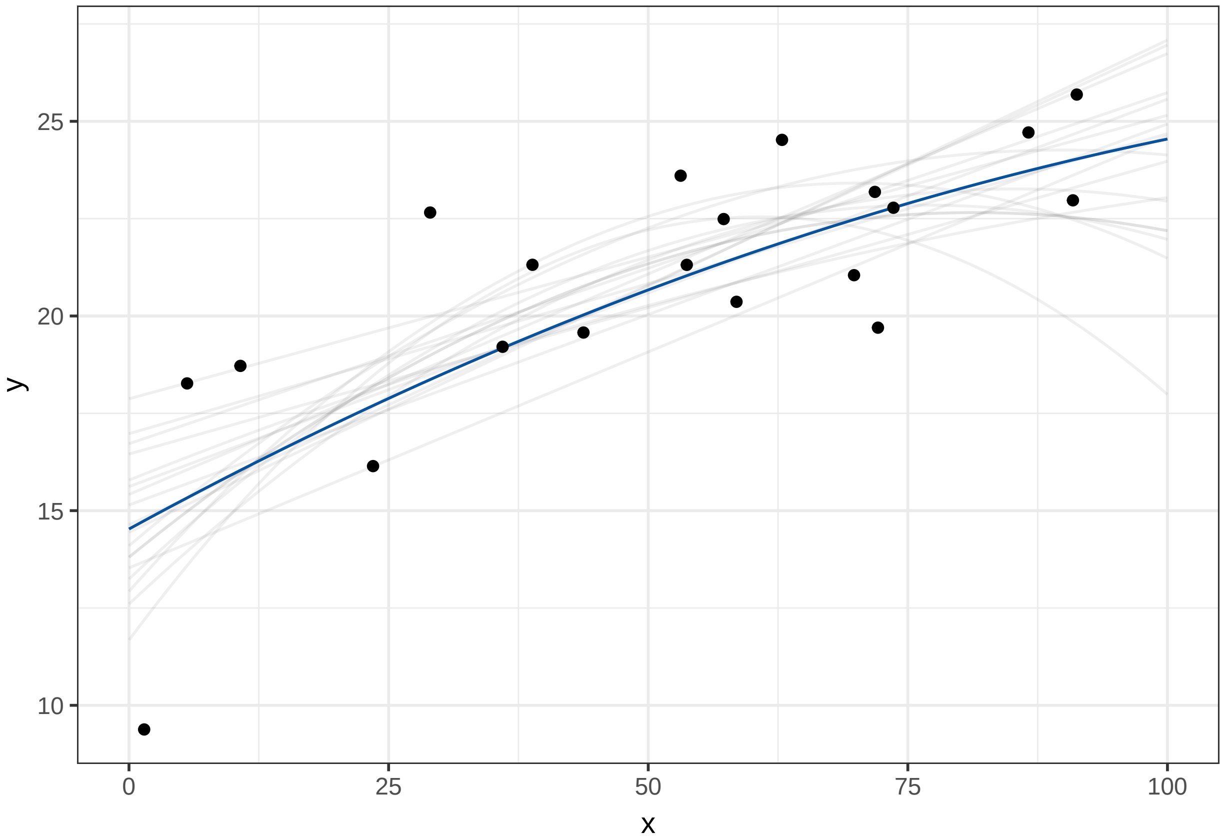

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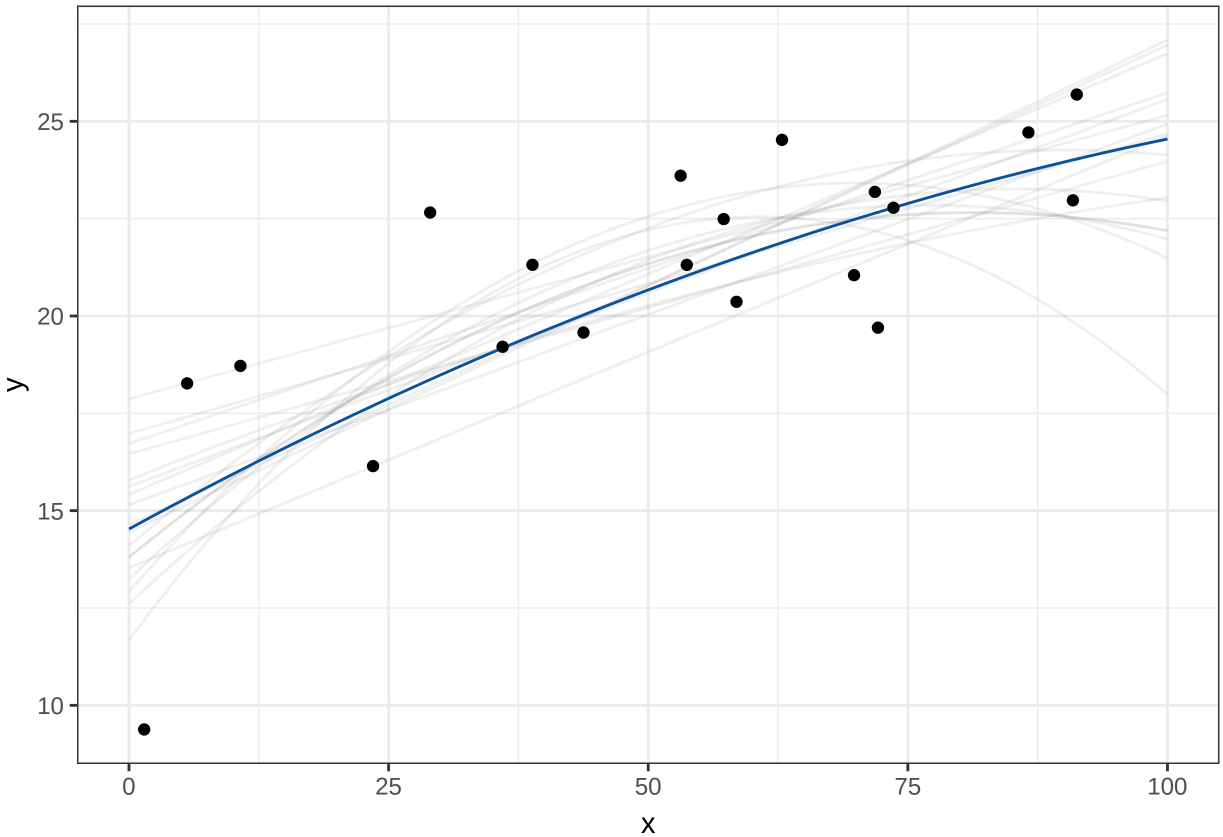

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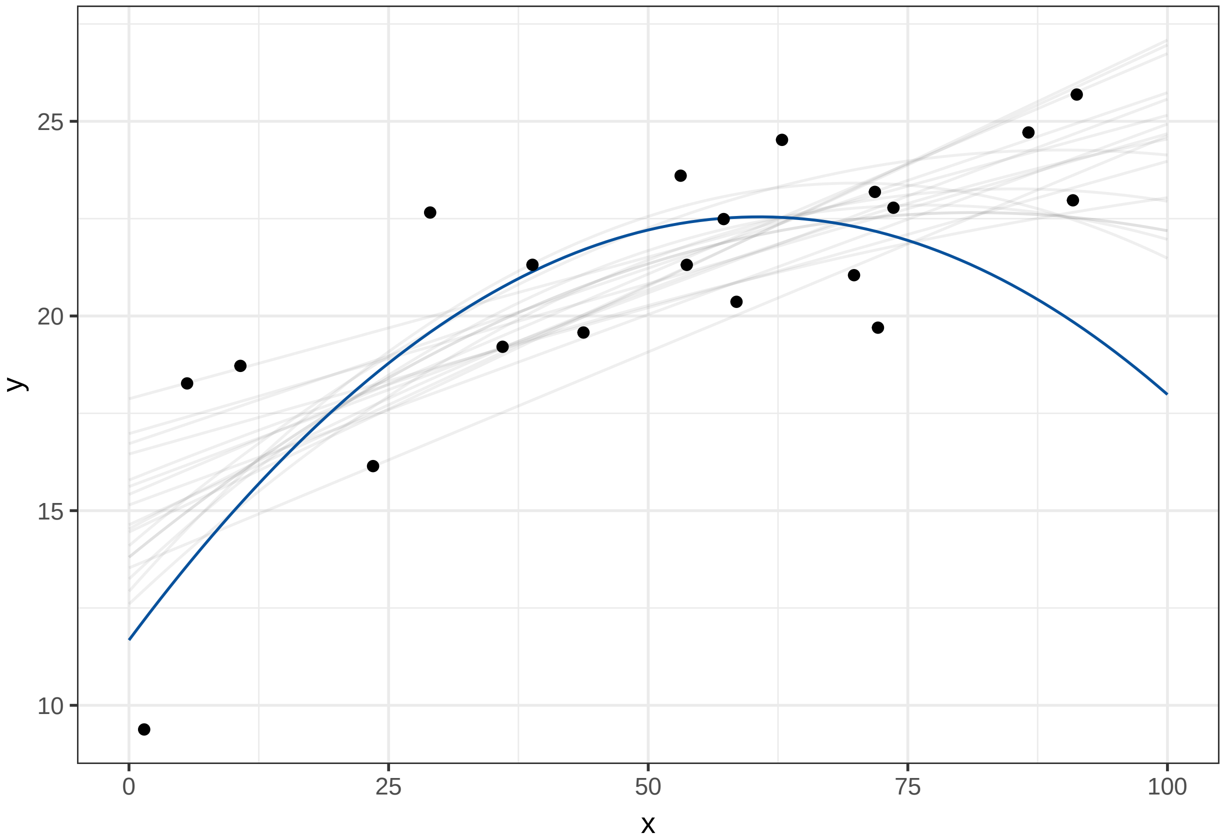

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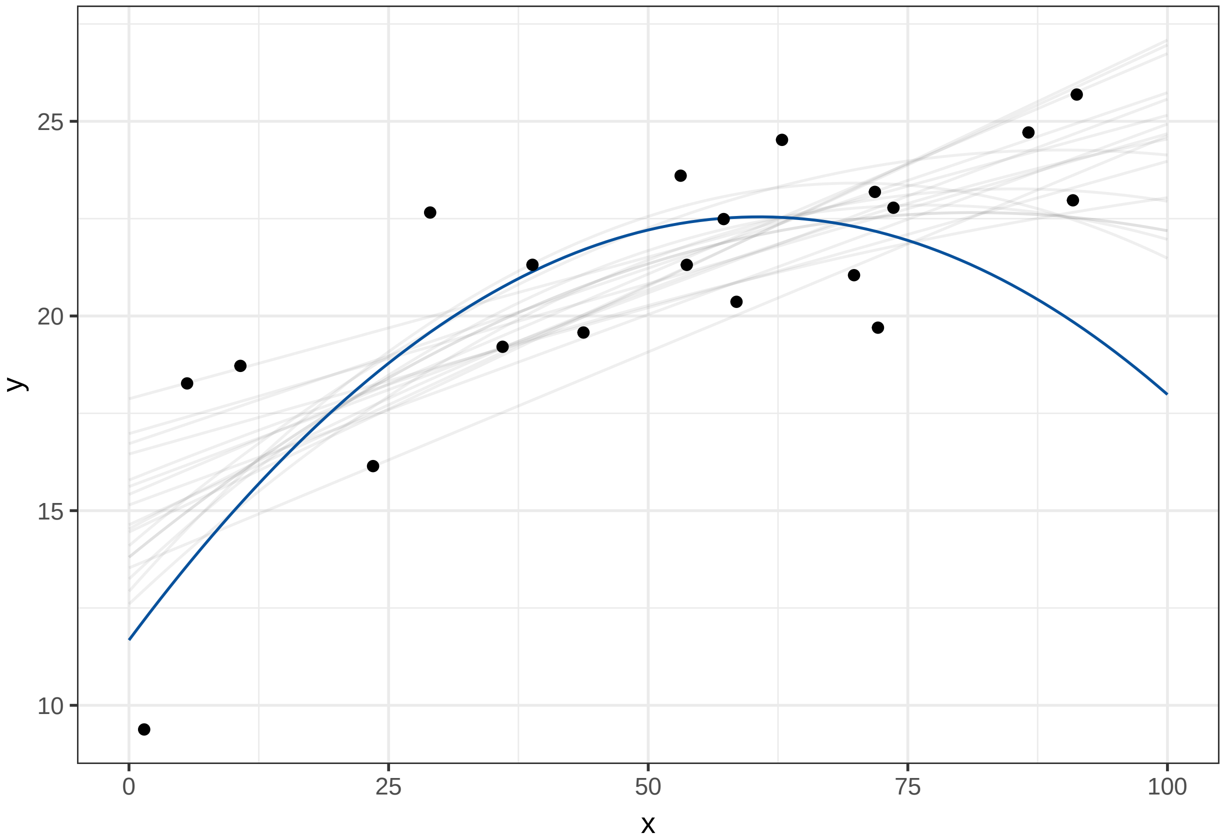
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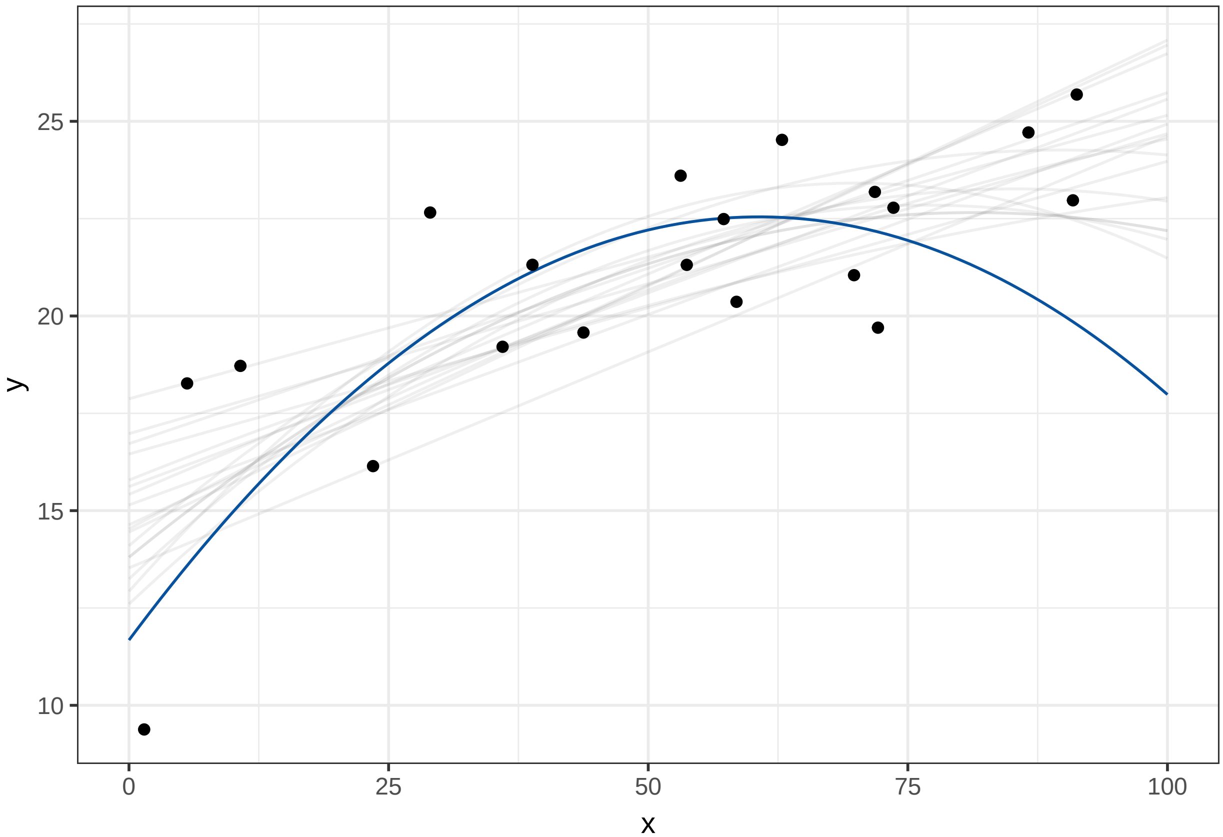

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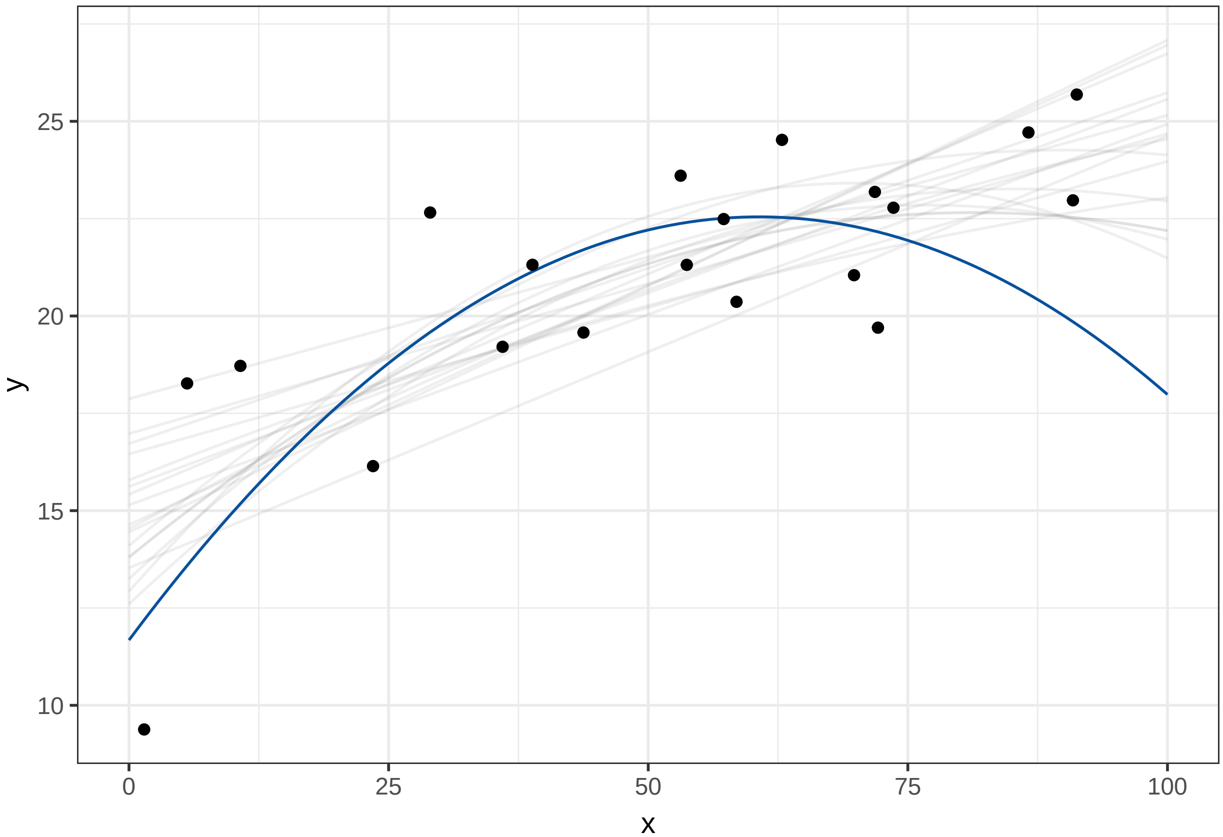
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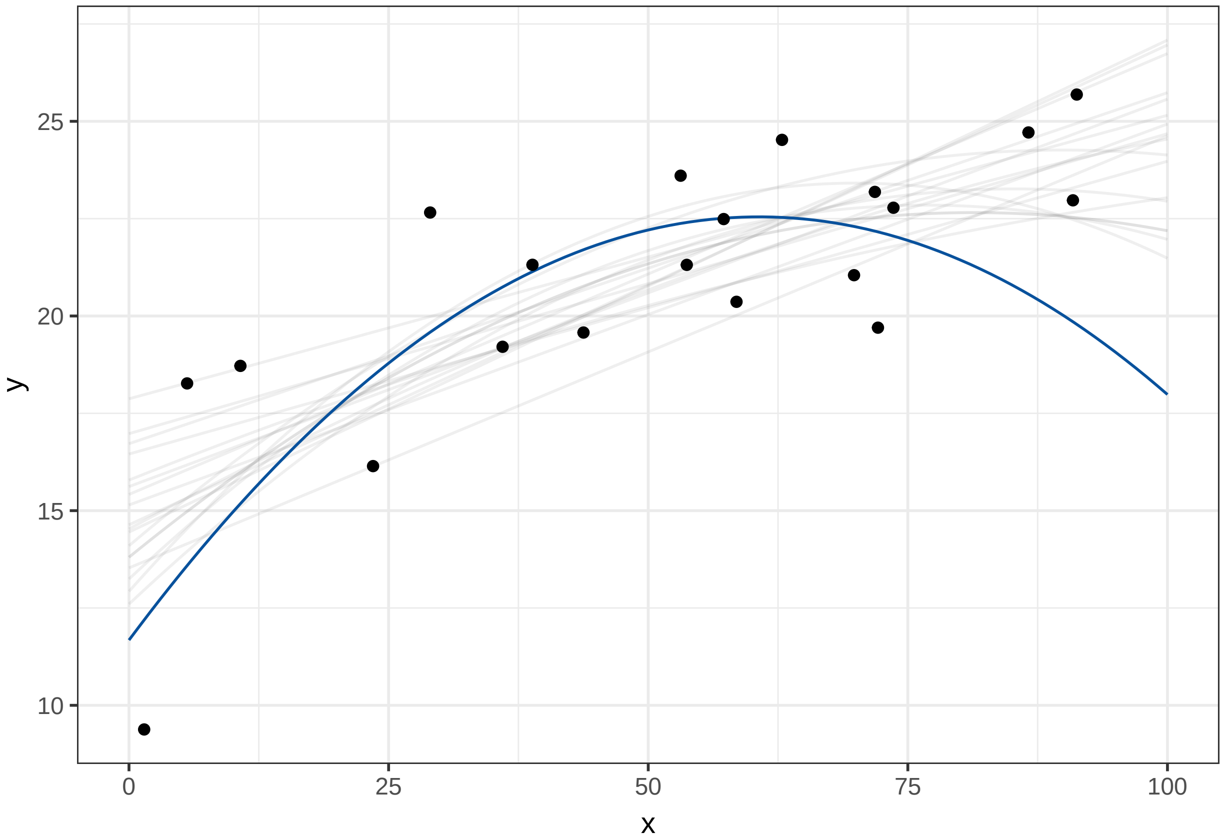
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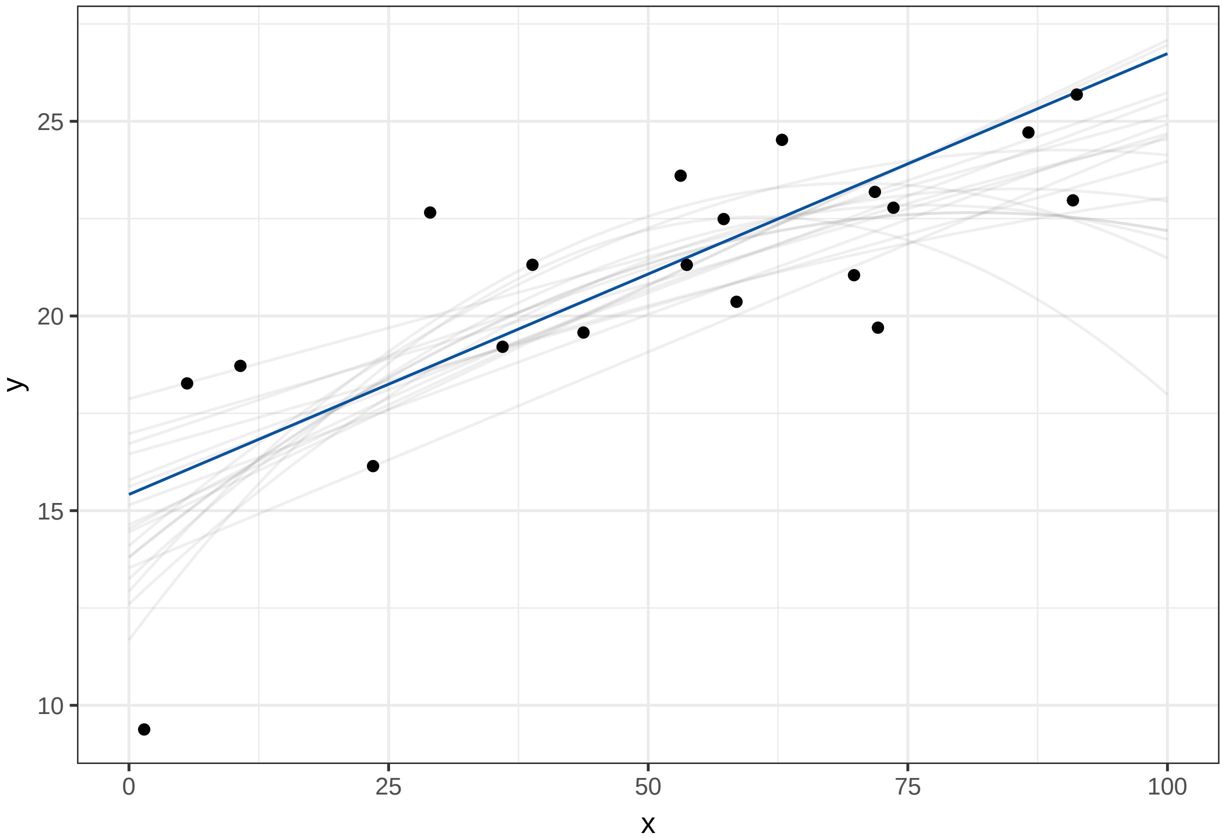
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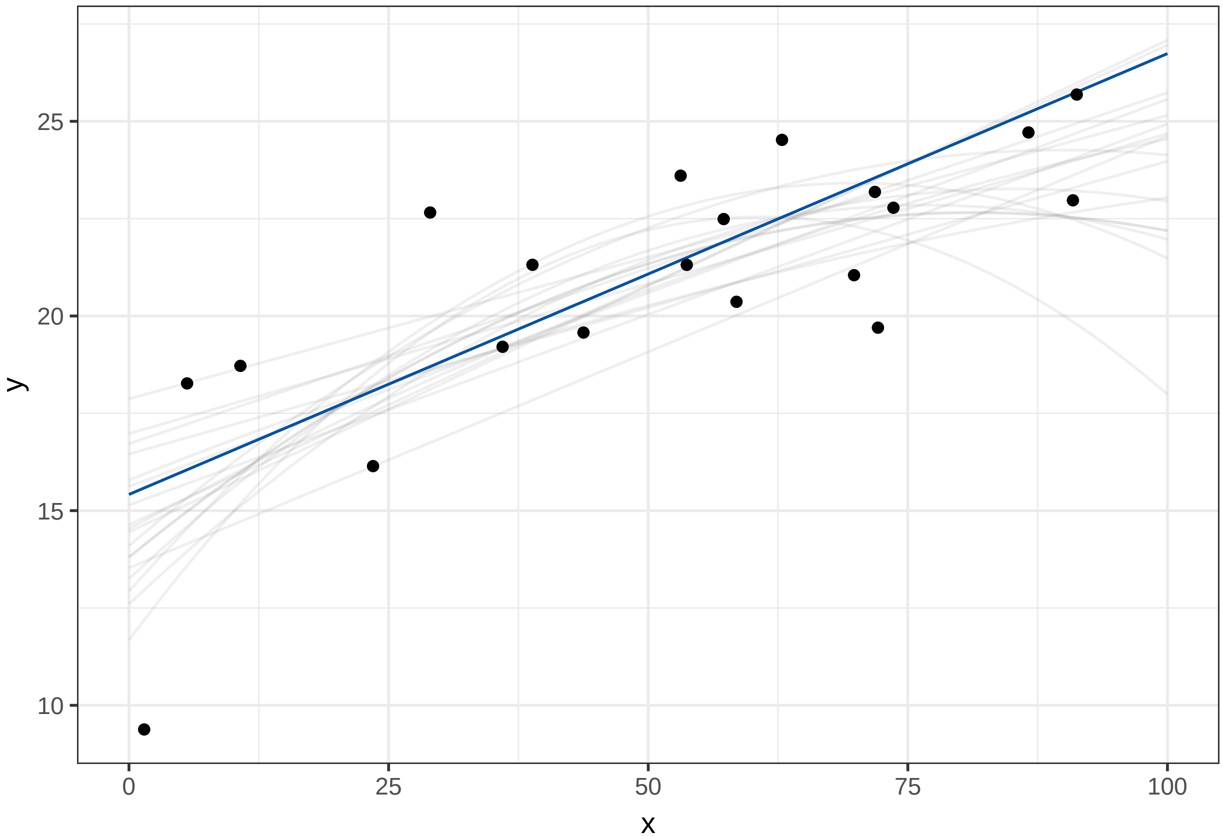
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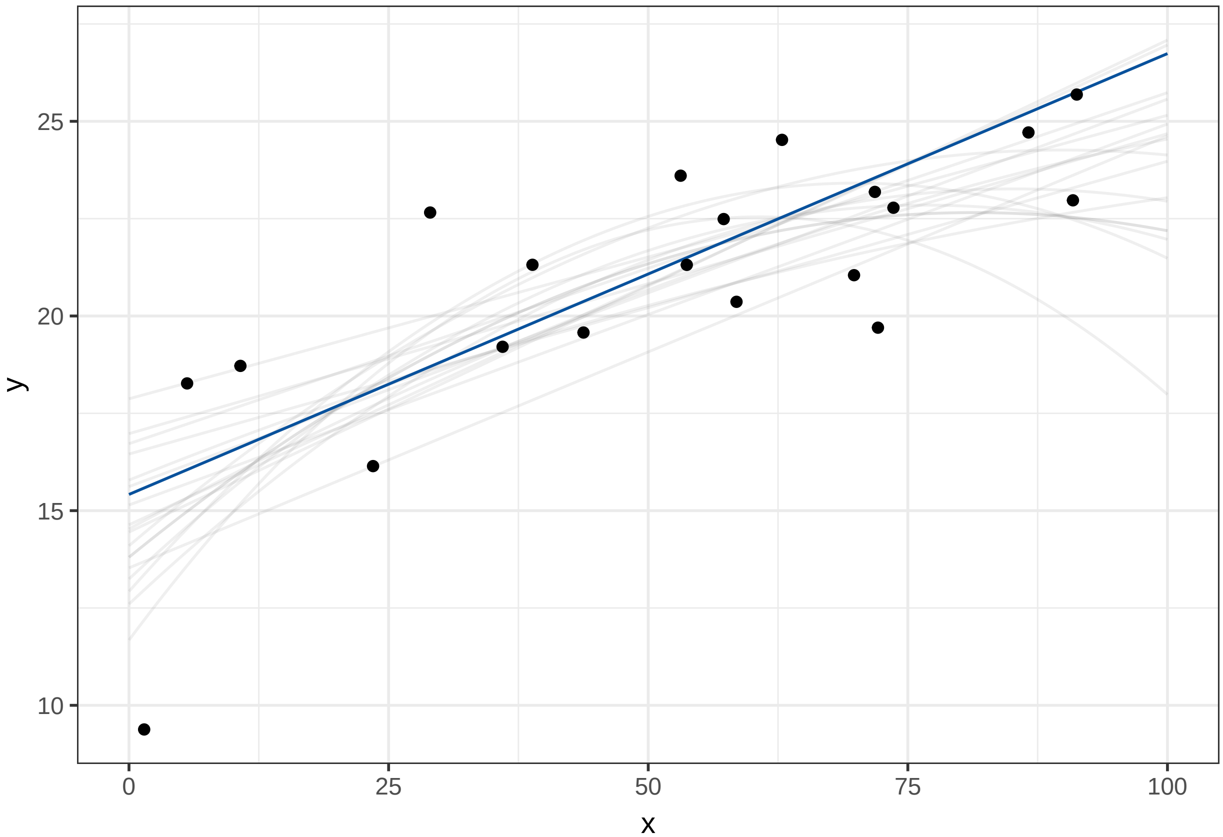

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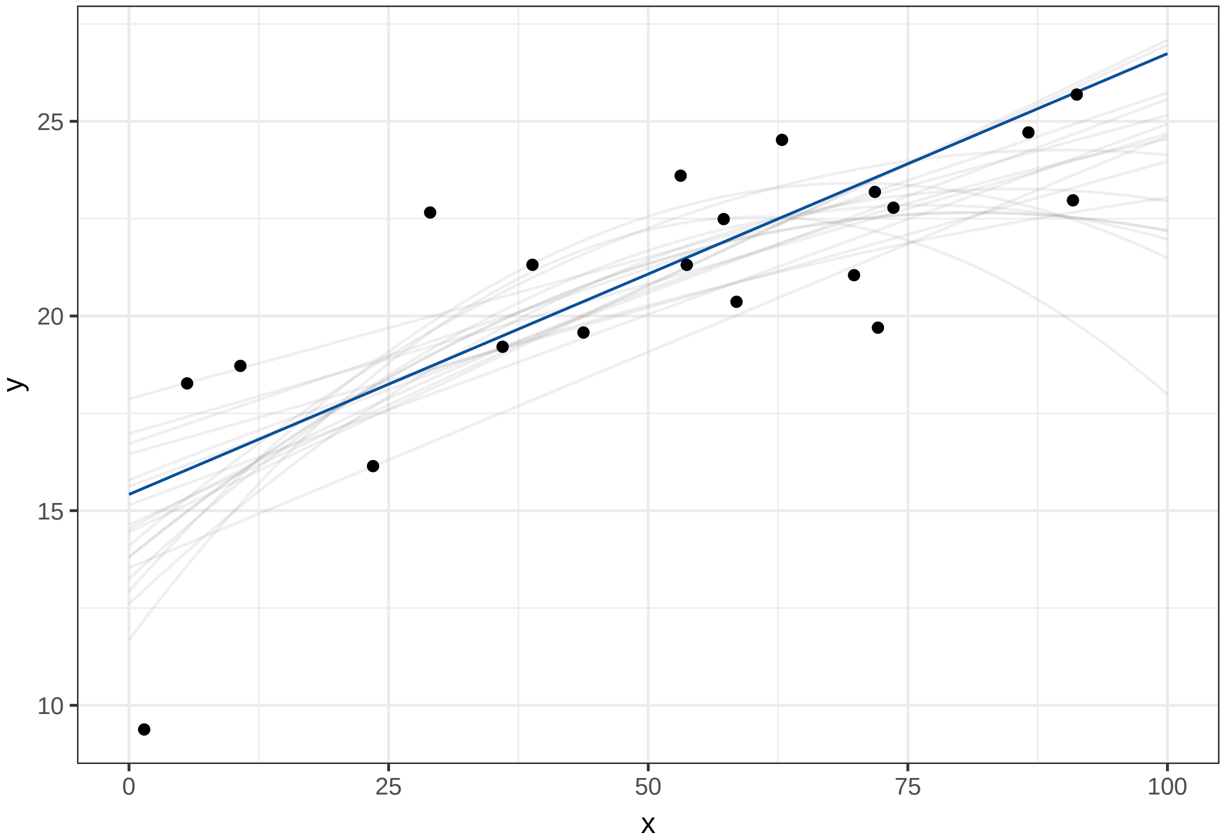
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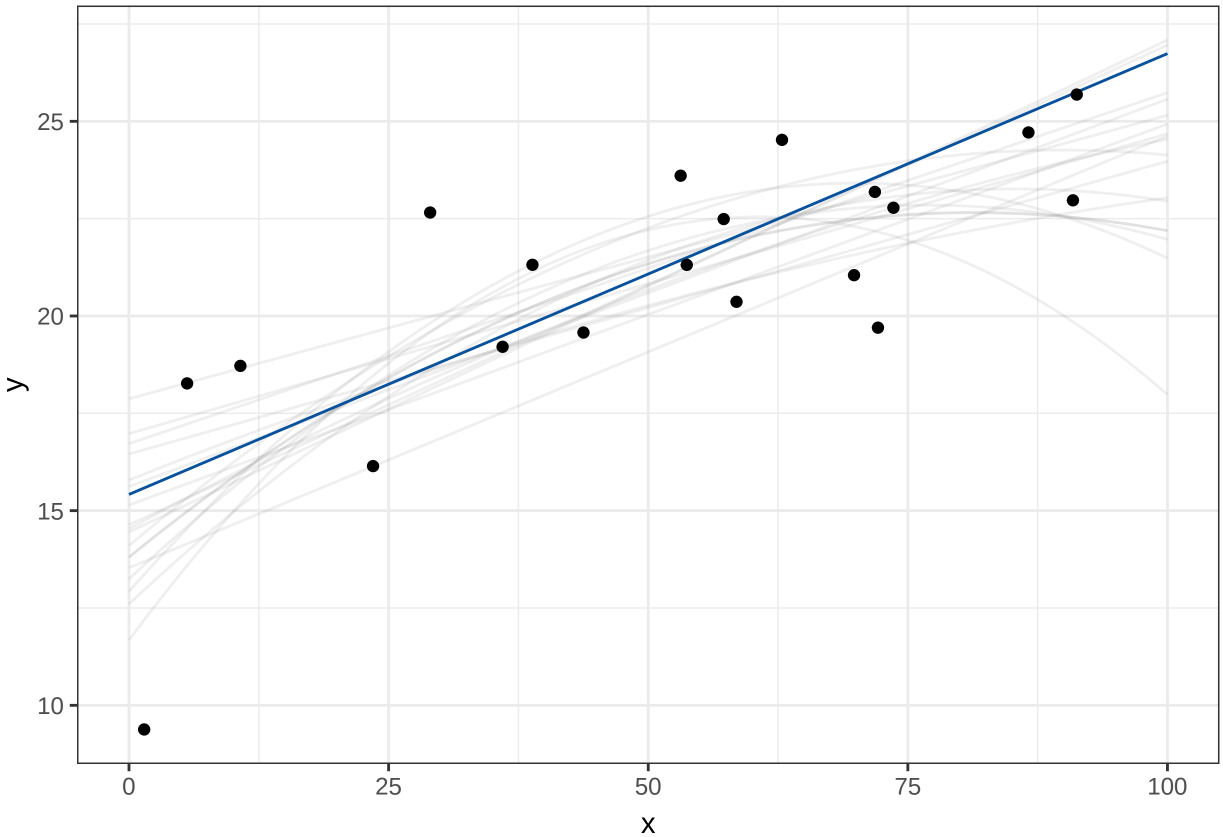

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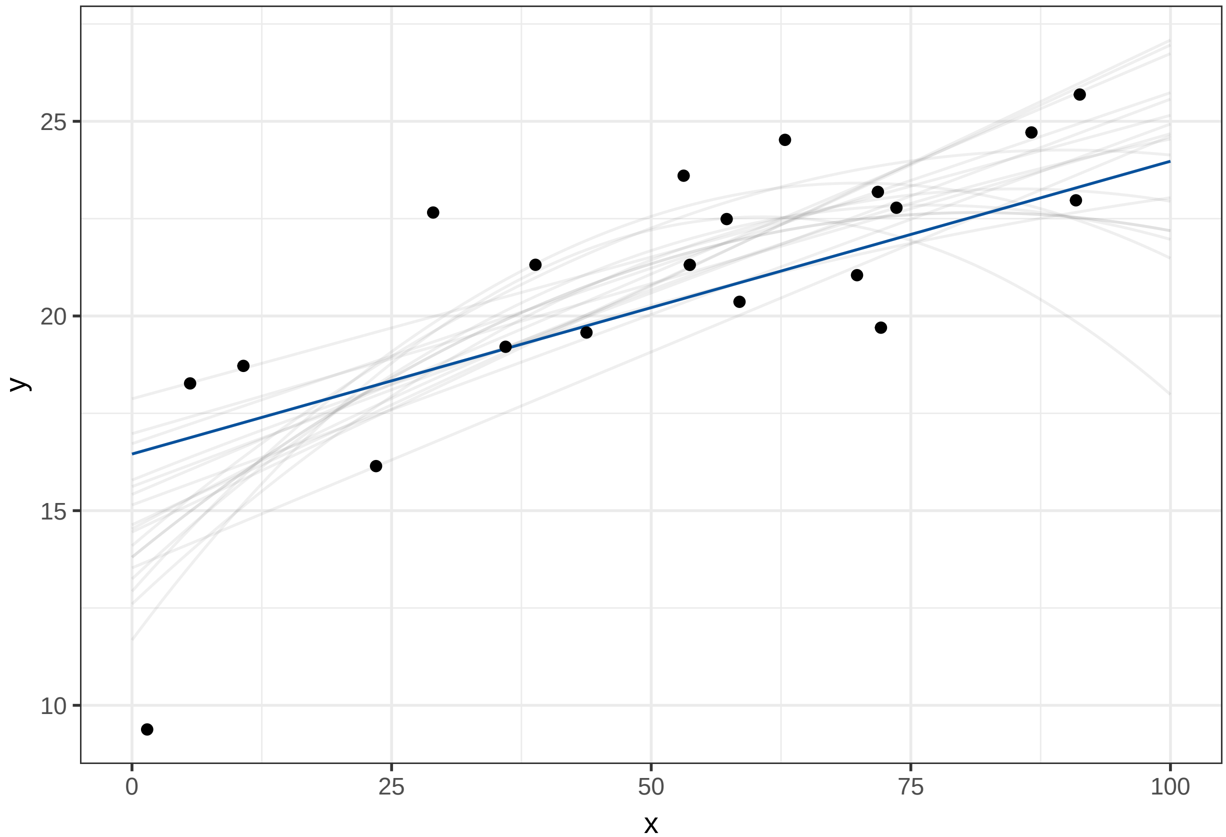

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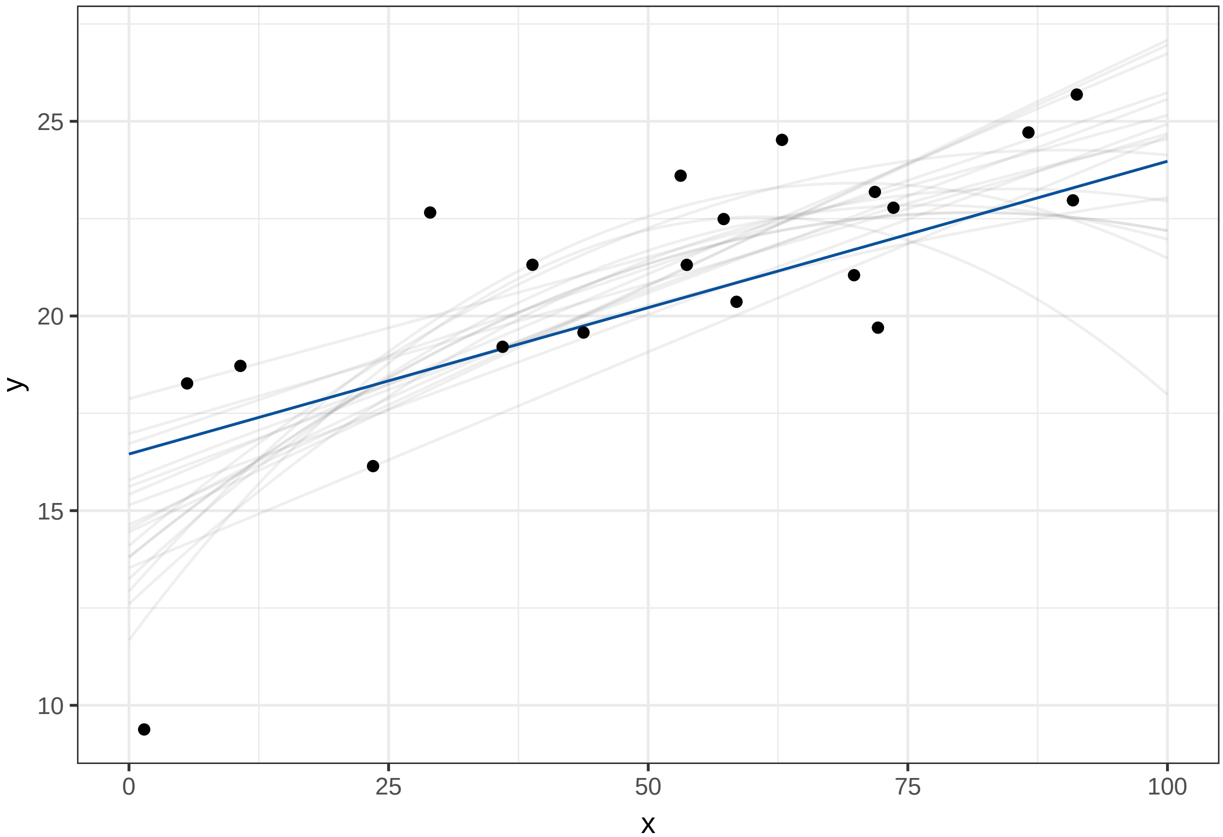

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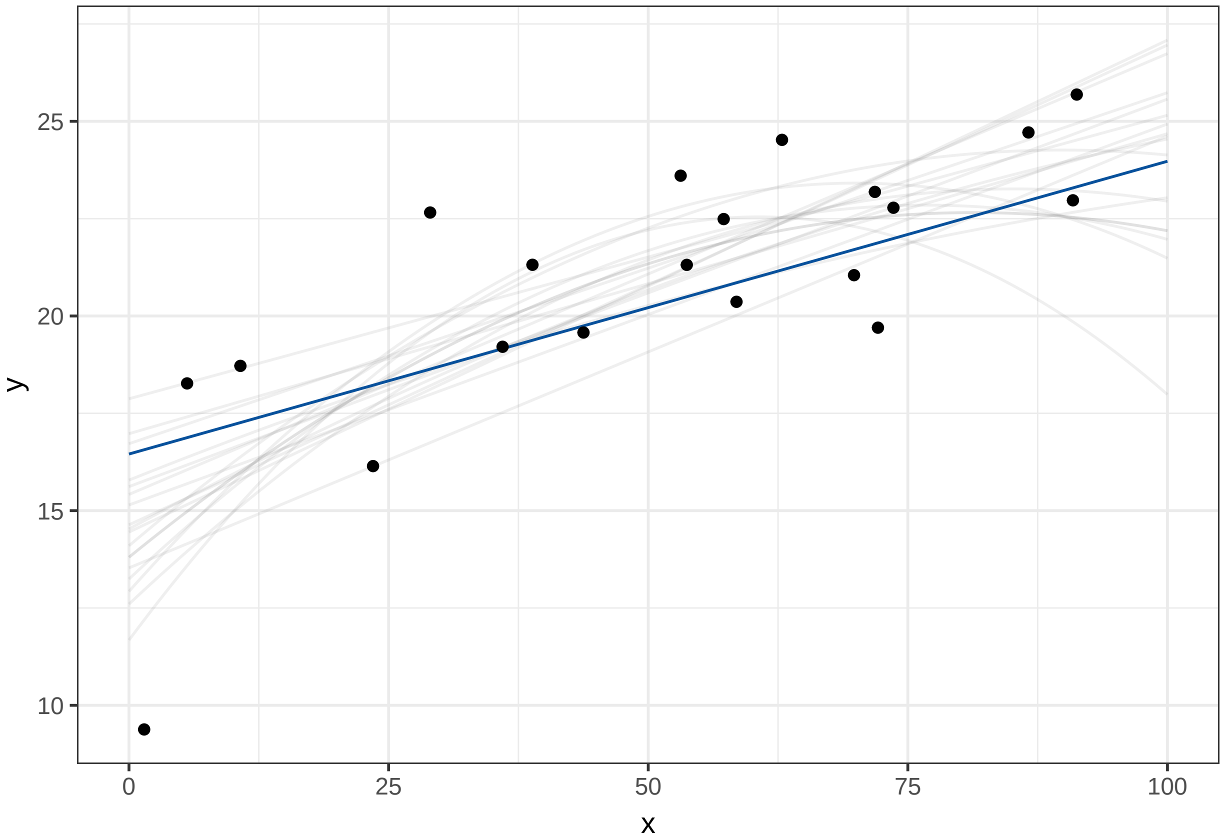

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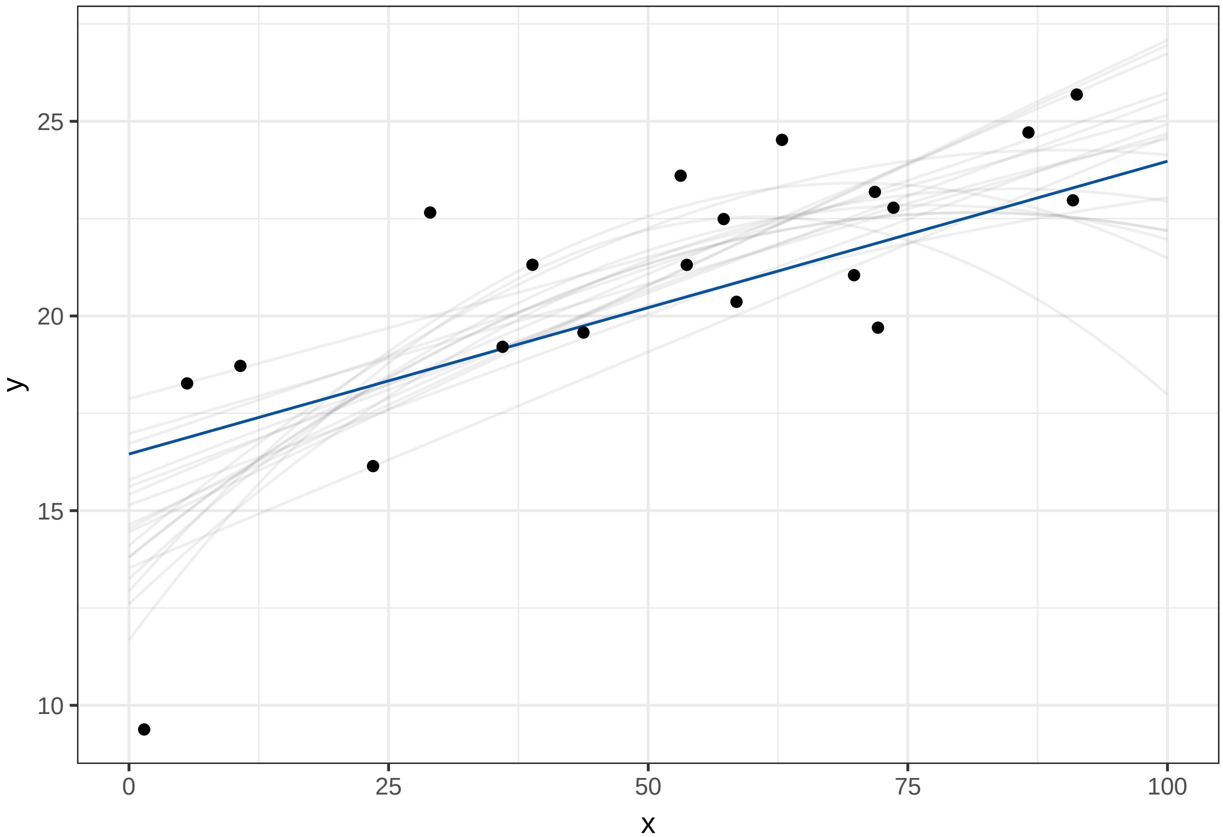

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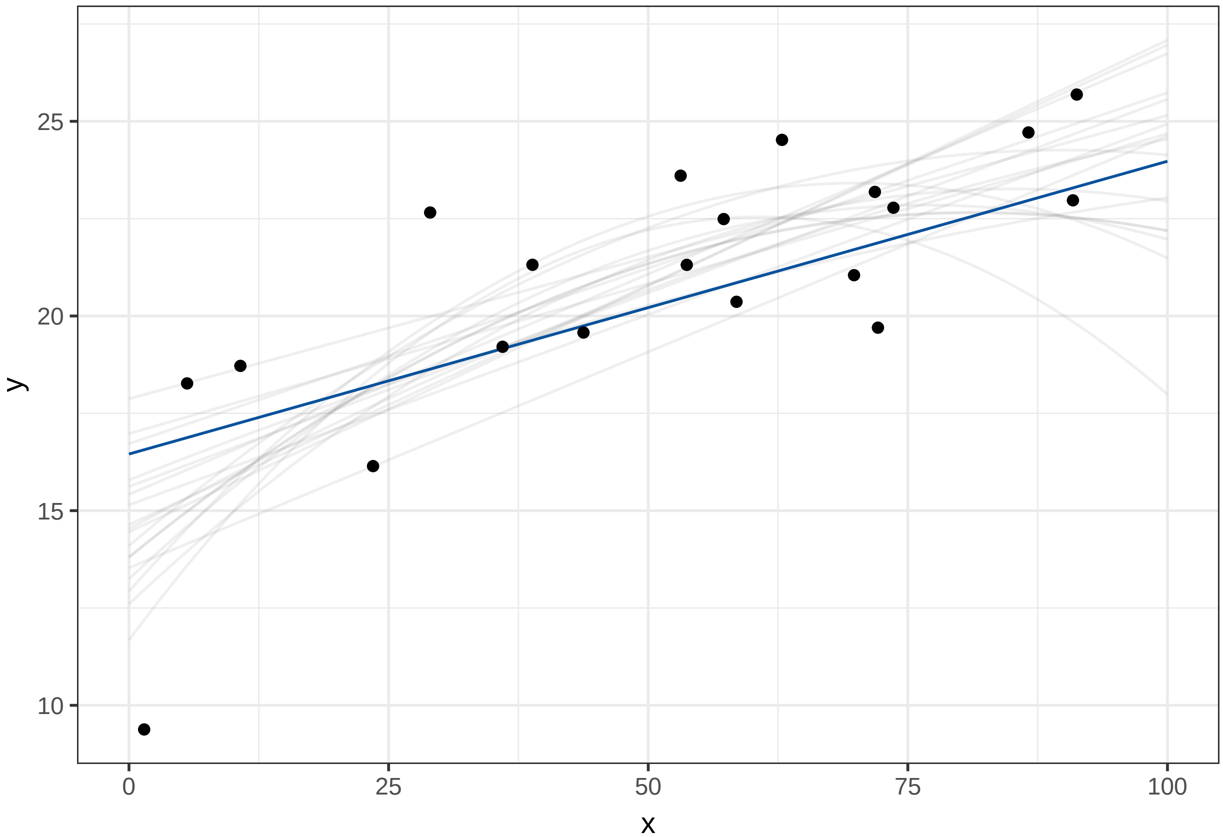

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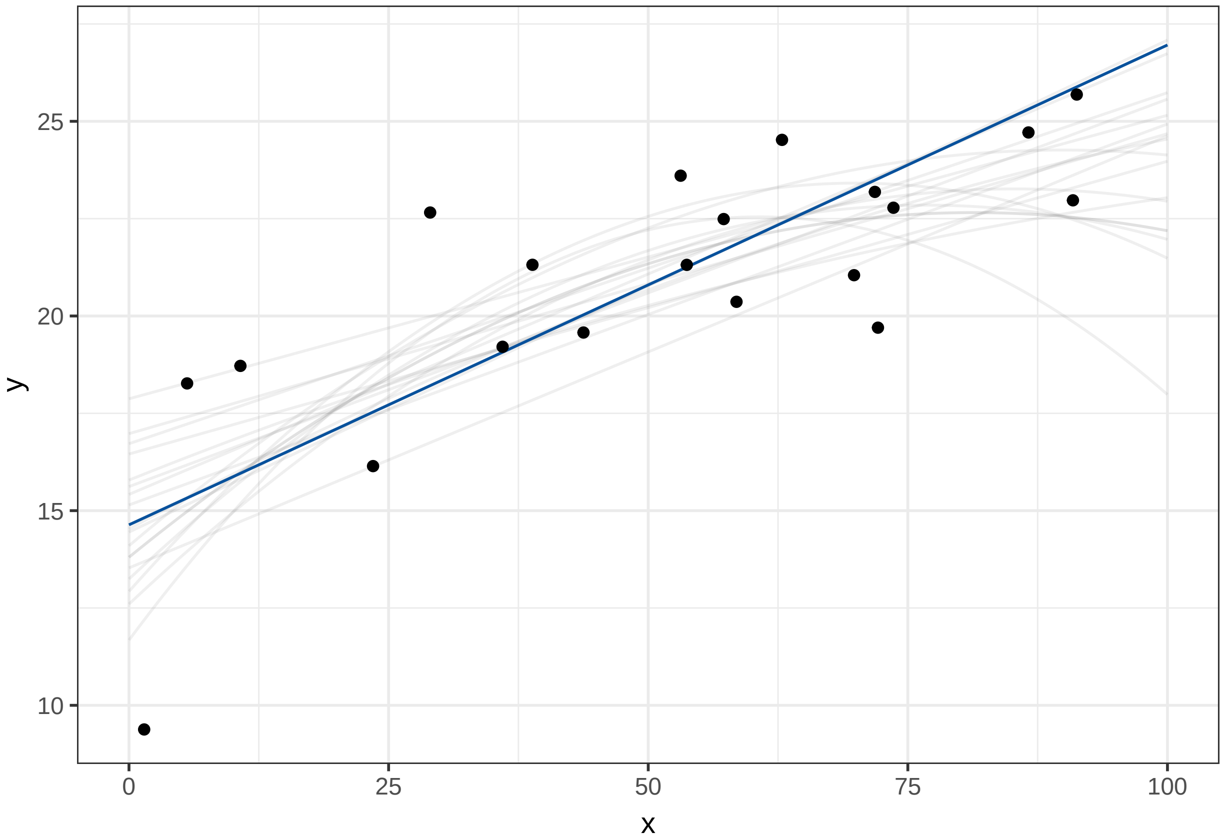

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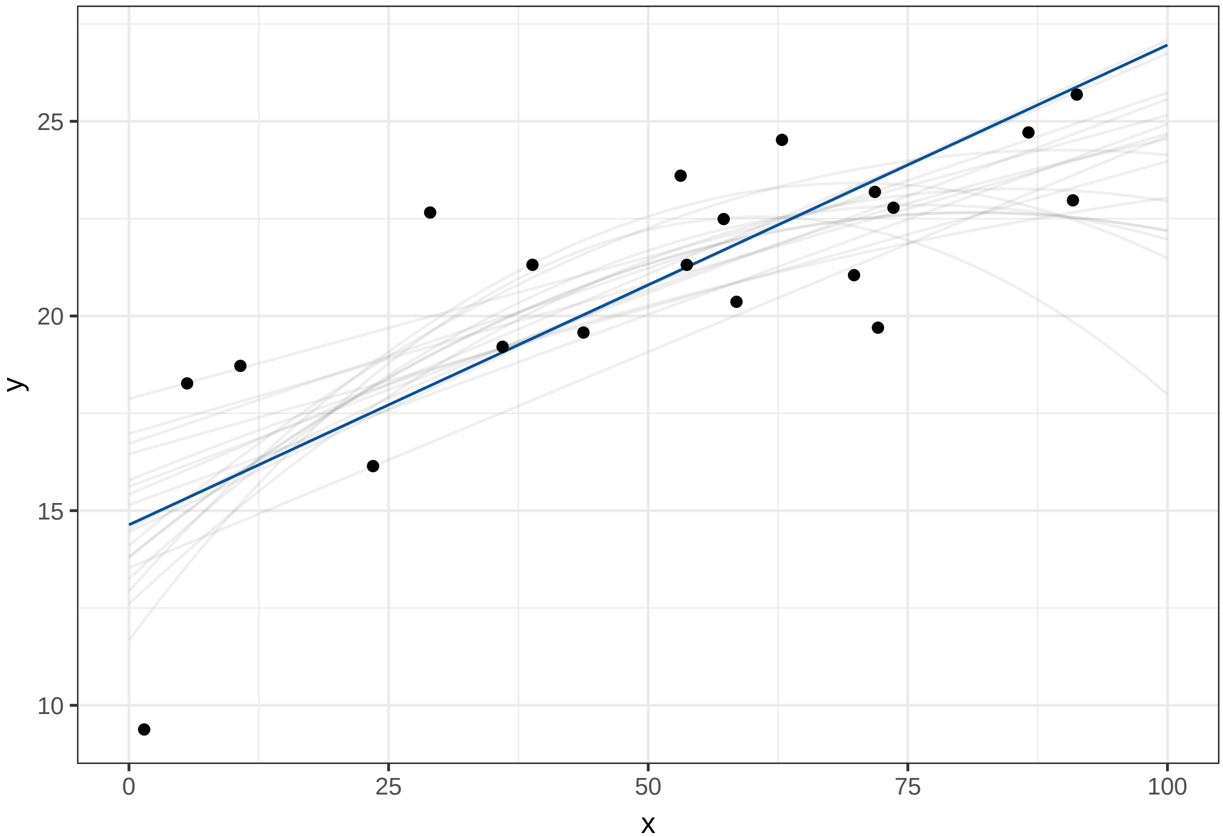

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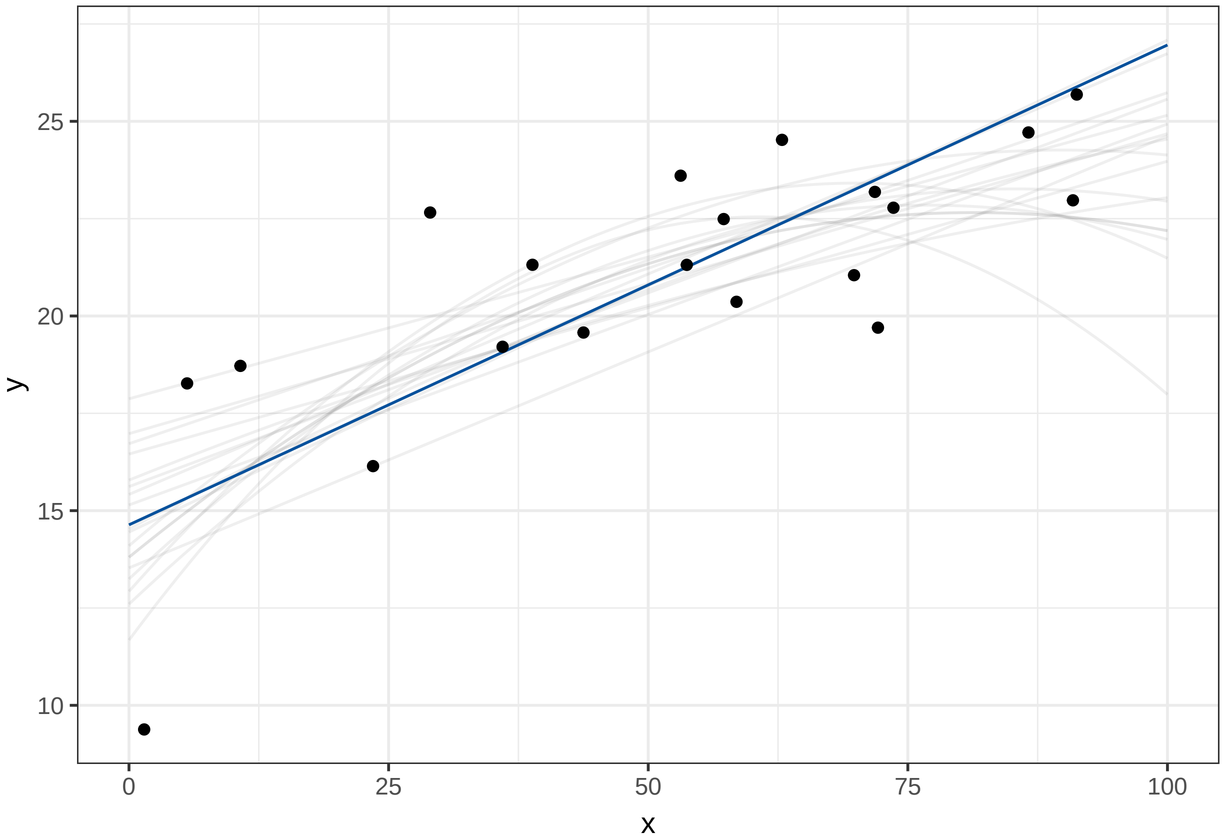

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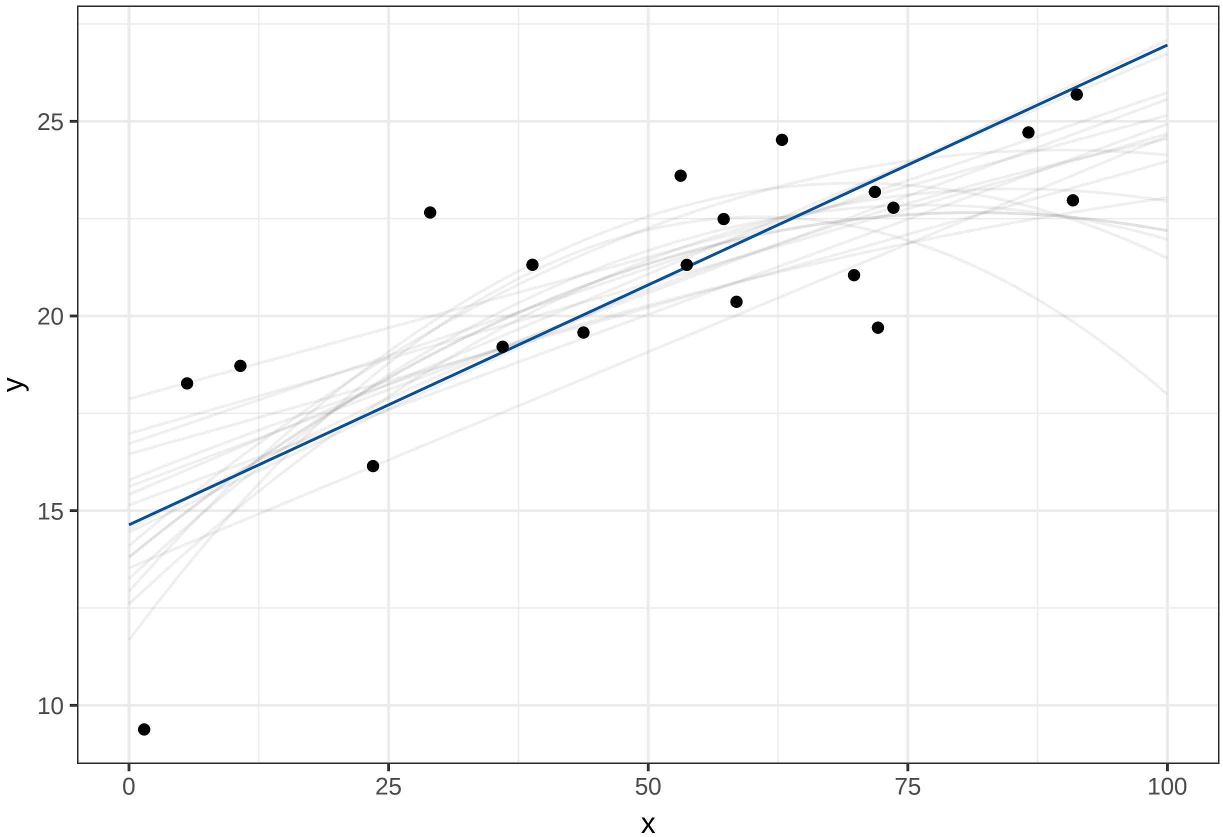

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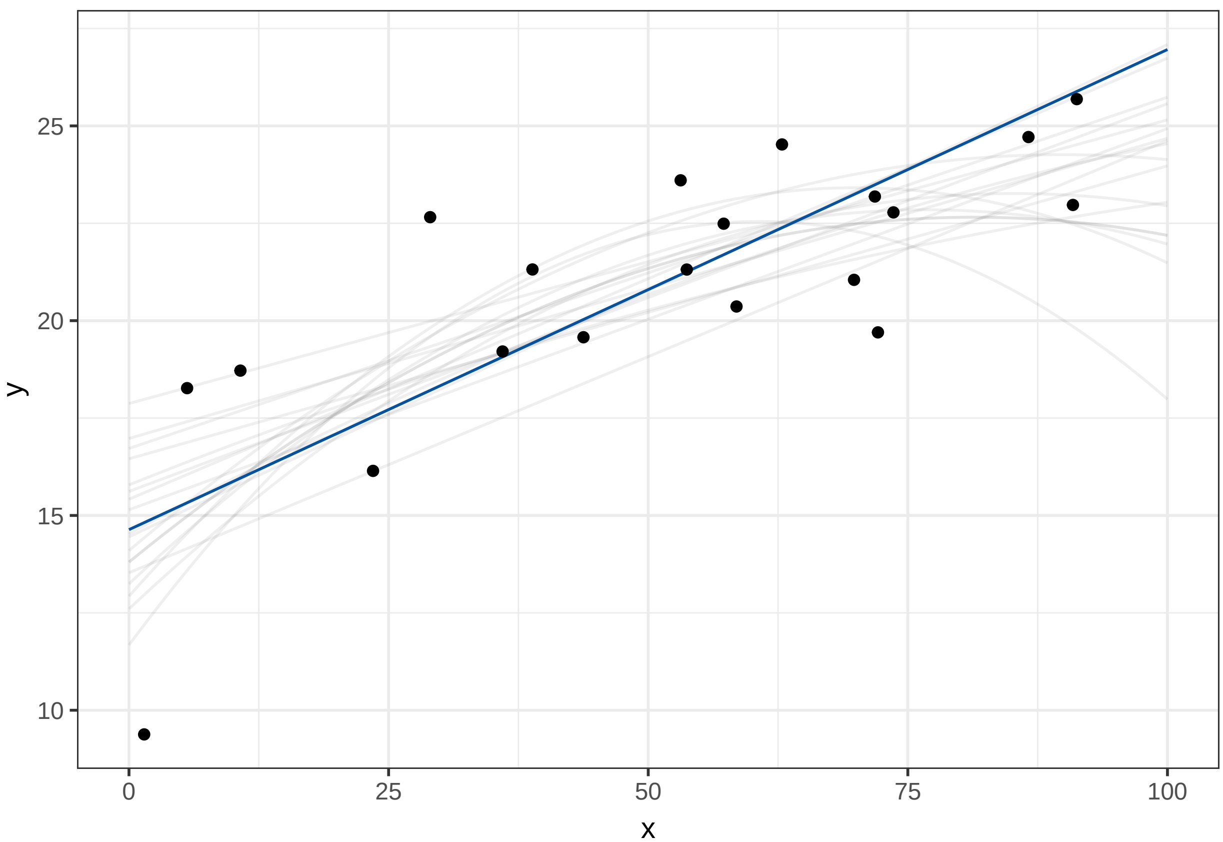

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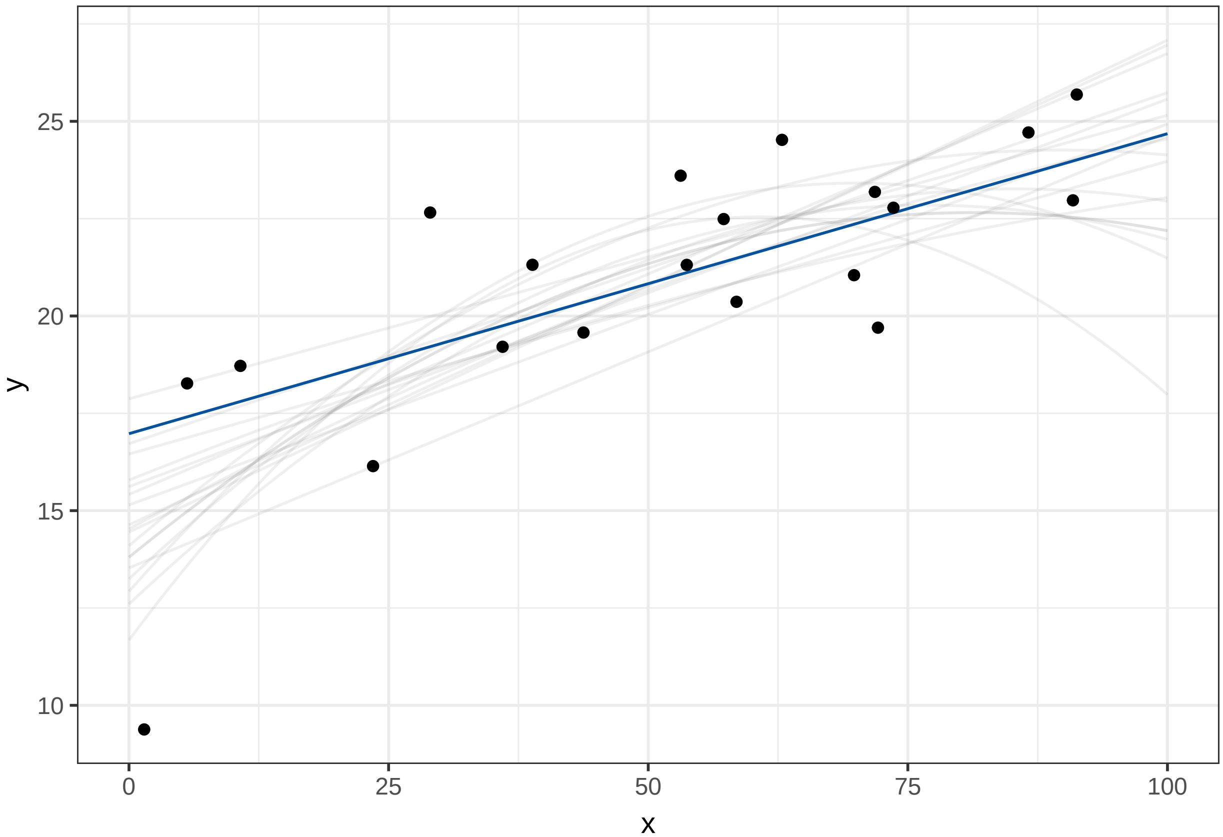
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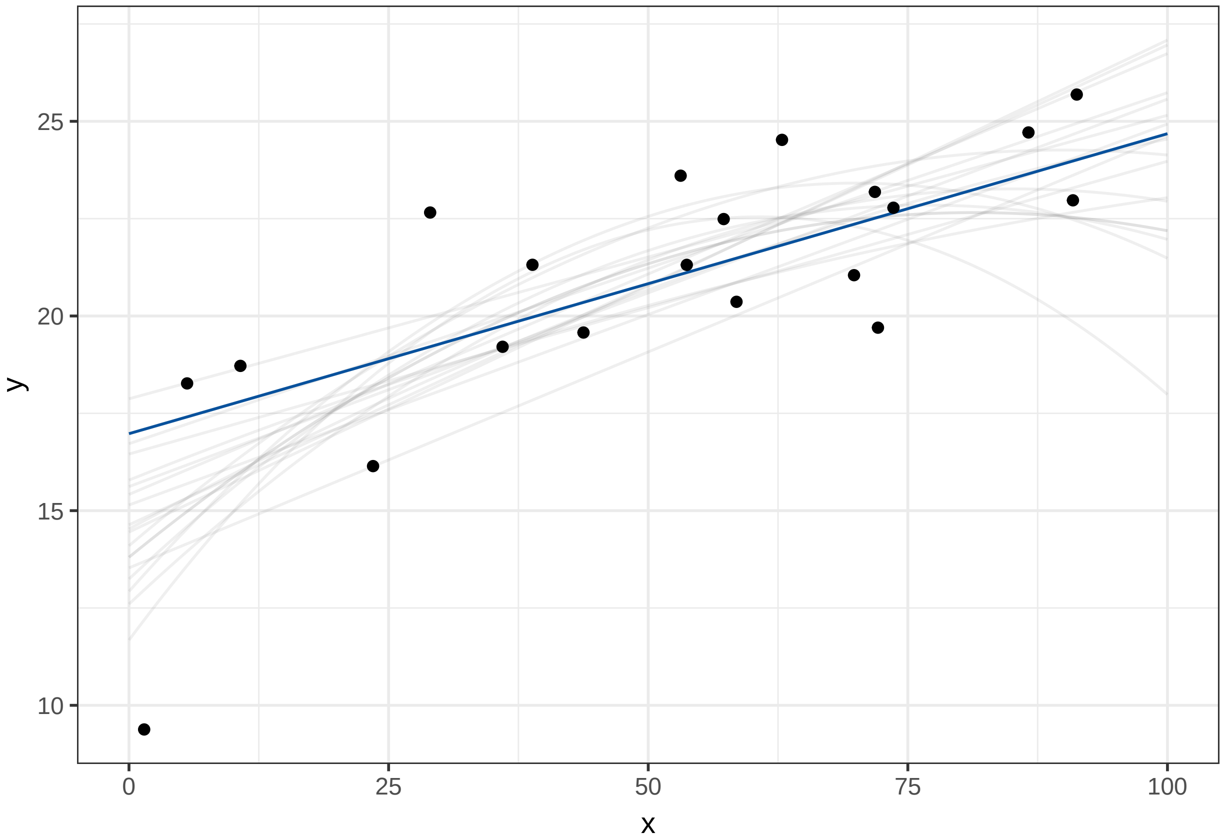
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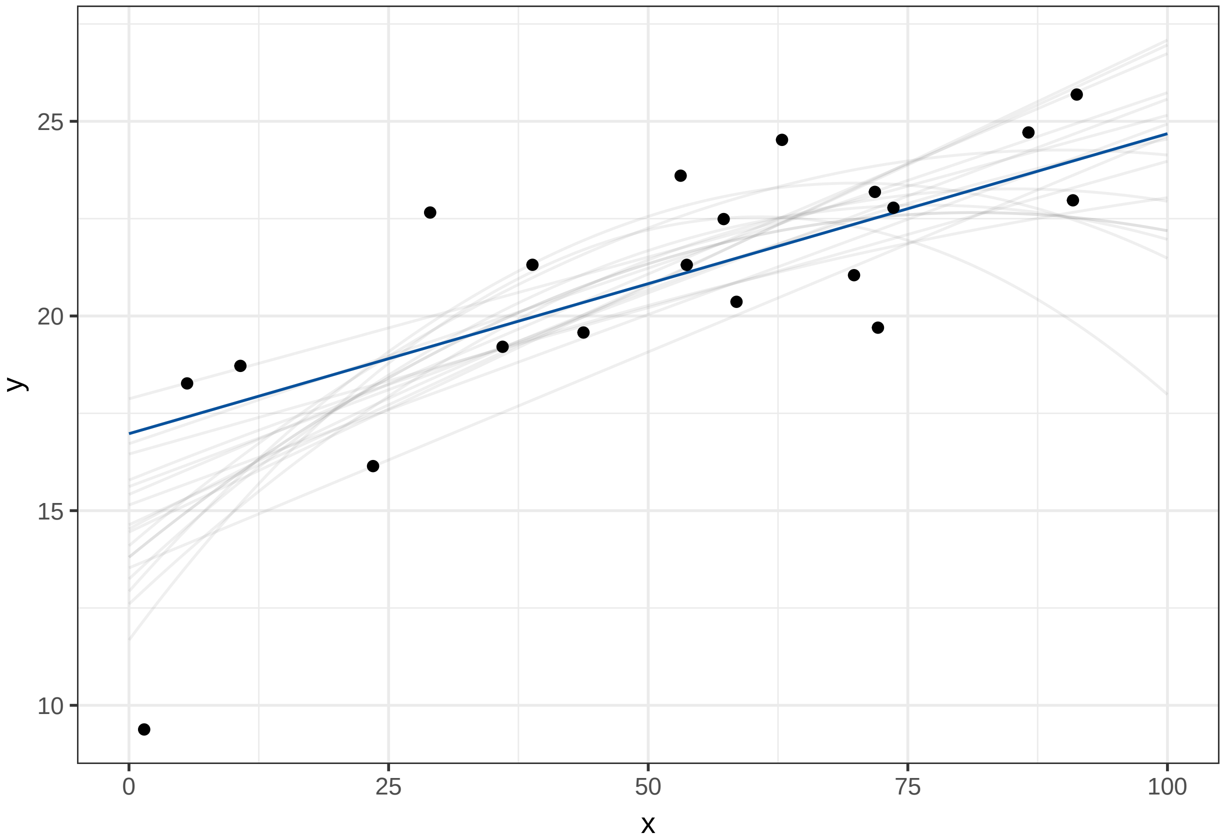
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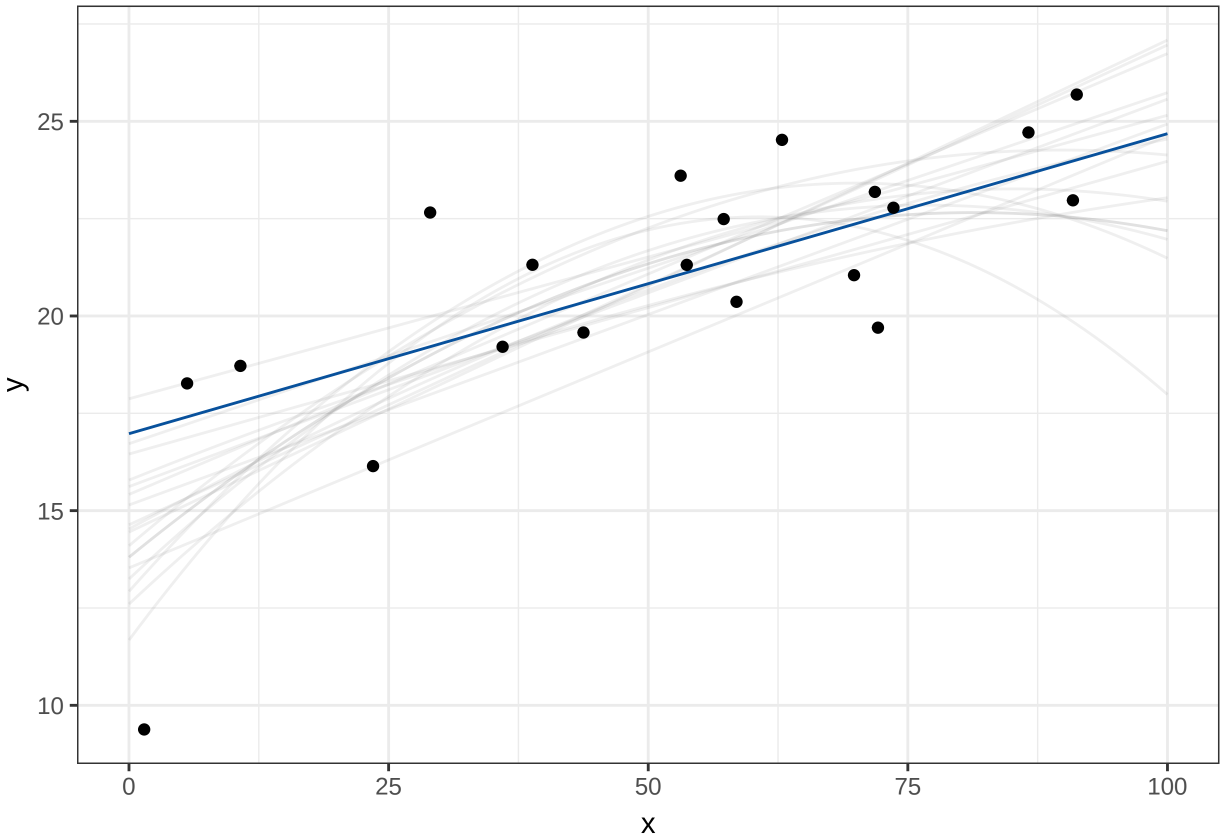

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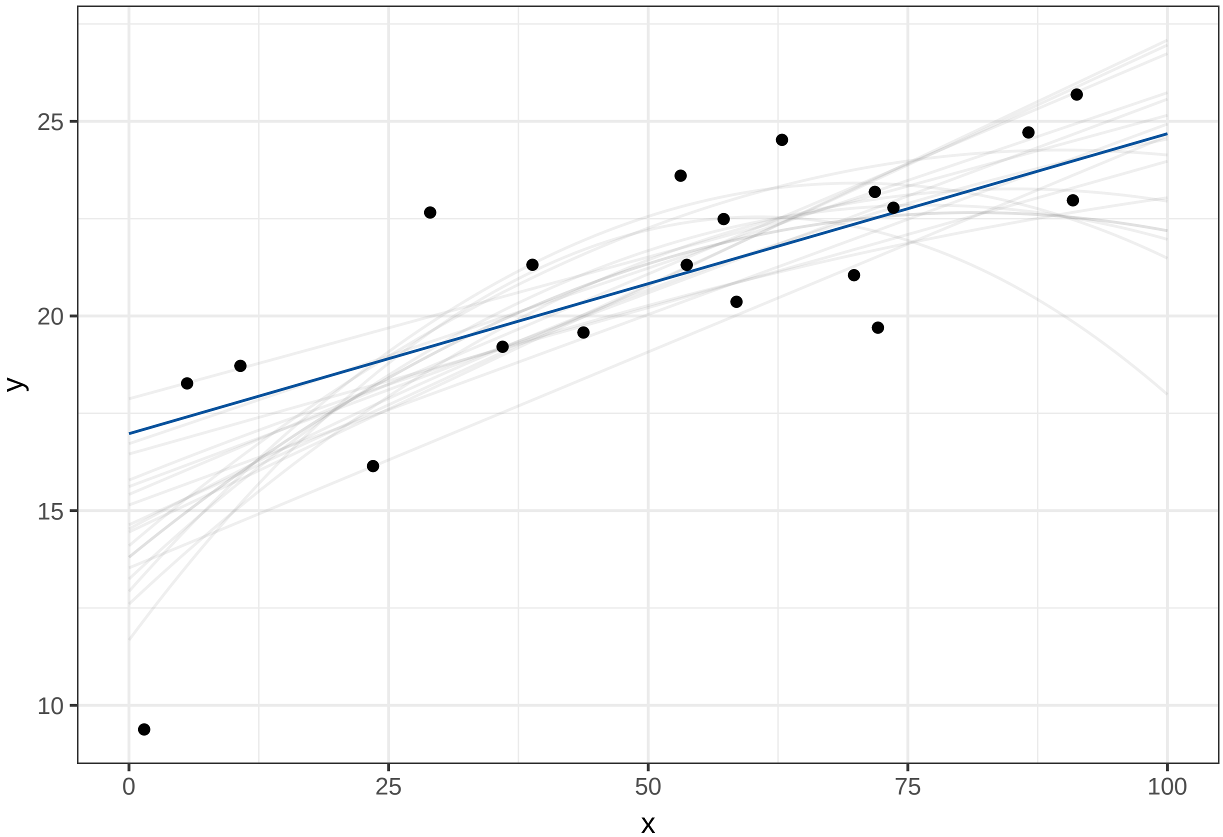

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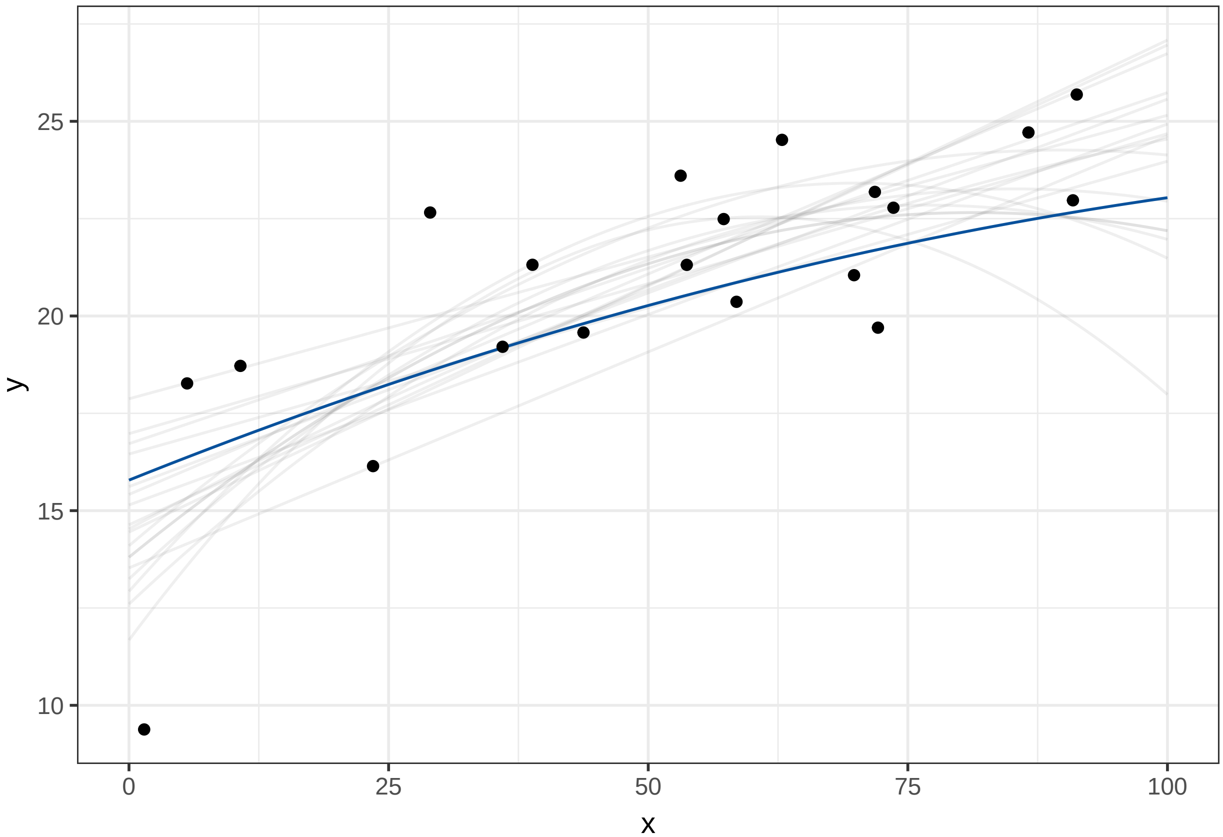

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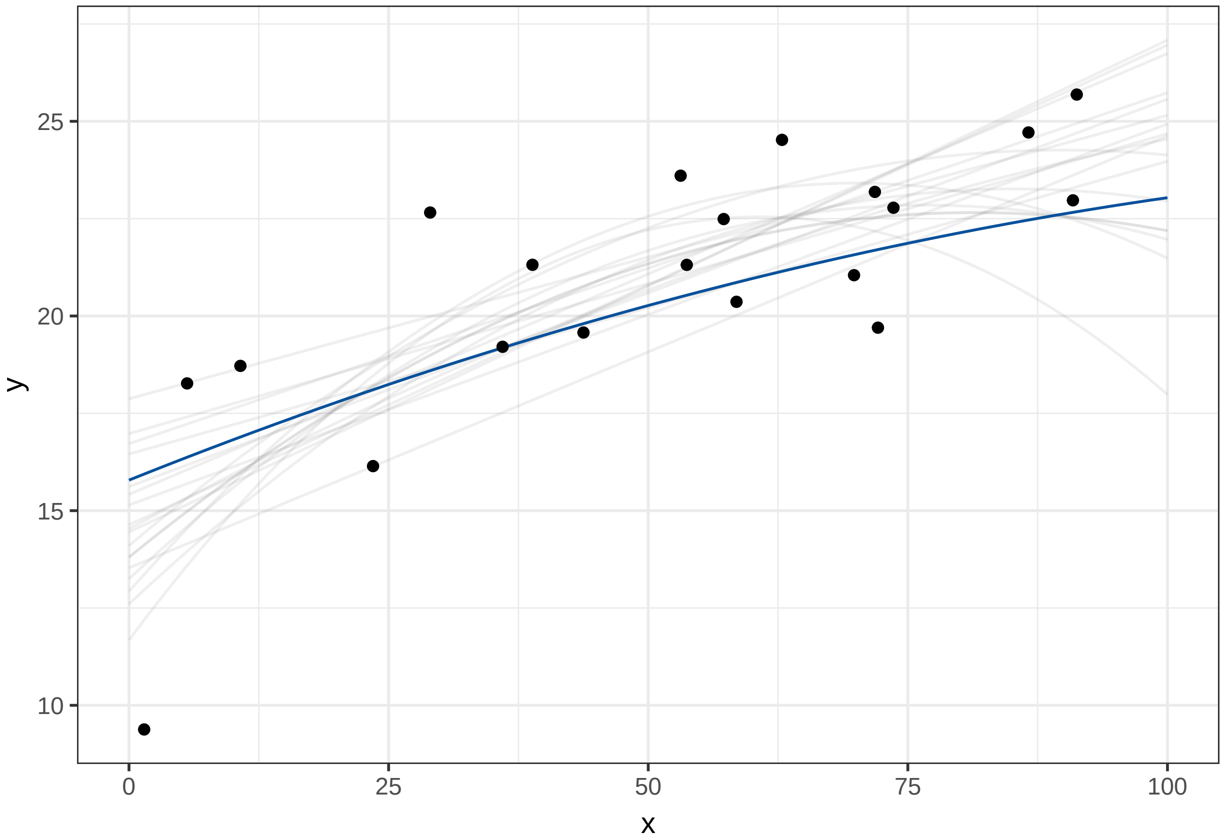

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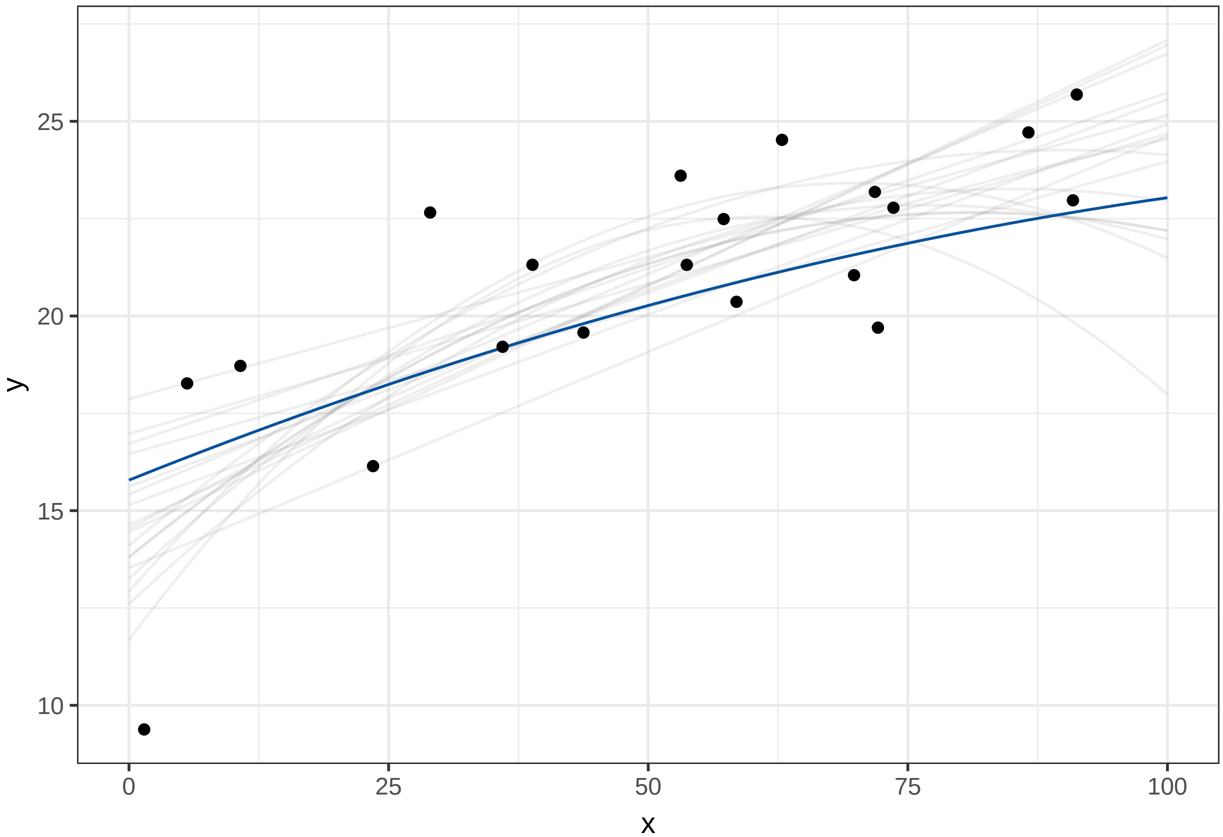

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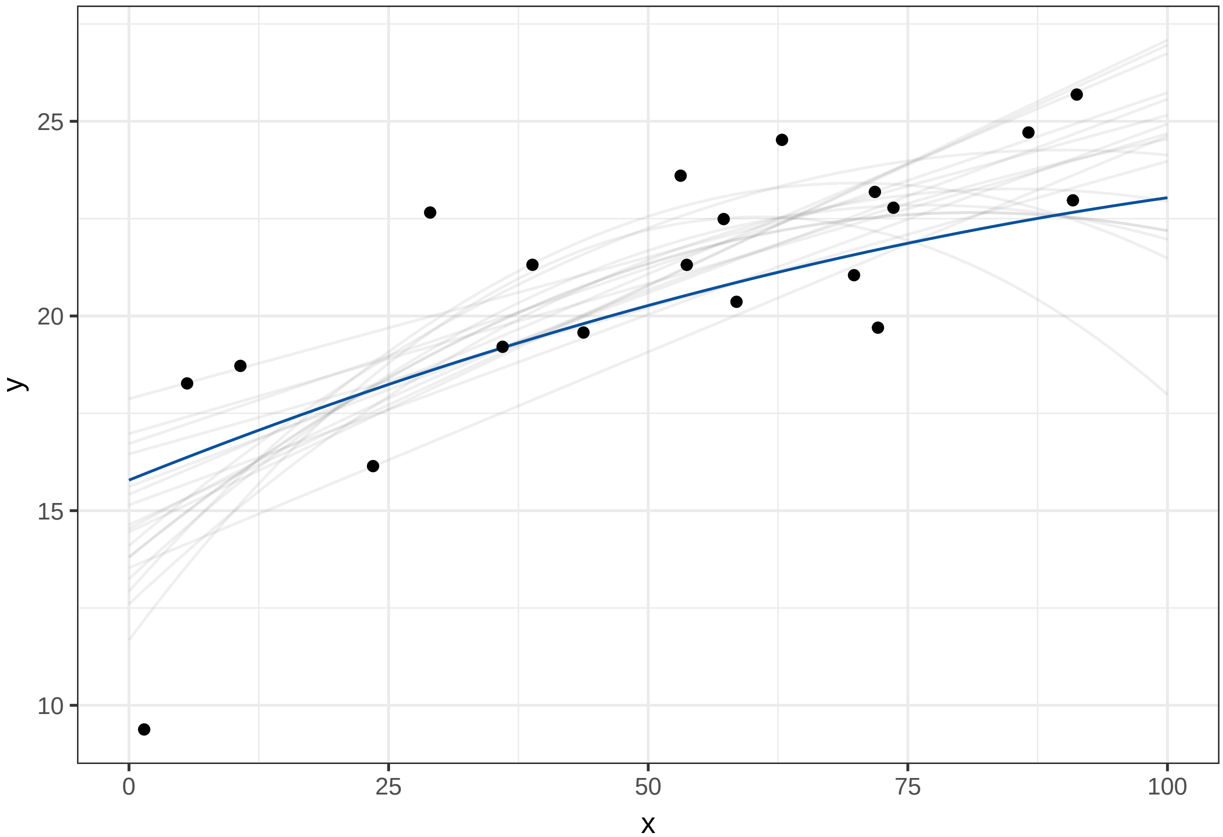

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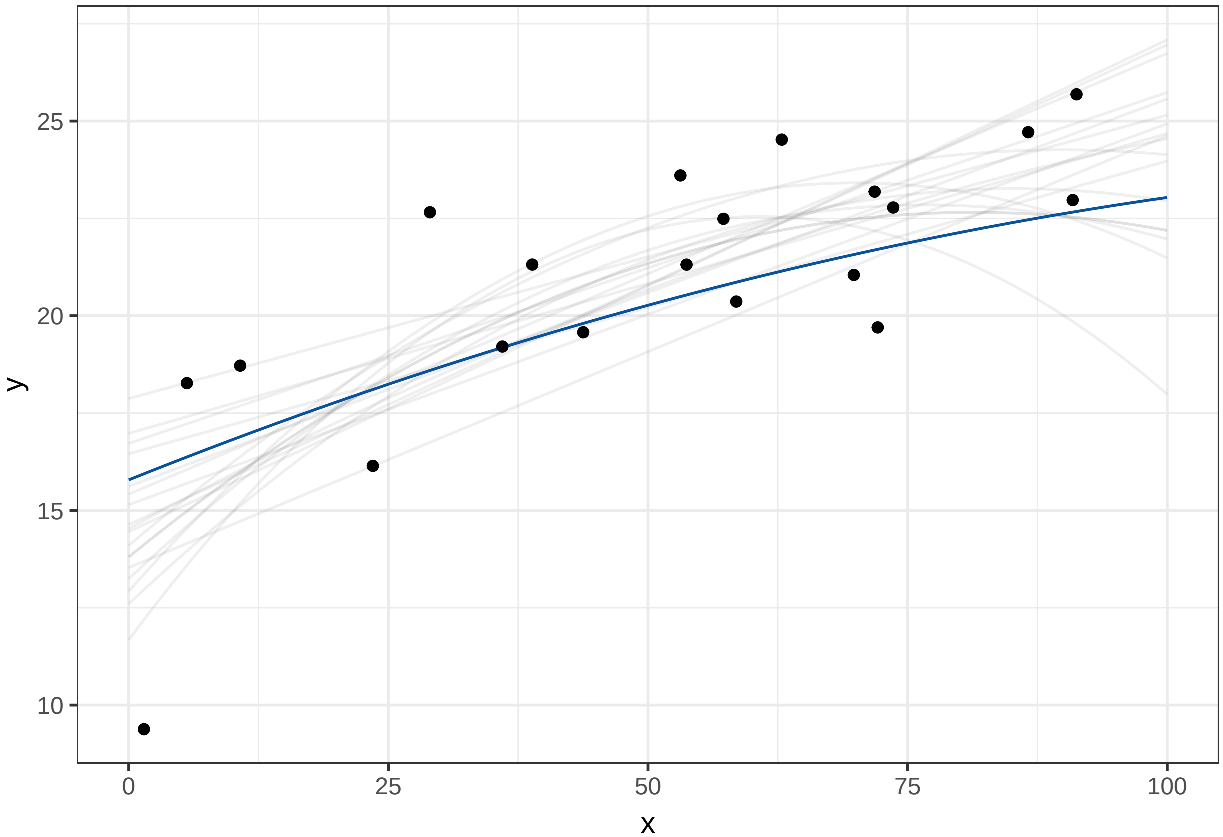

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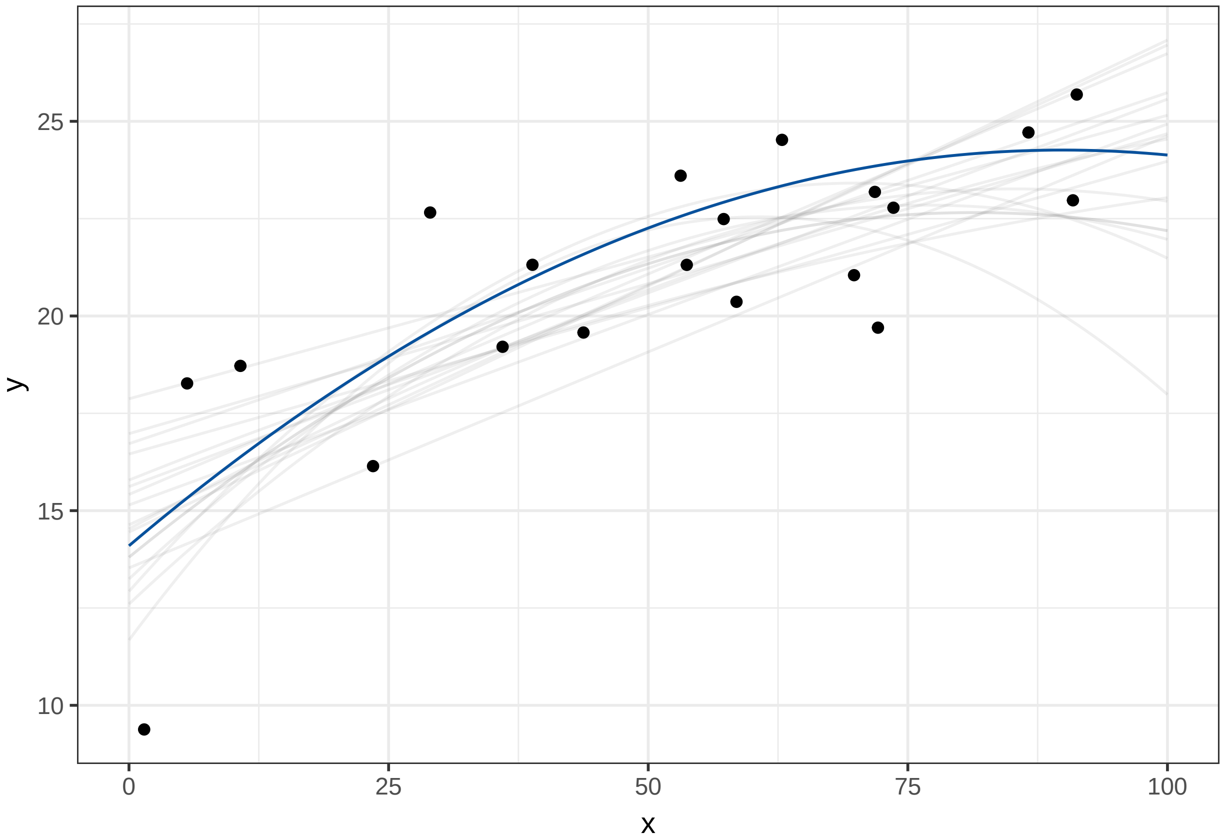

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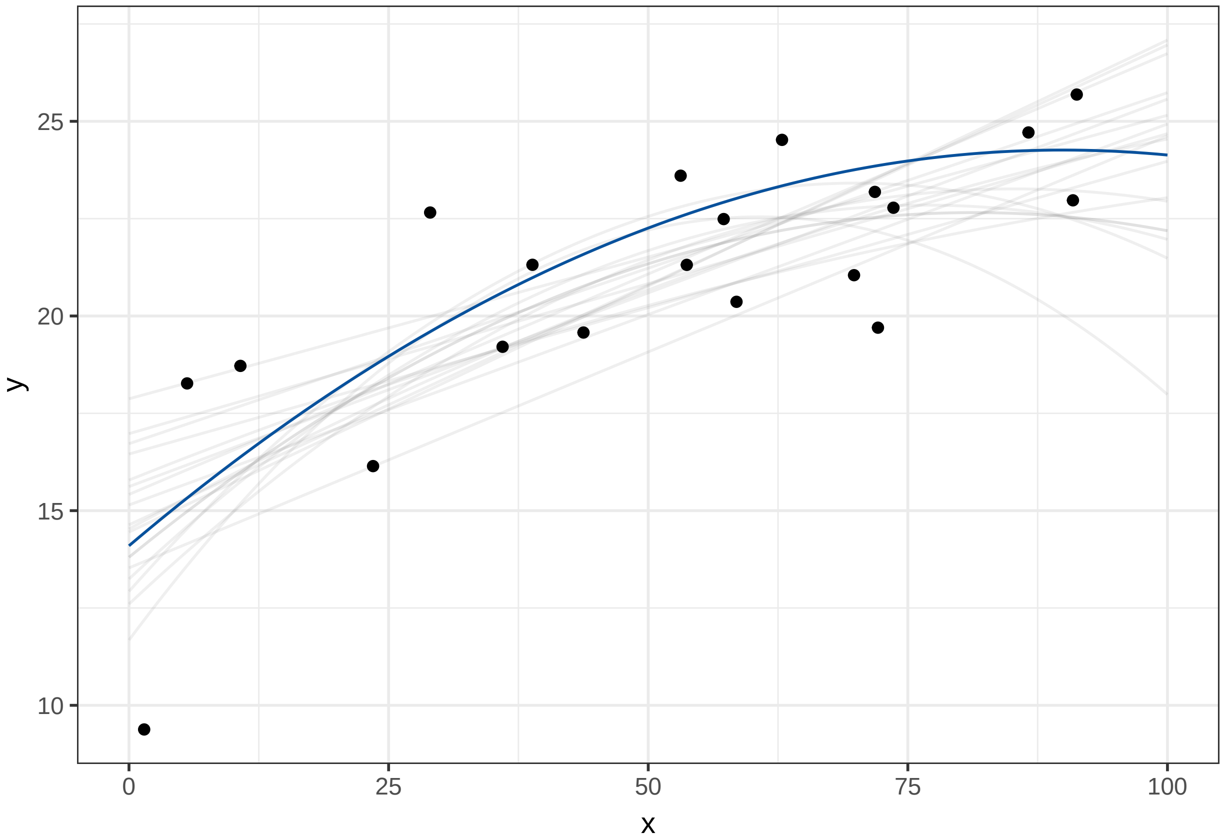
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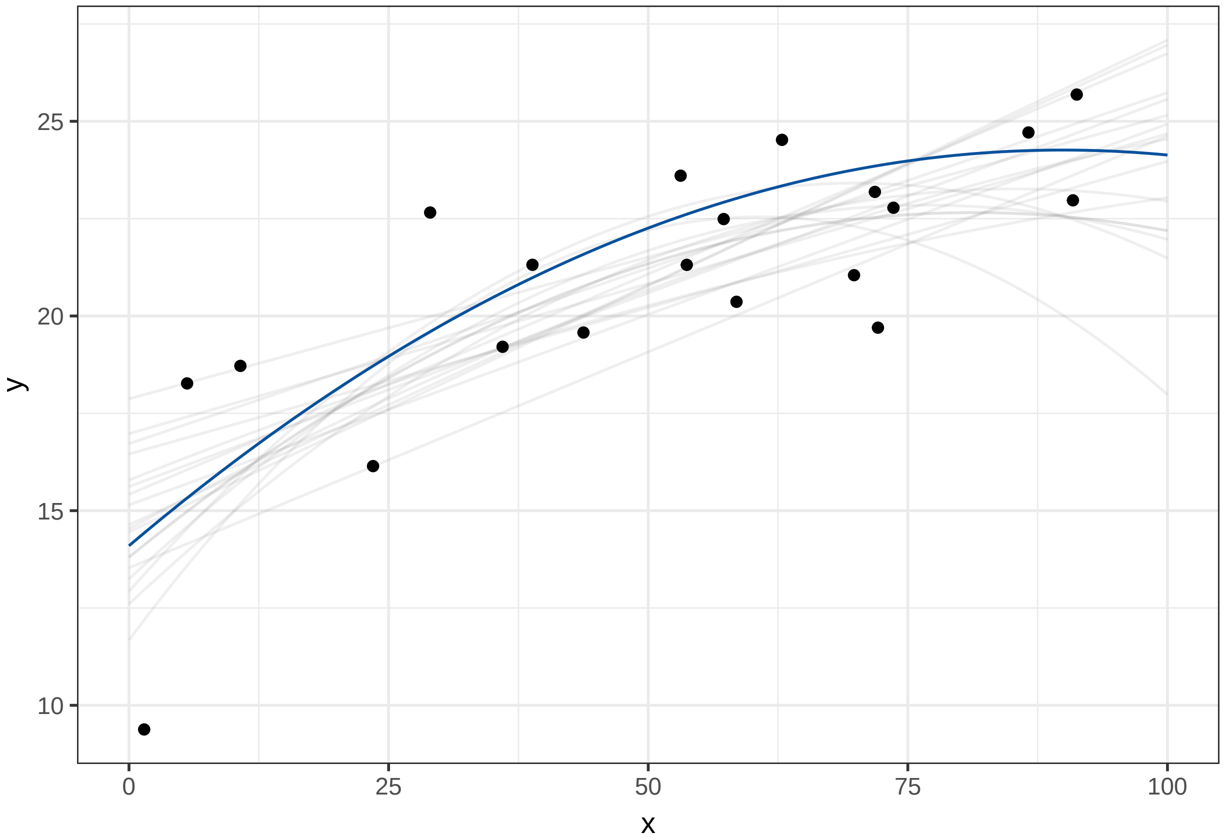
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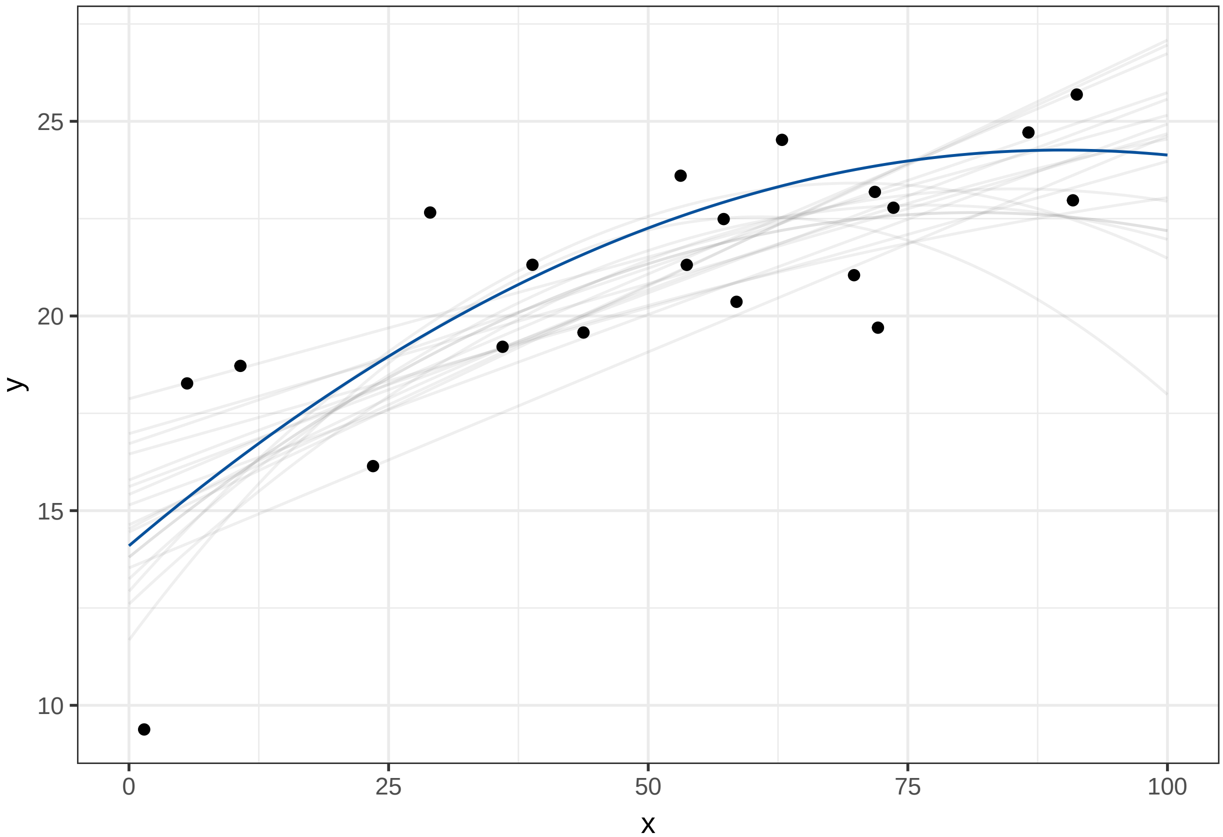
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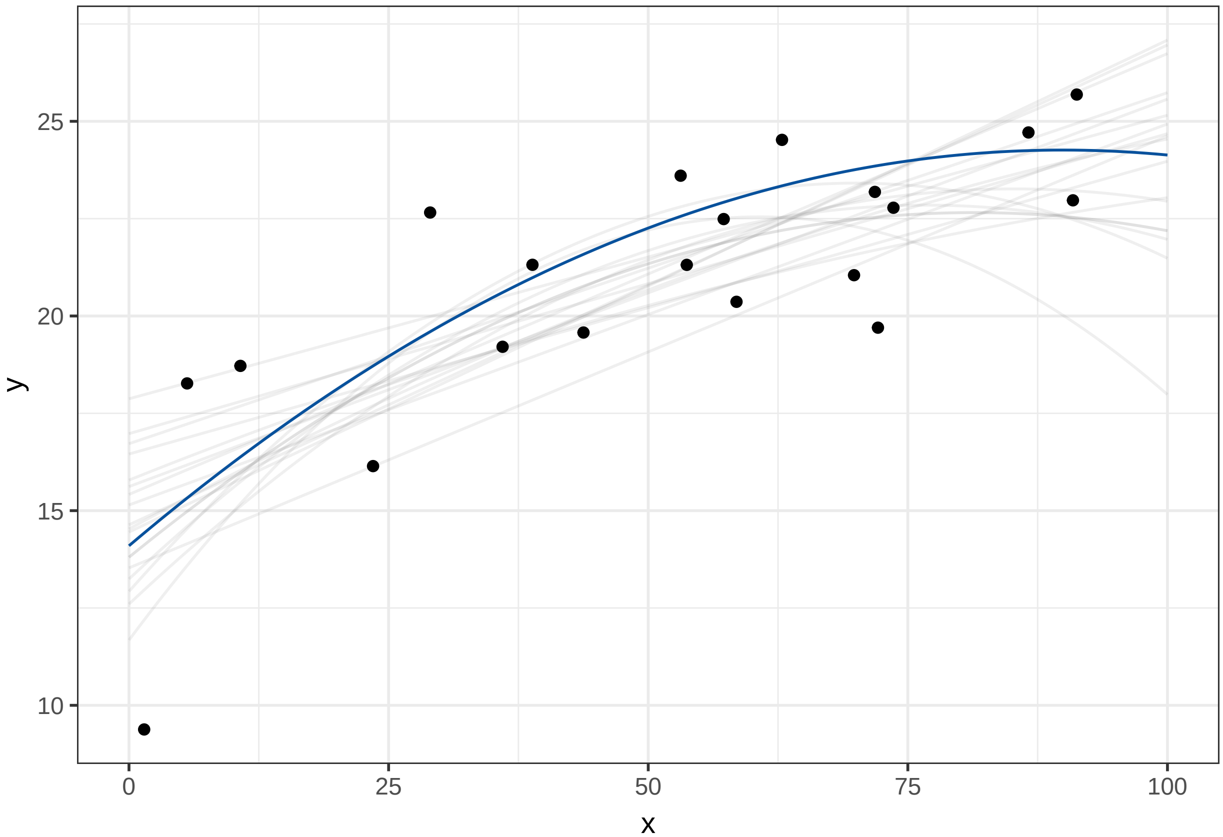
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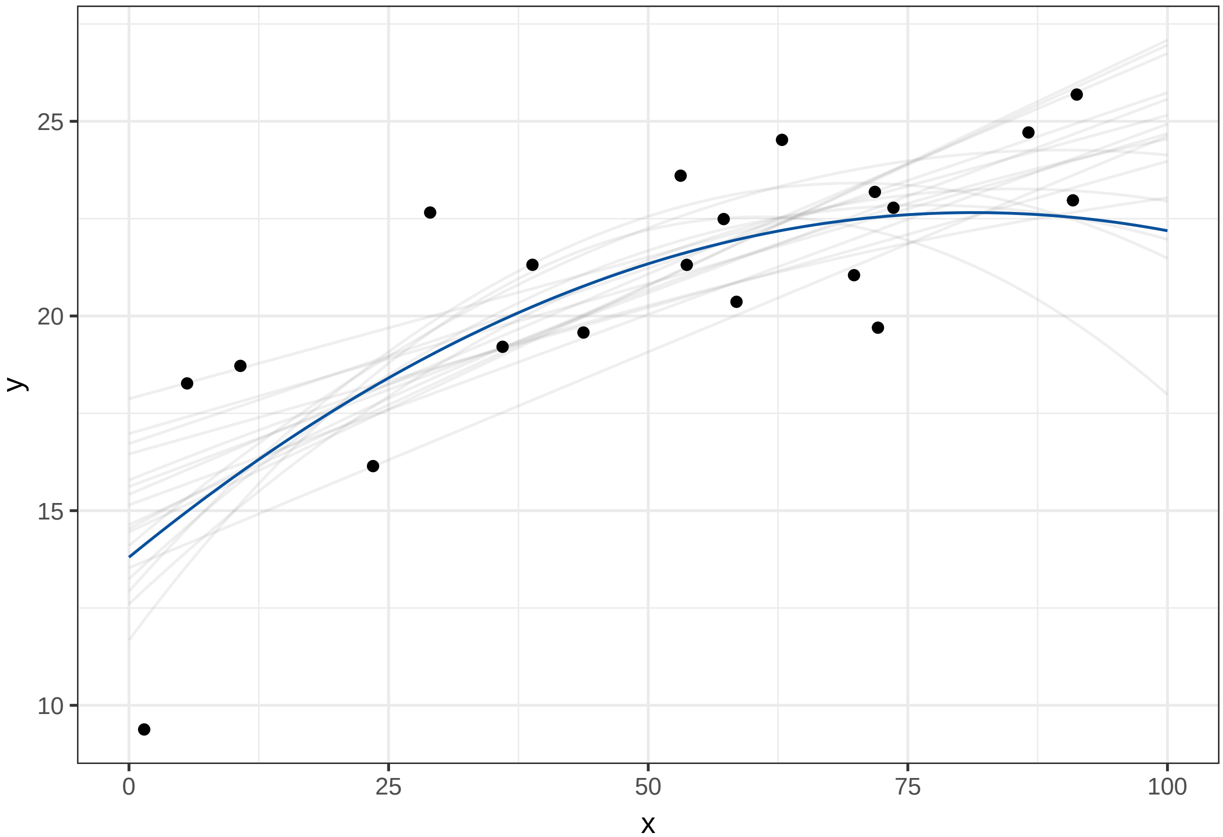

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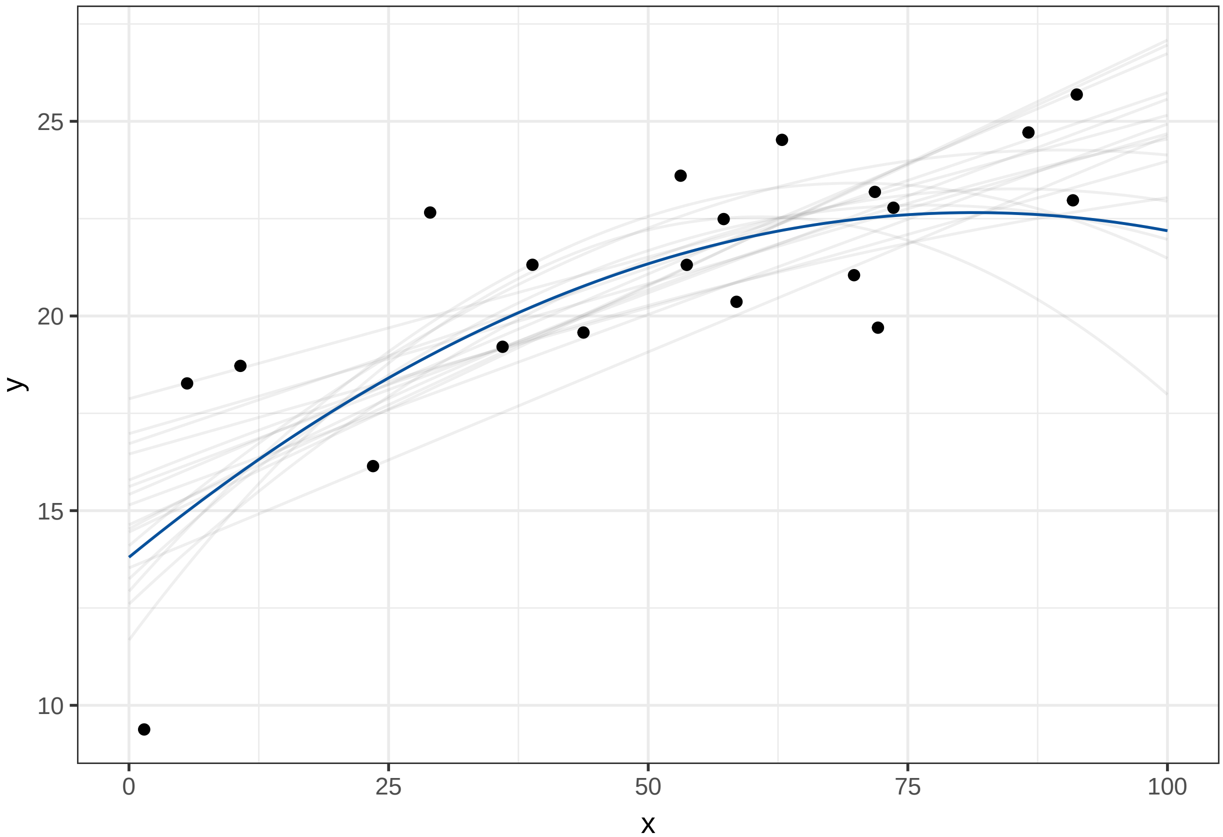

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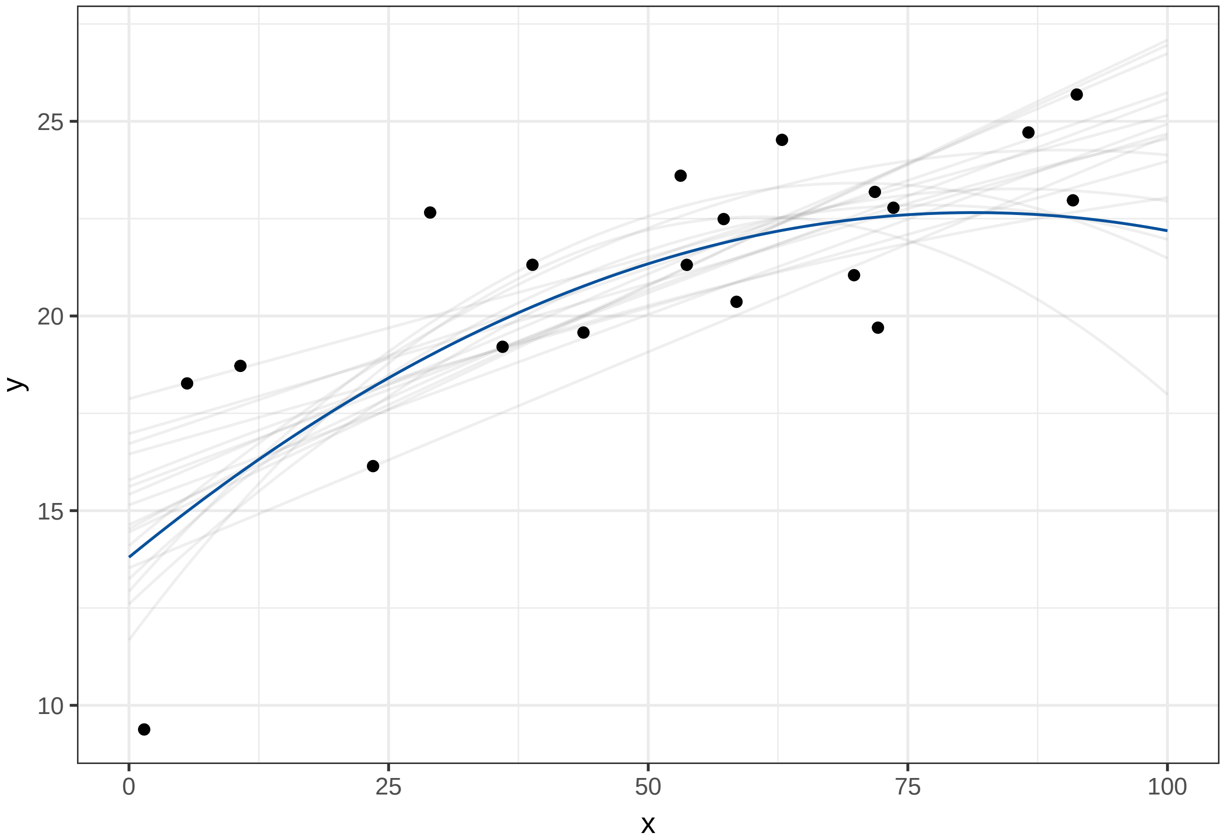

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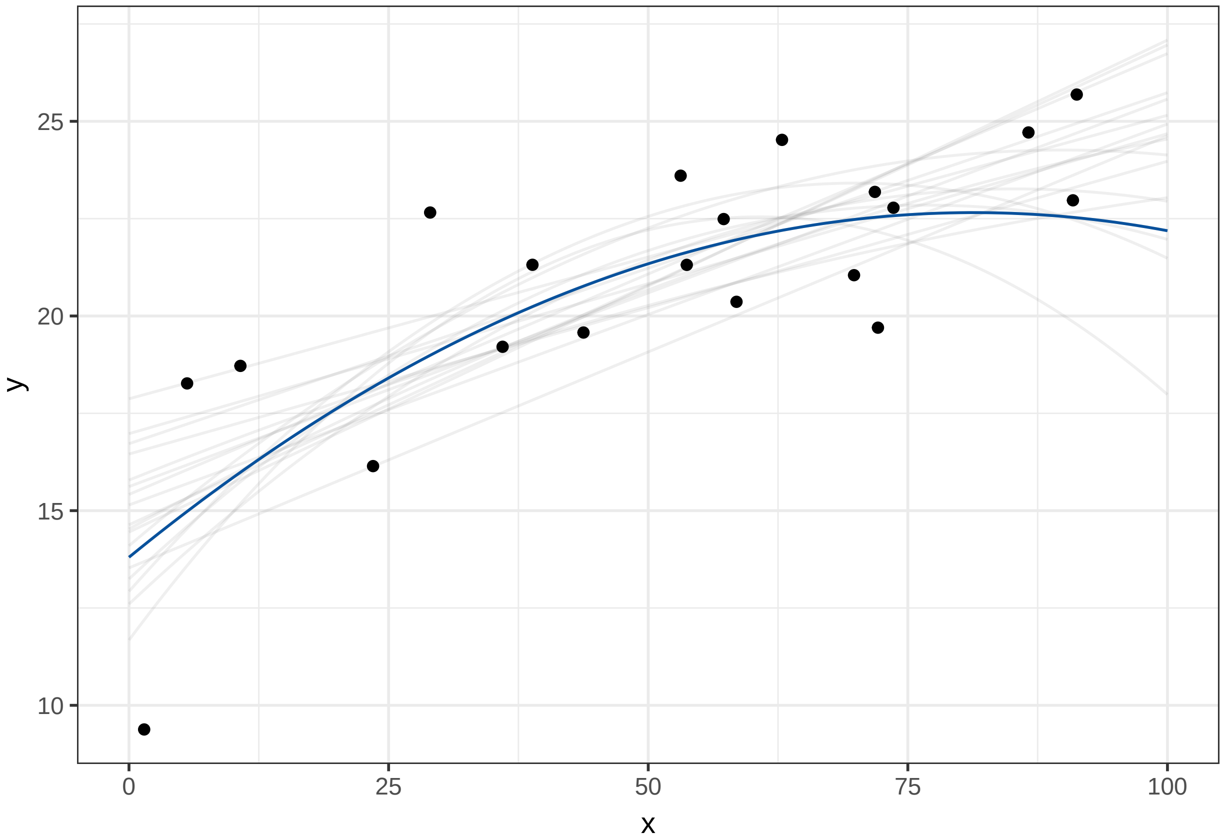

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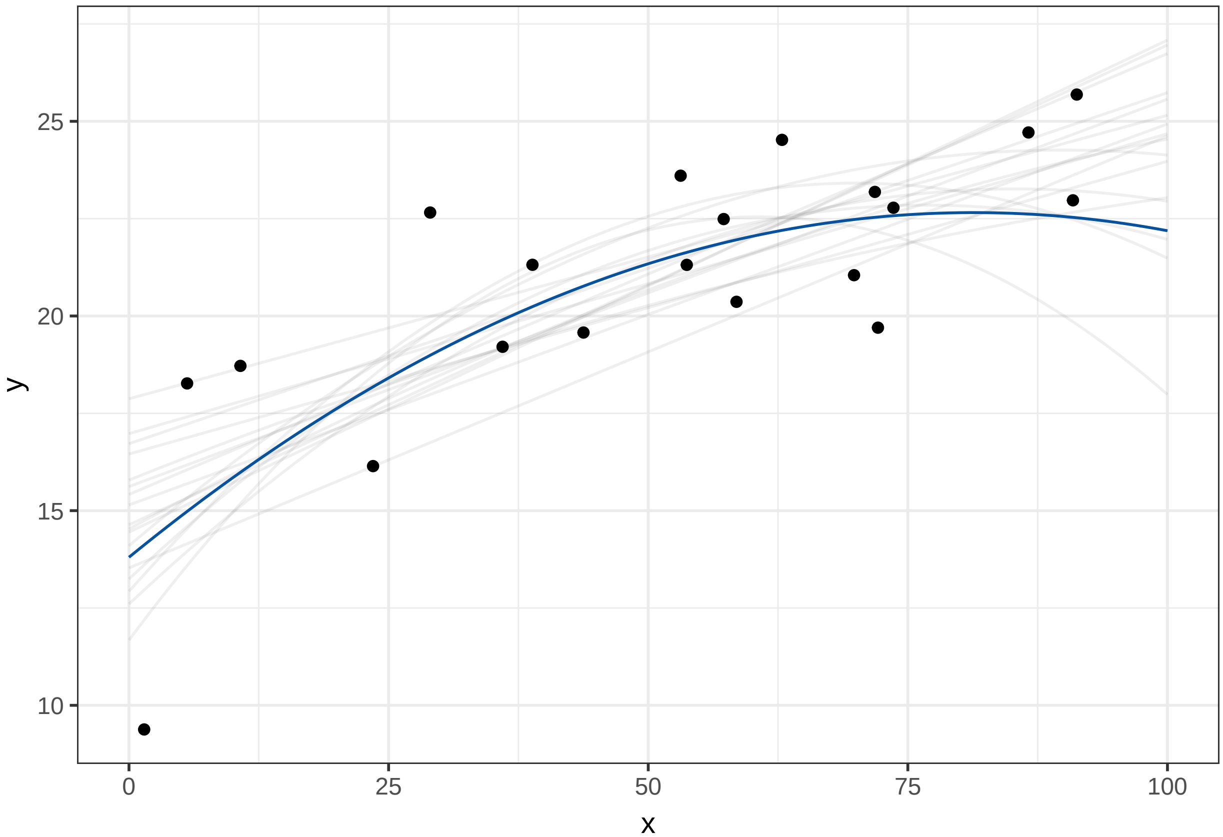

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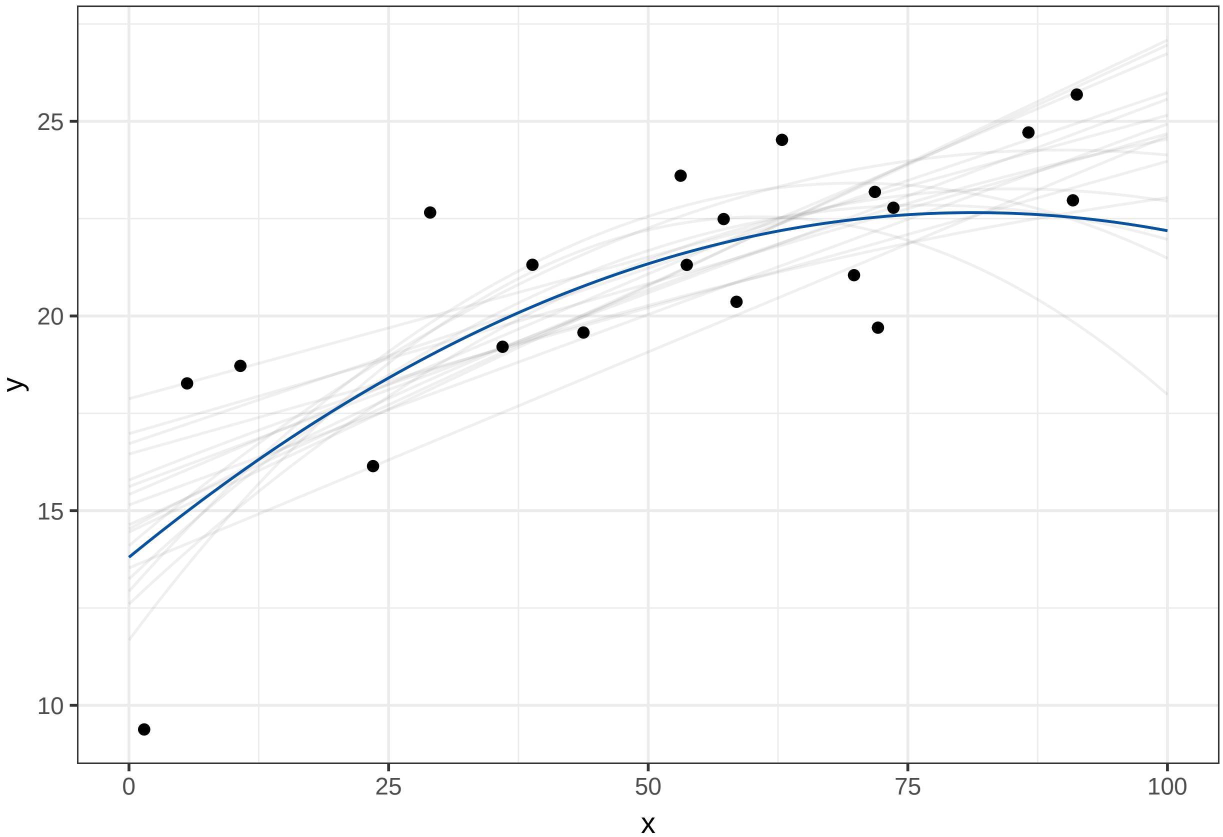

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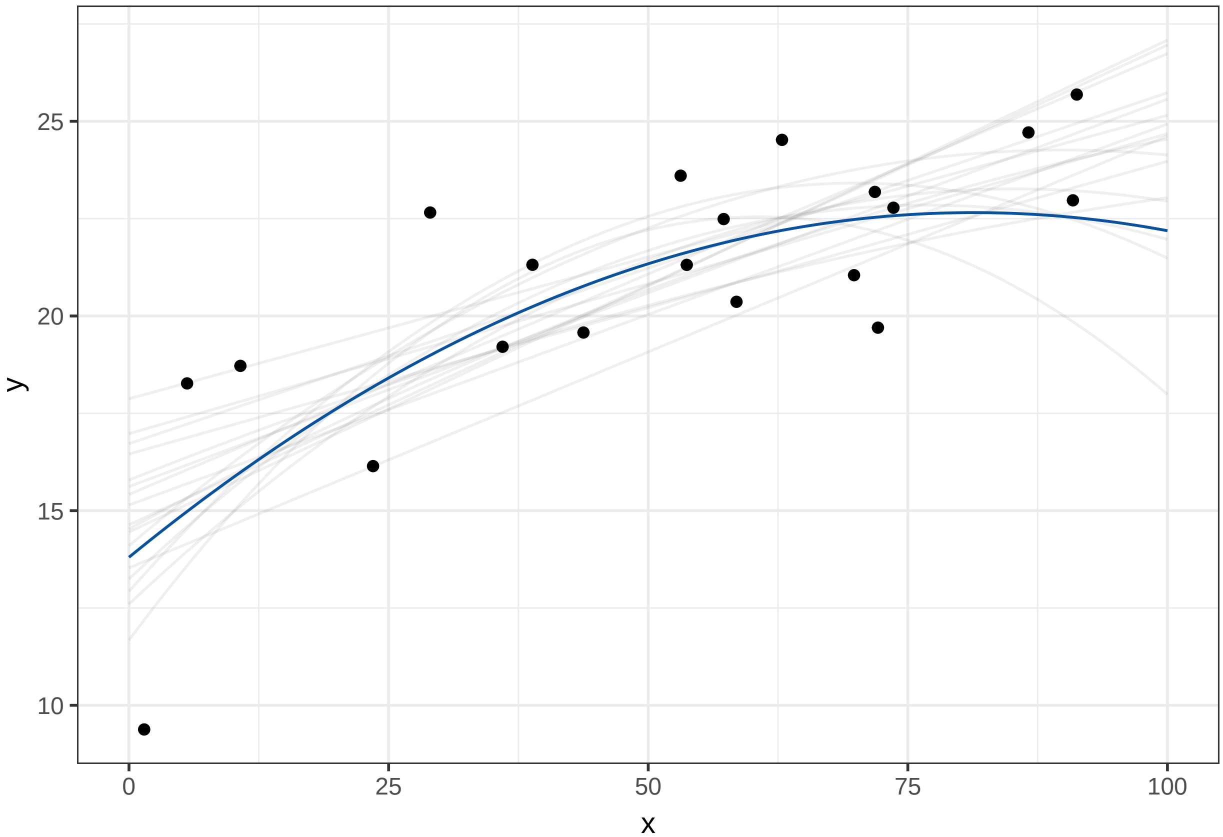

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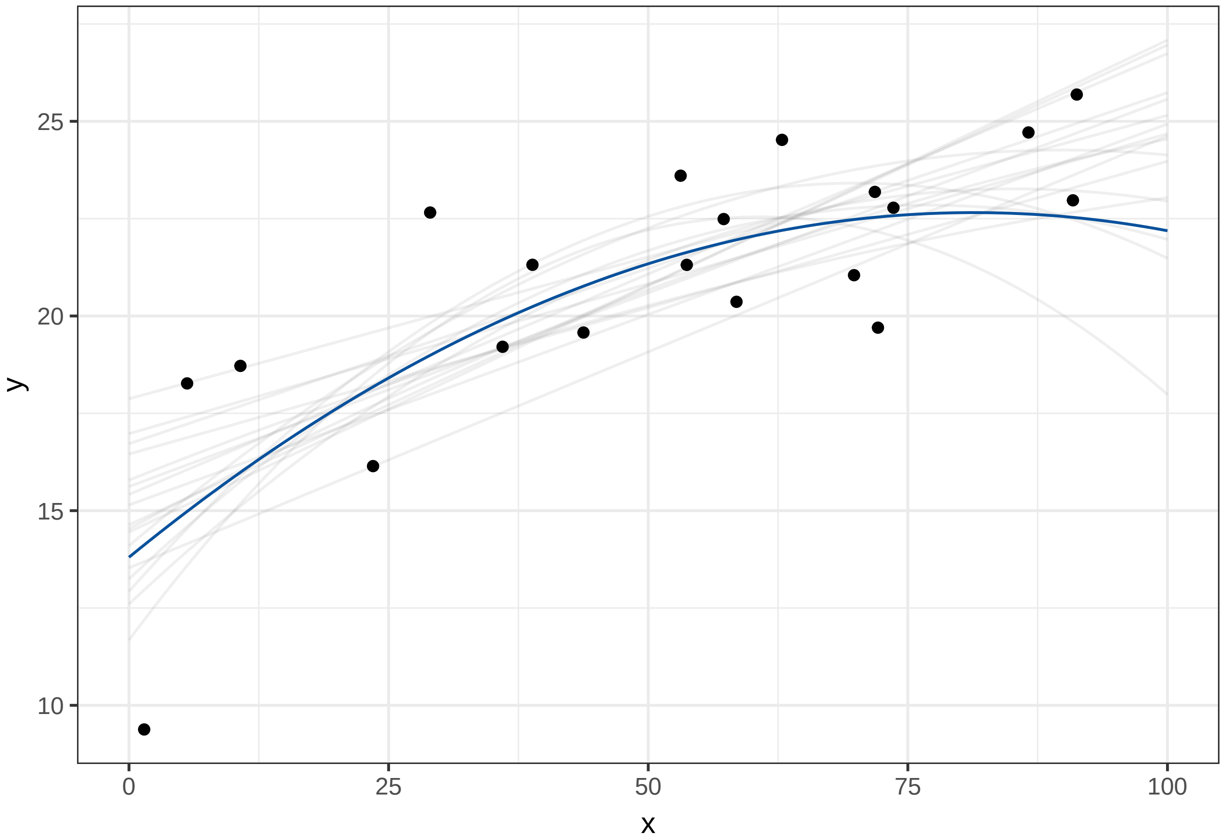
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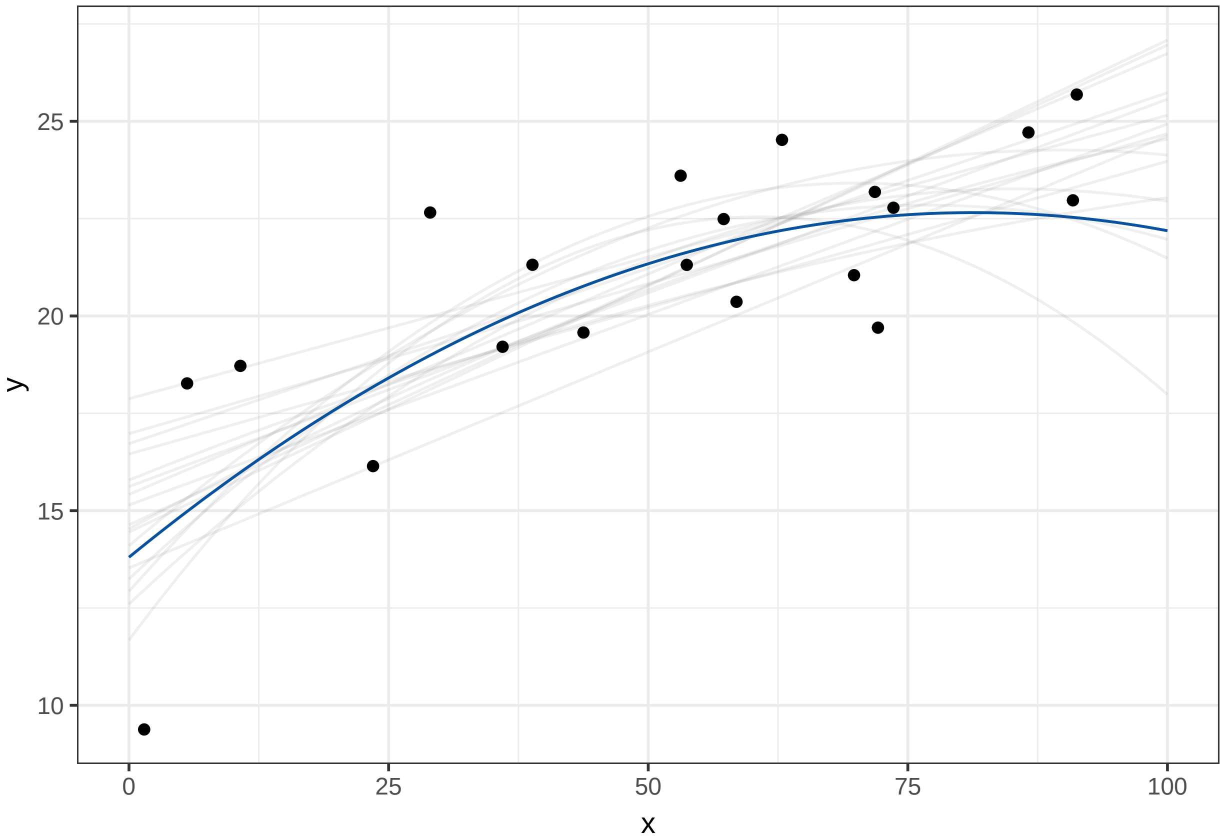

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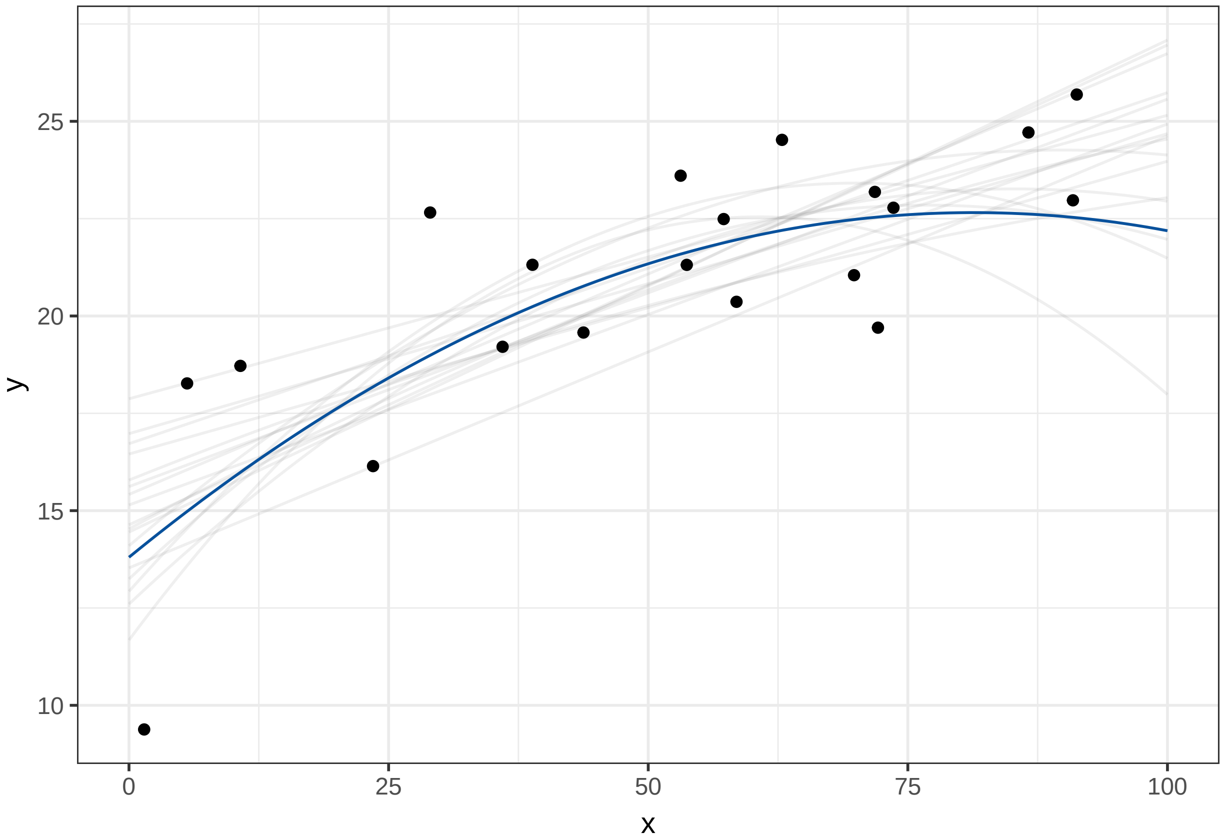

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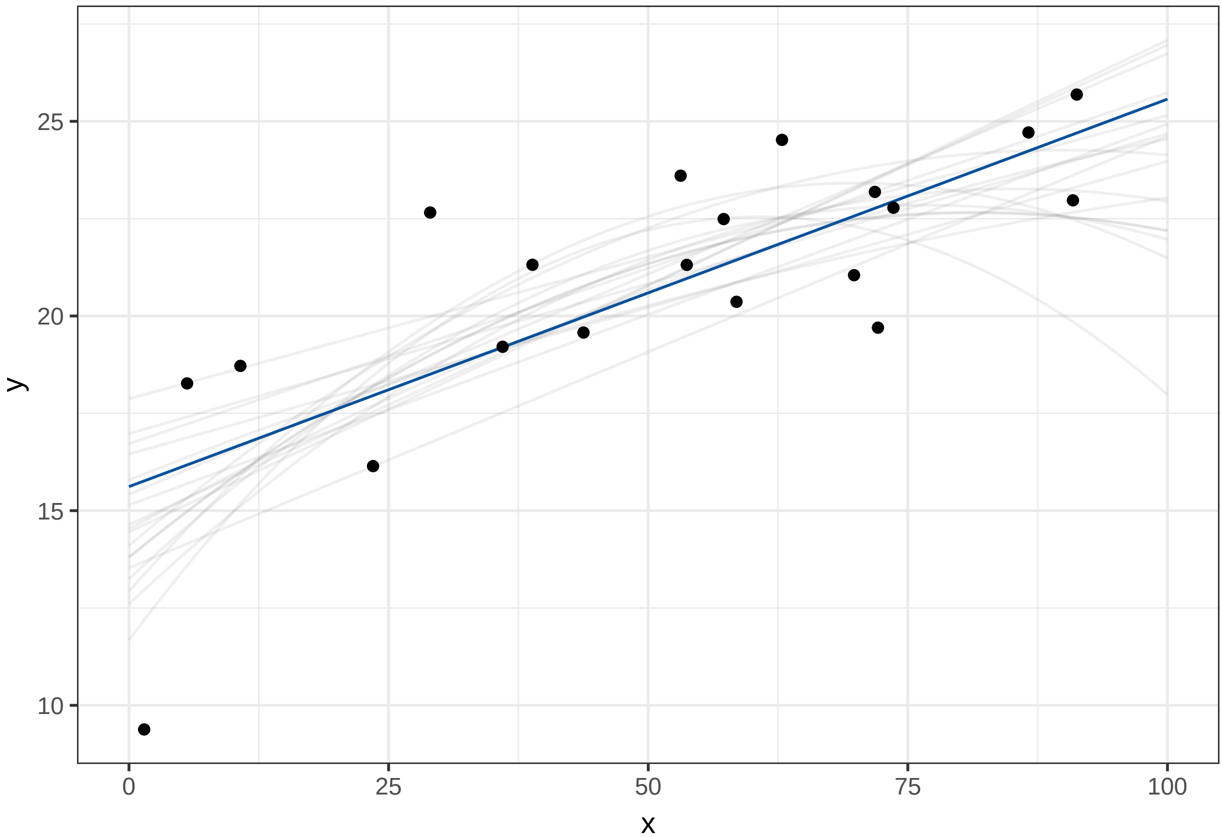
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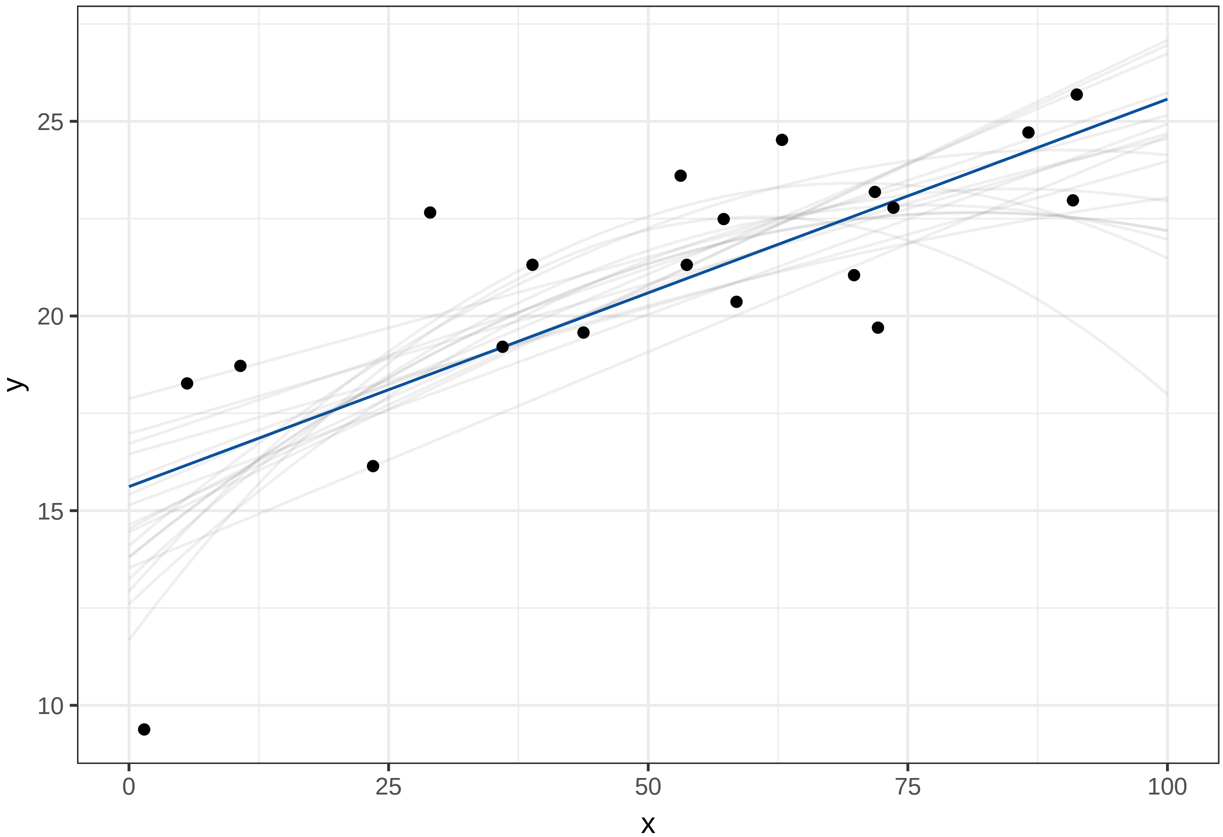

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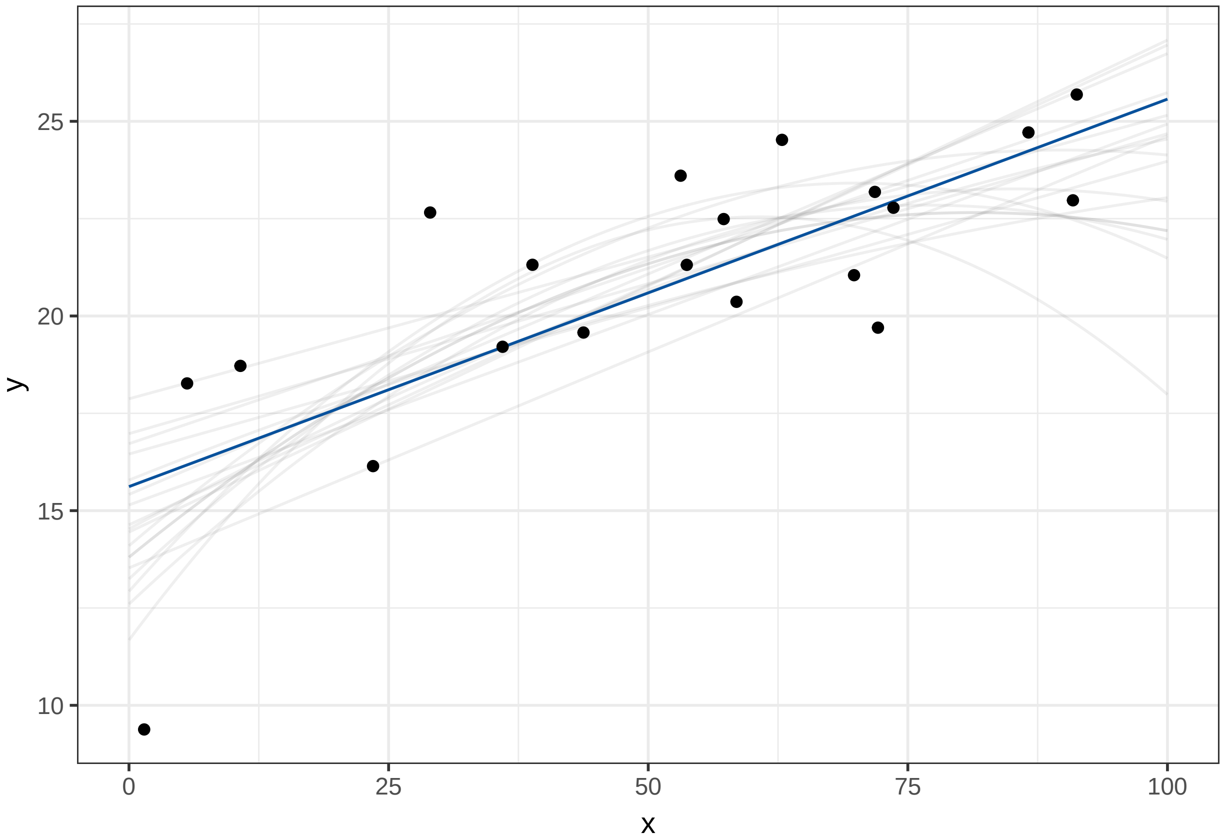
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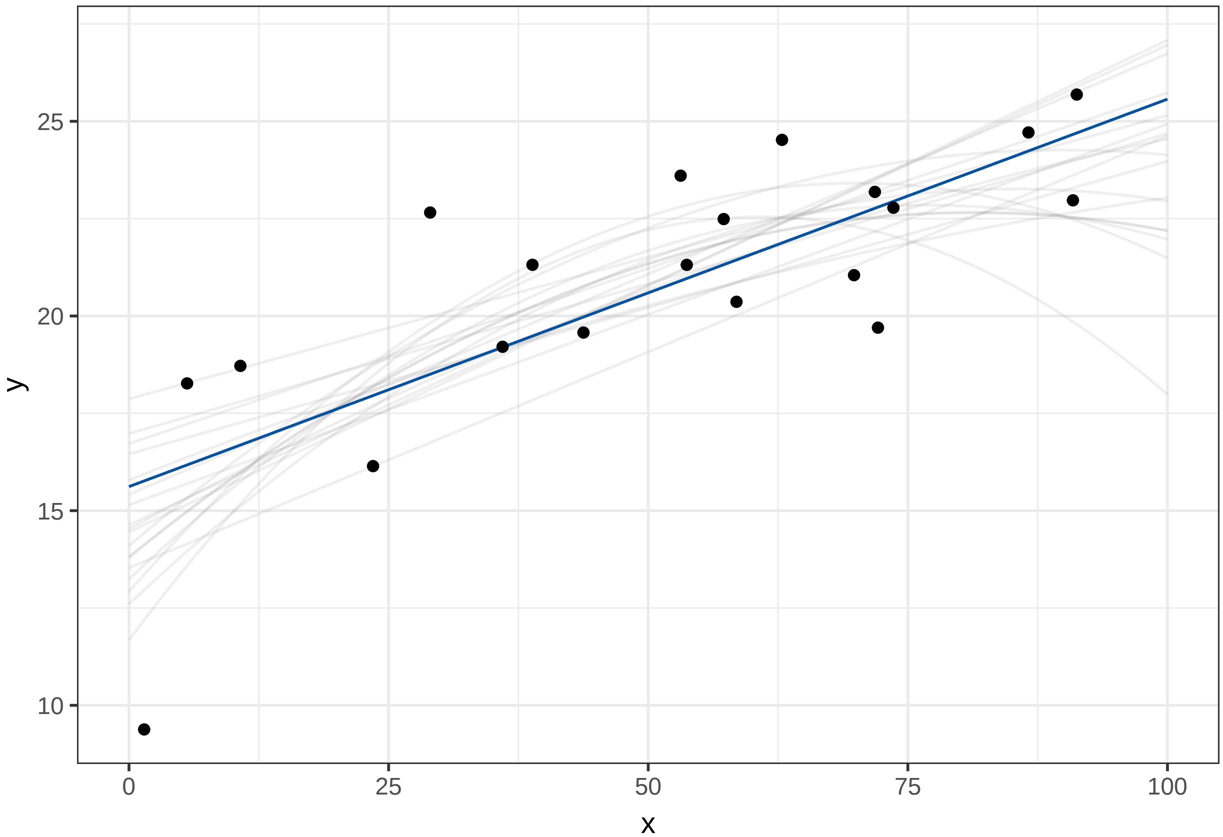

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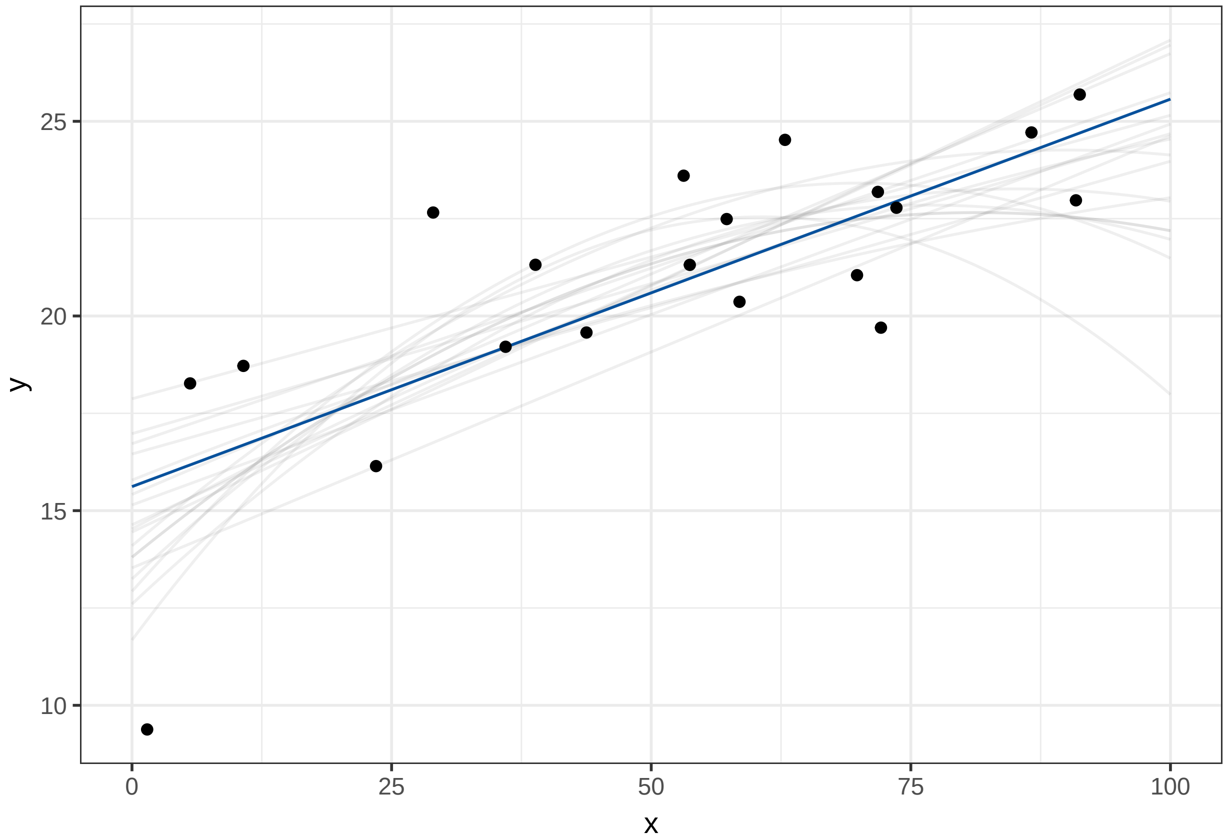

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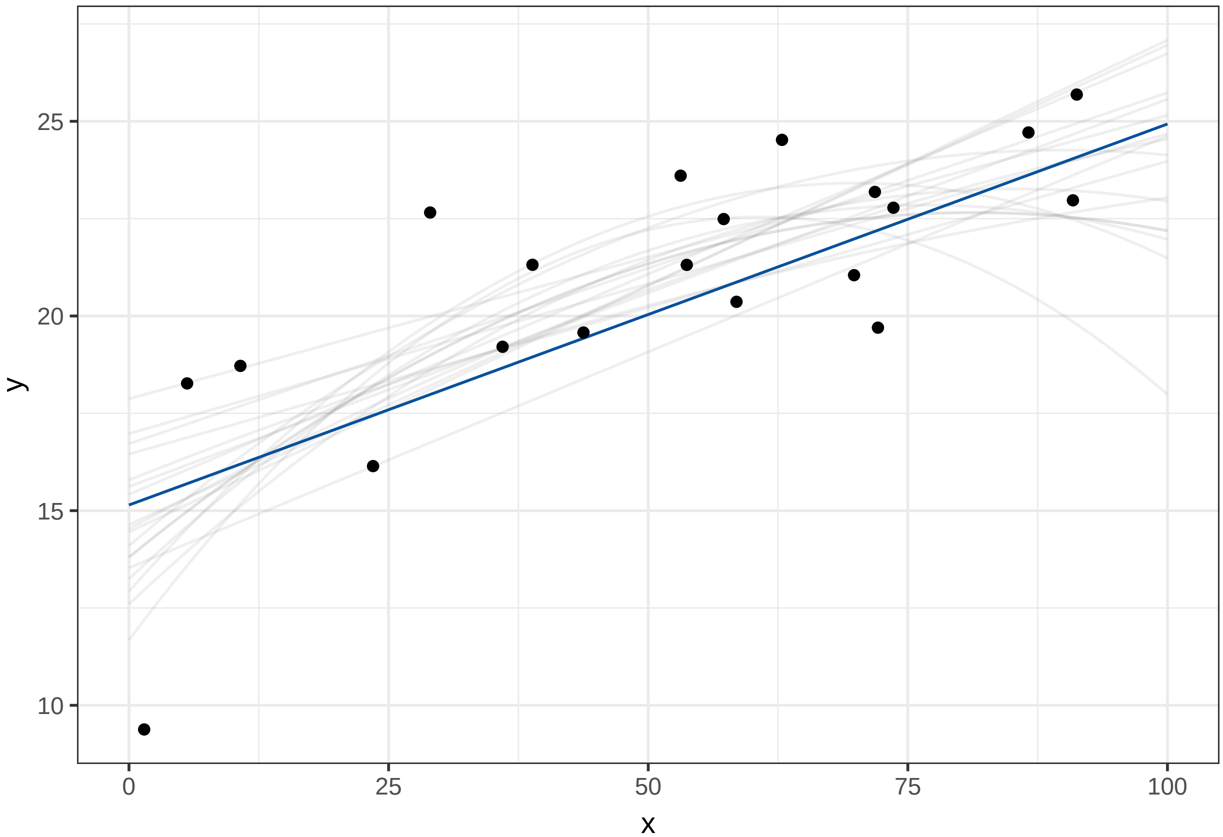

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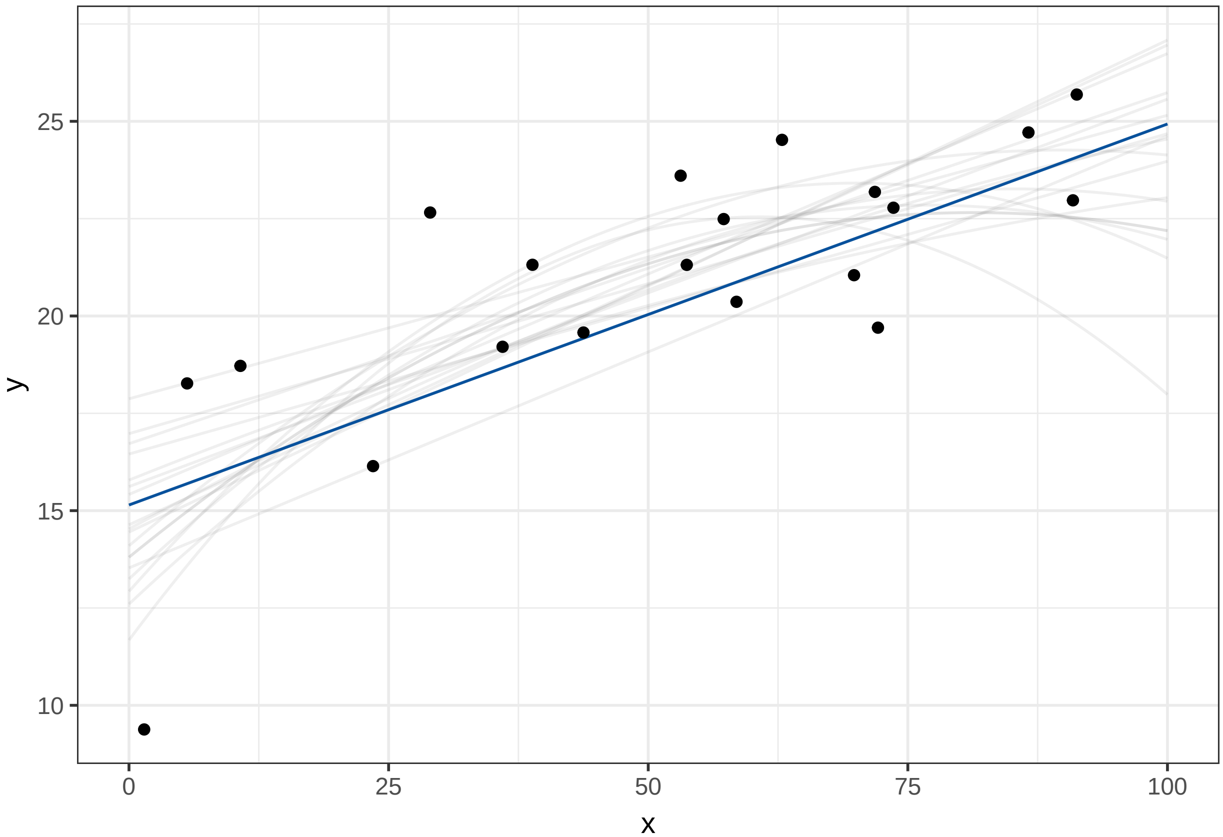

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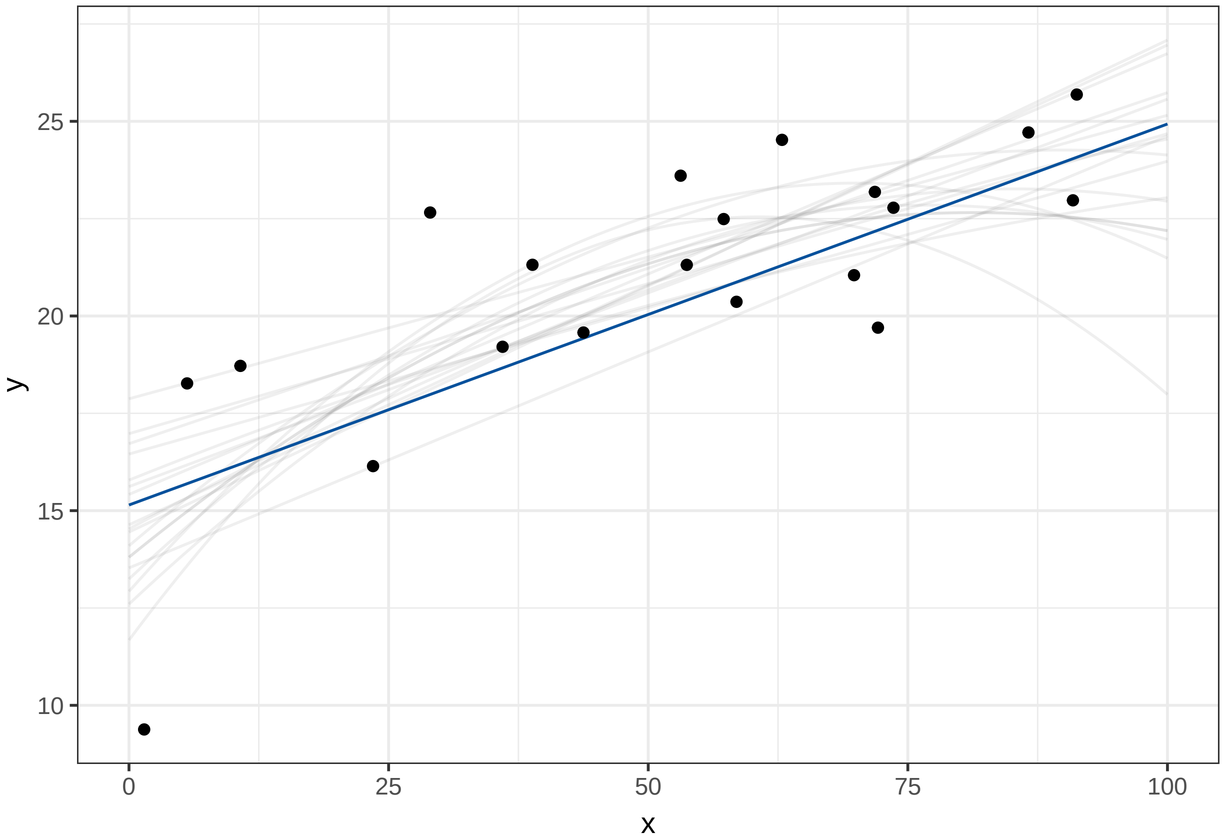

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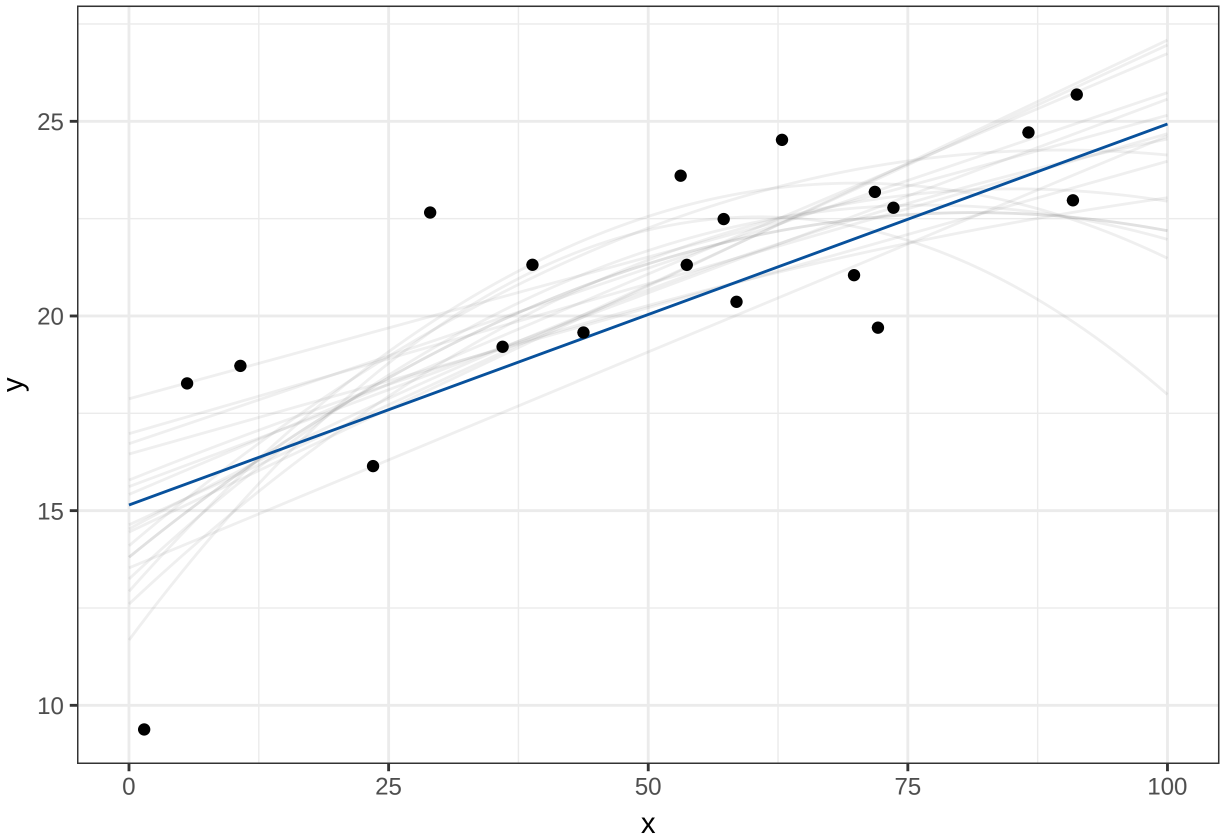

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y
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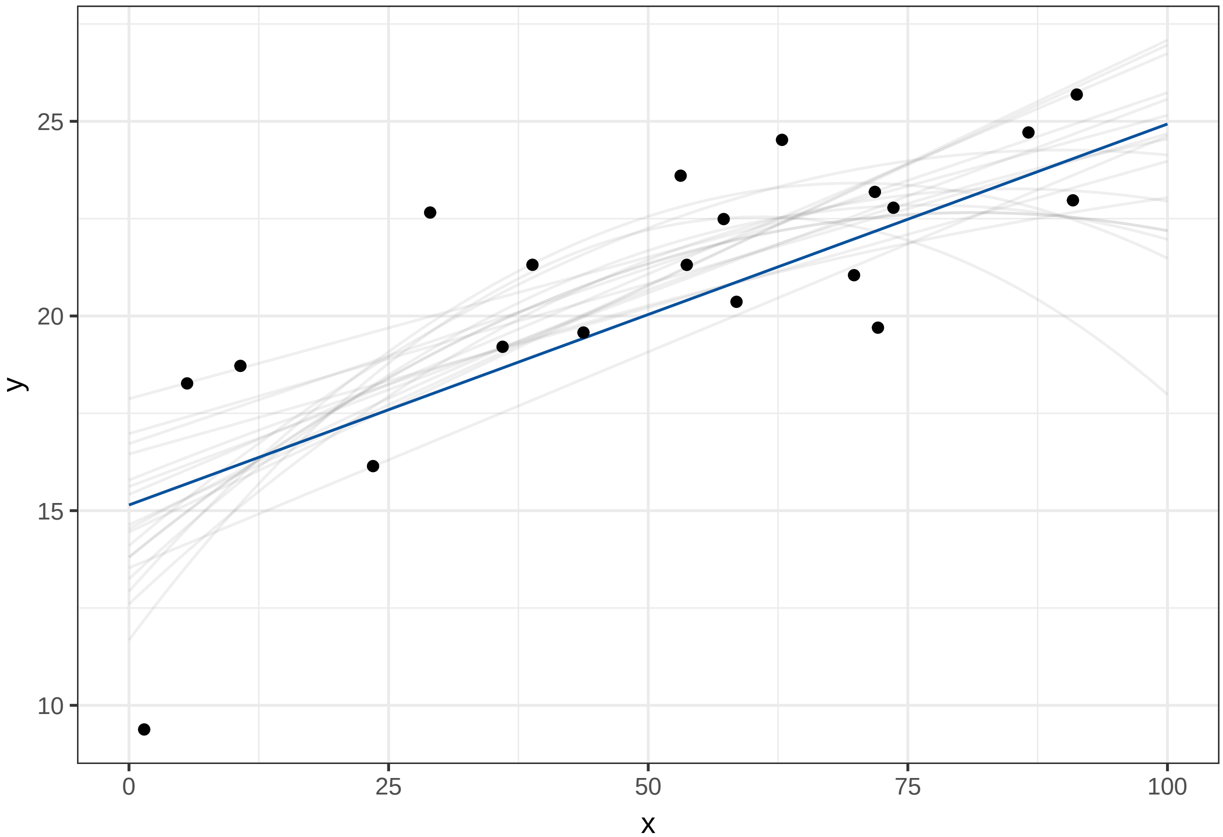
x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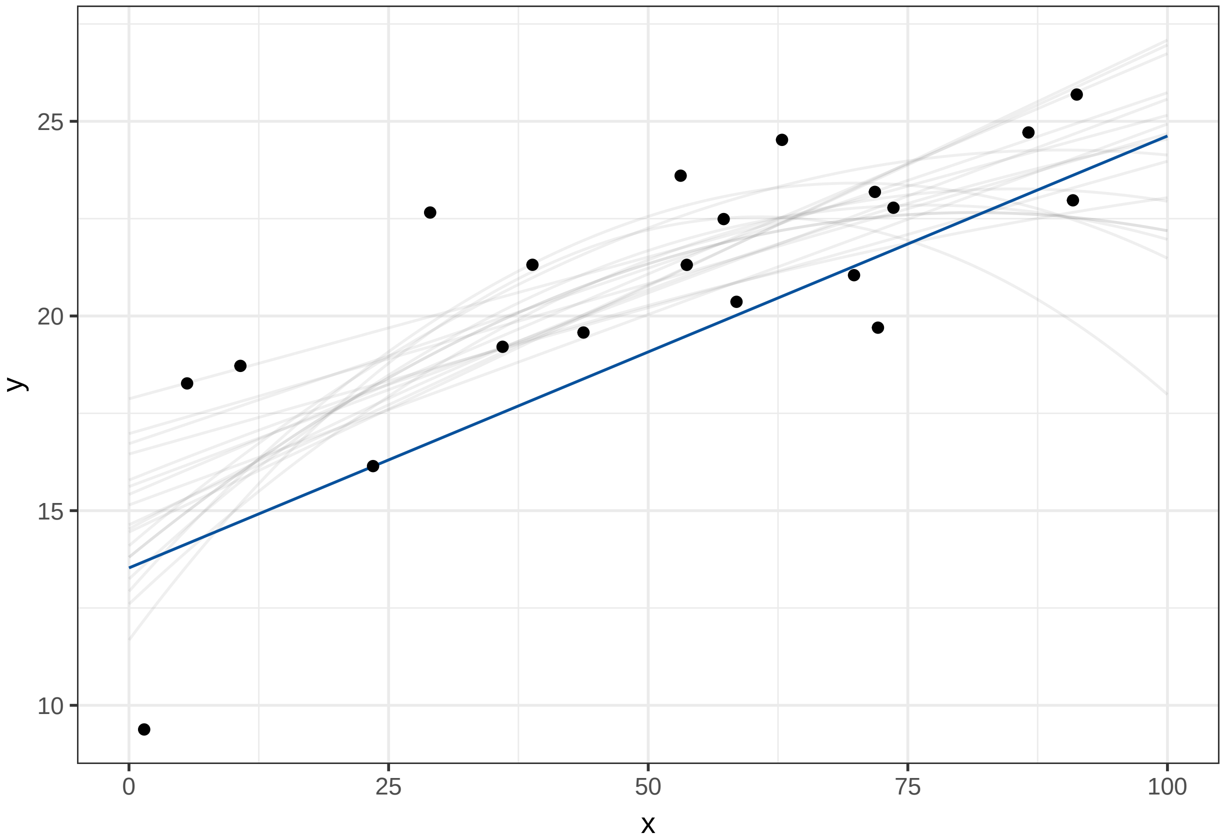

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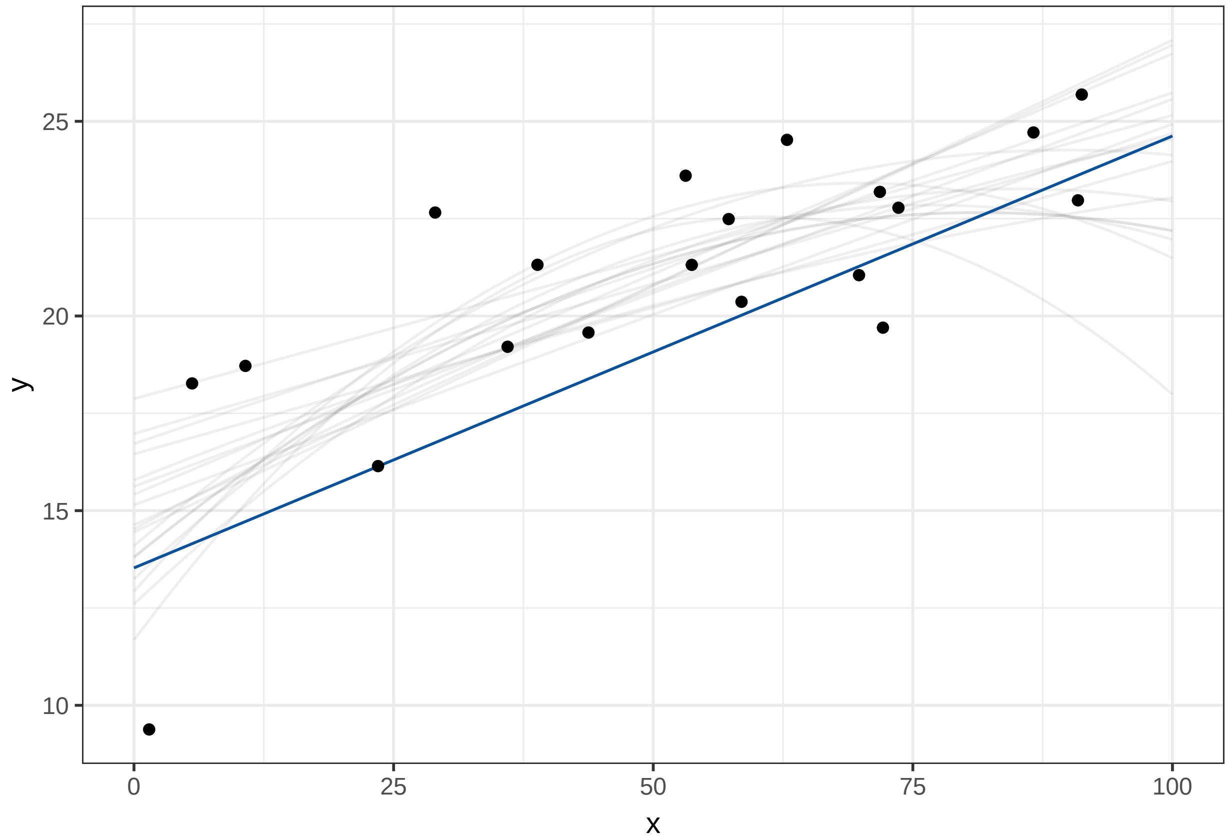

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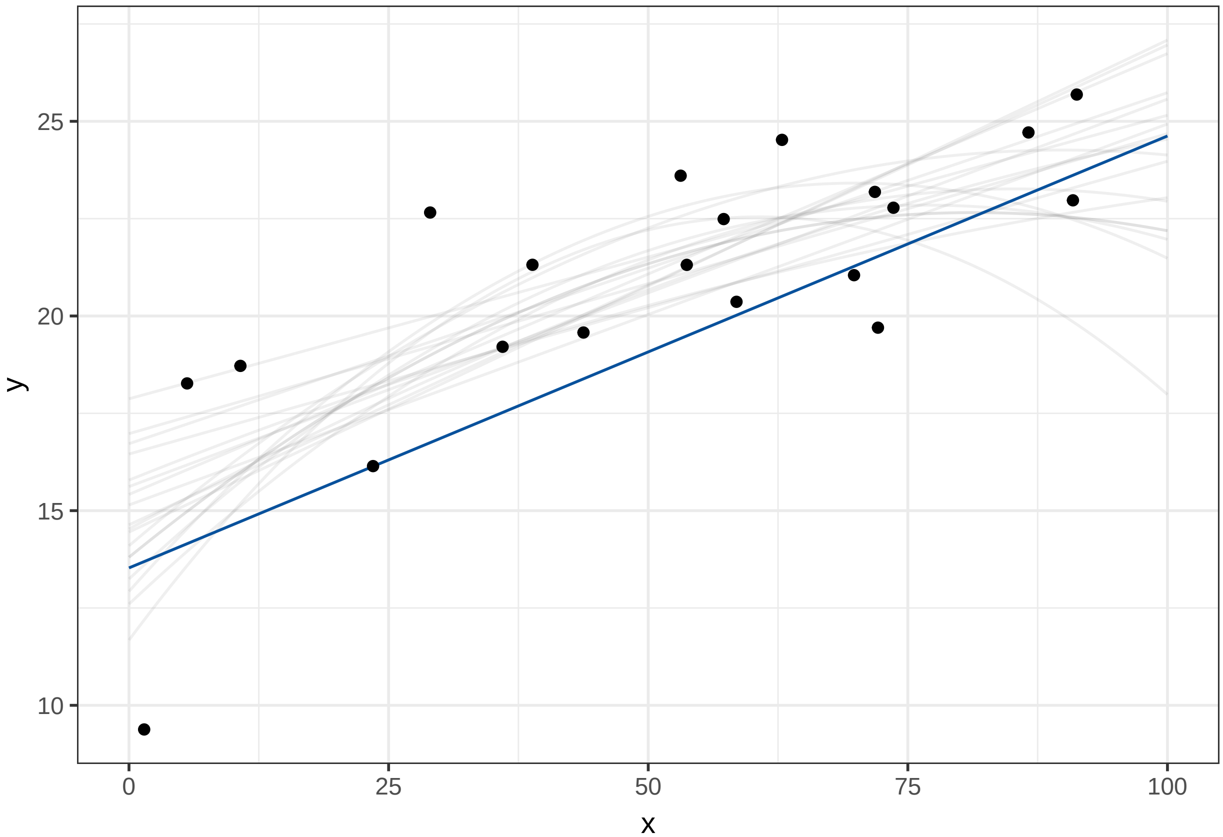

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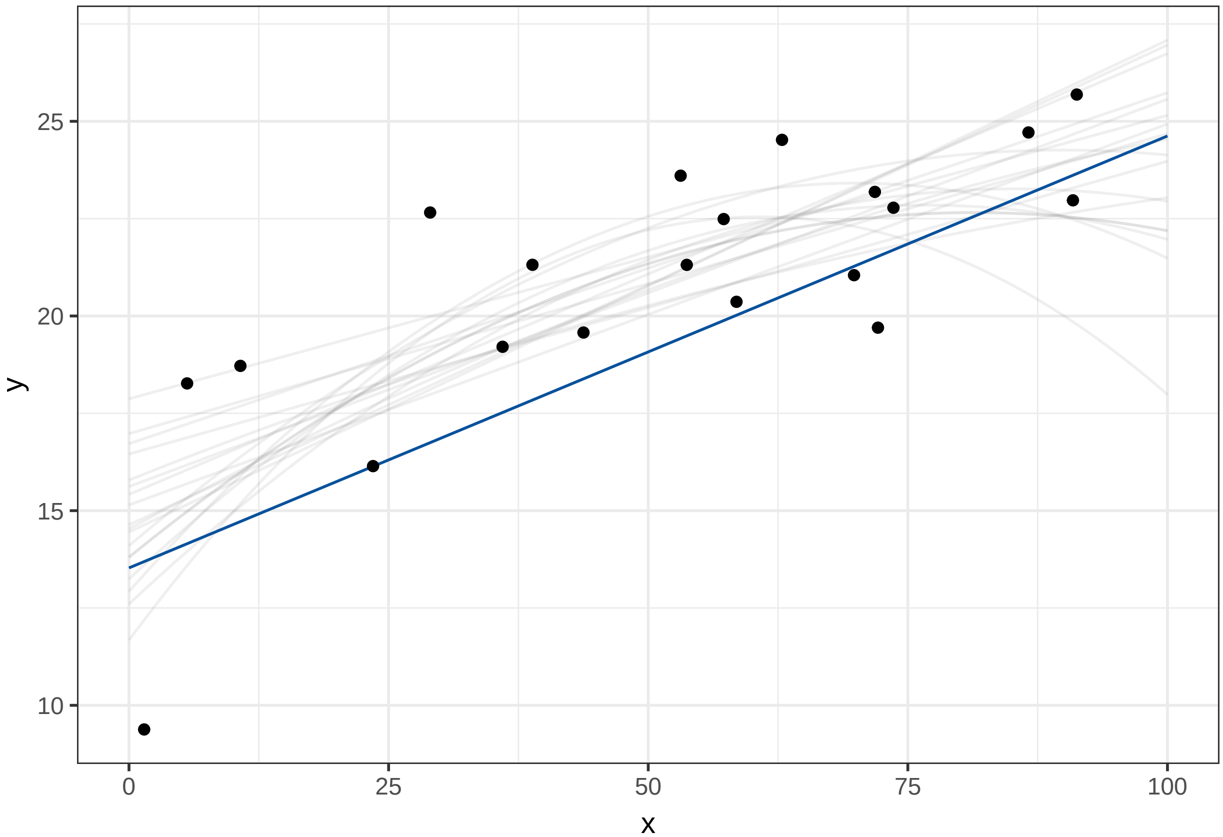
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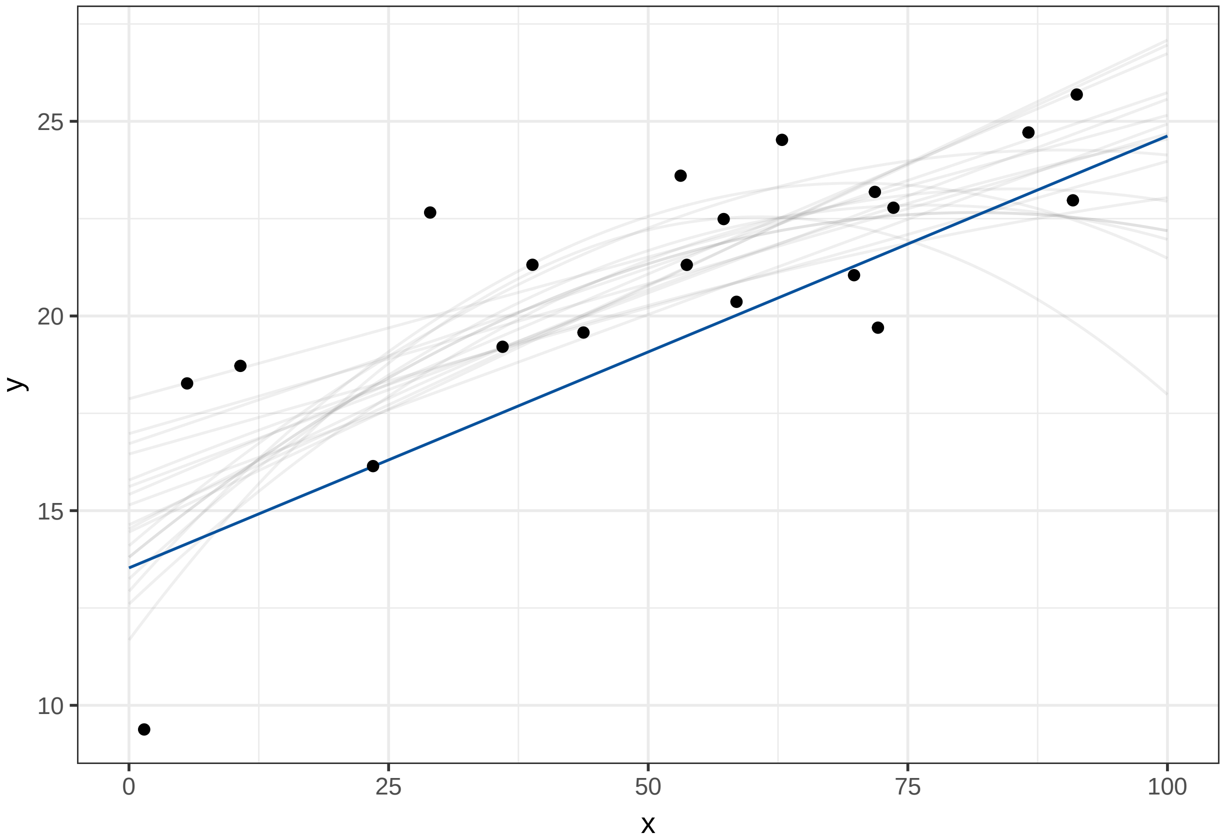

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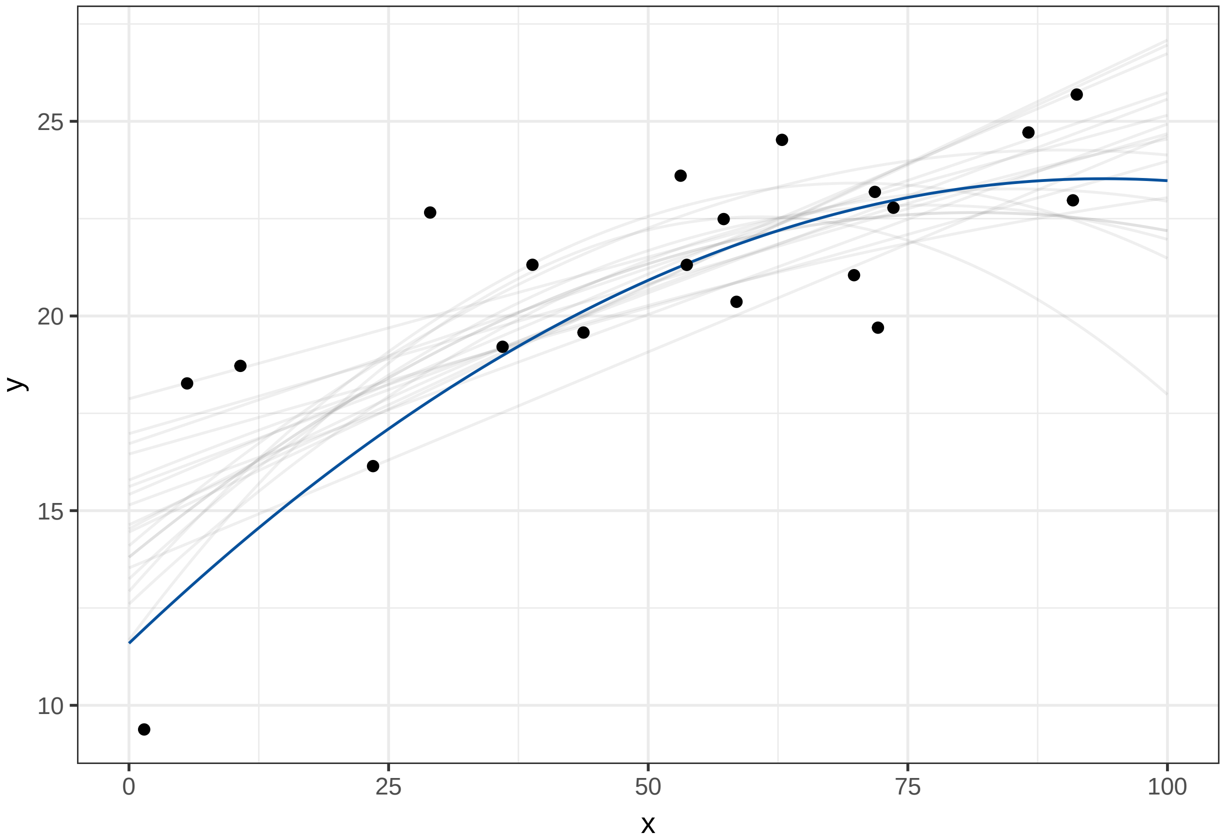

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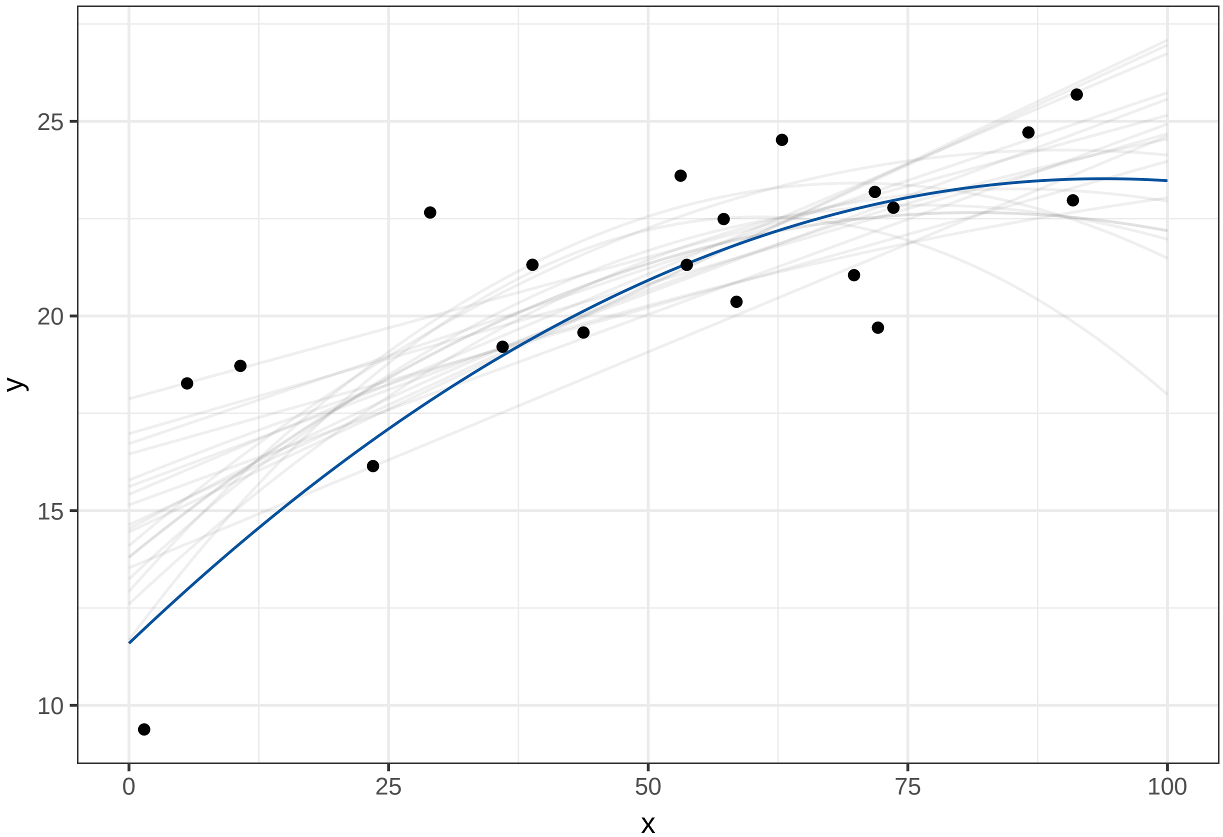
x



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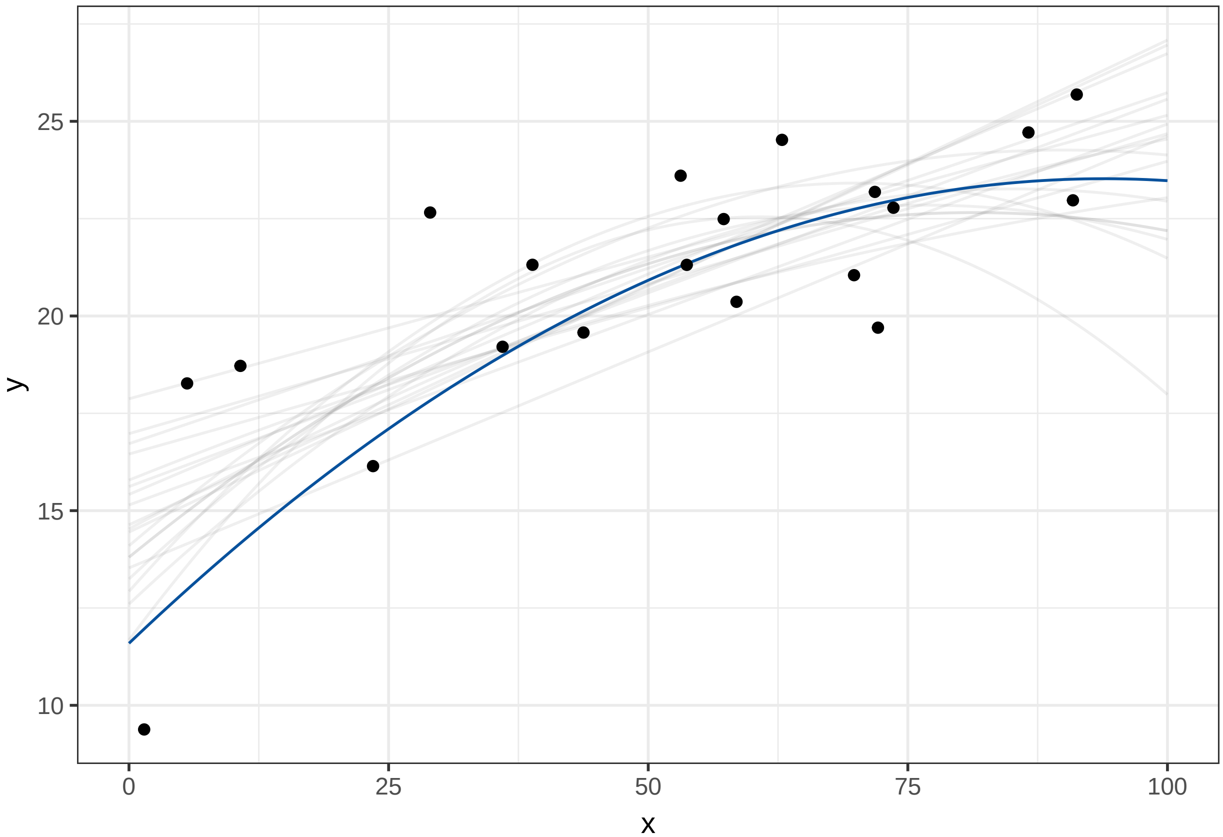

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y
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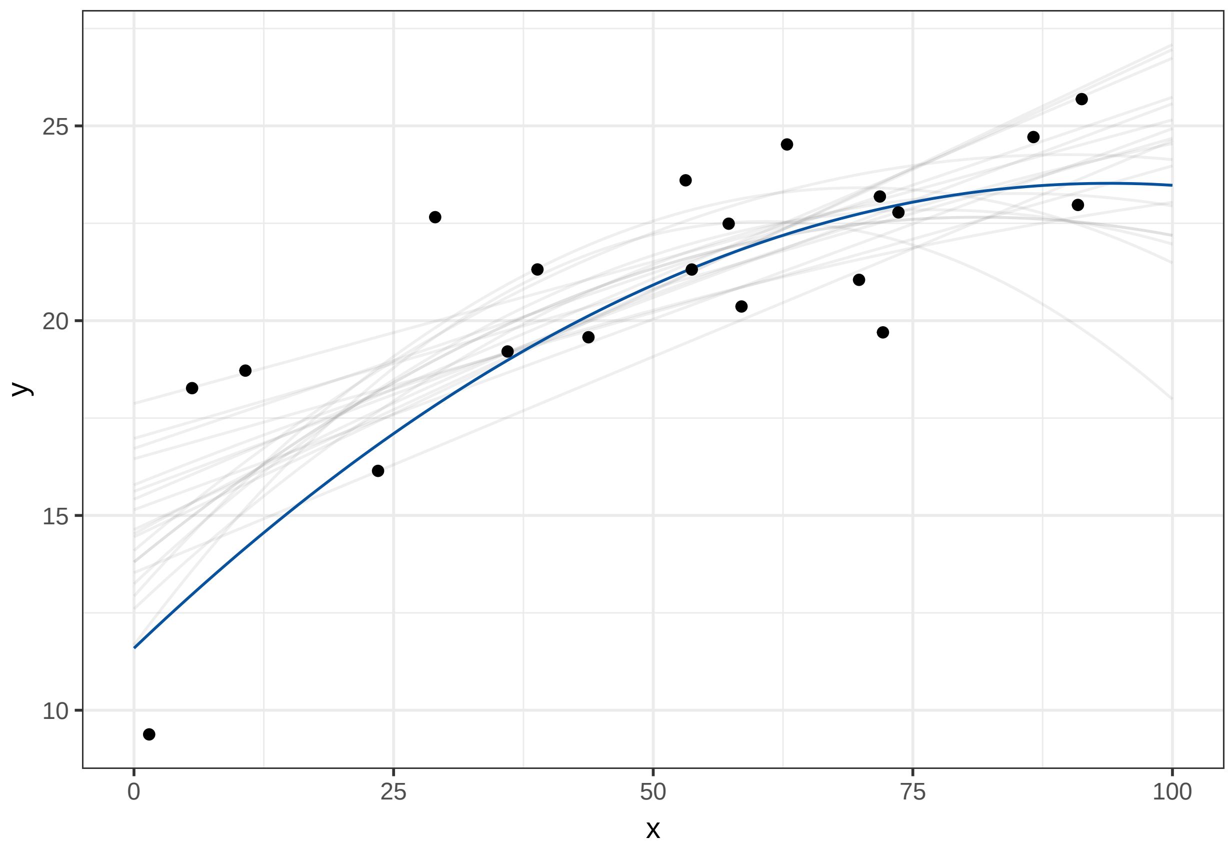
x



Comparison to interval and interval analysis

Intervals determined by the 1st and 99th percentiles for uncertainty in parameters and 1st and 99th percentiles for the variability.

There is a high agreement between output from interval analysis and probabilistic analysis, because the intervals are informed by the probabilistic analysis and the model is relatively simple.

Interval analysis of the linear model

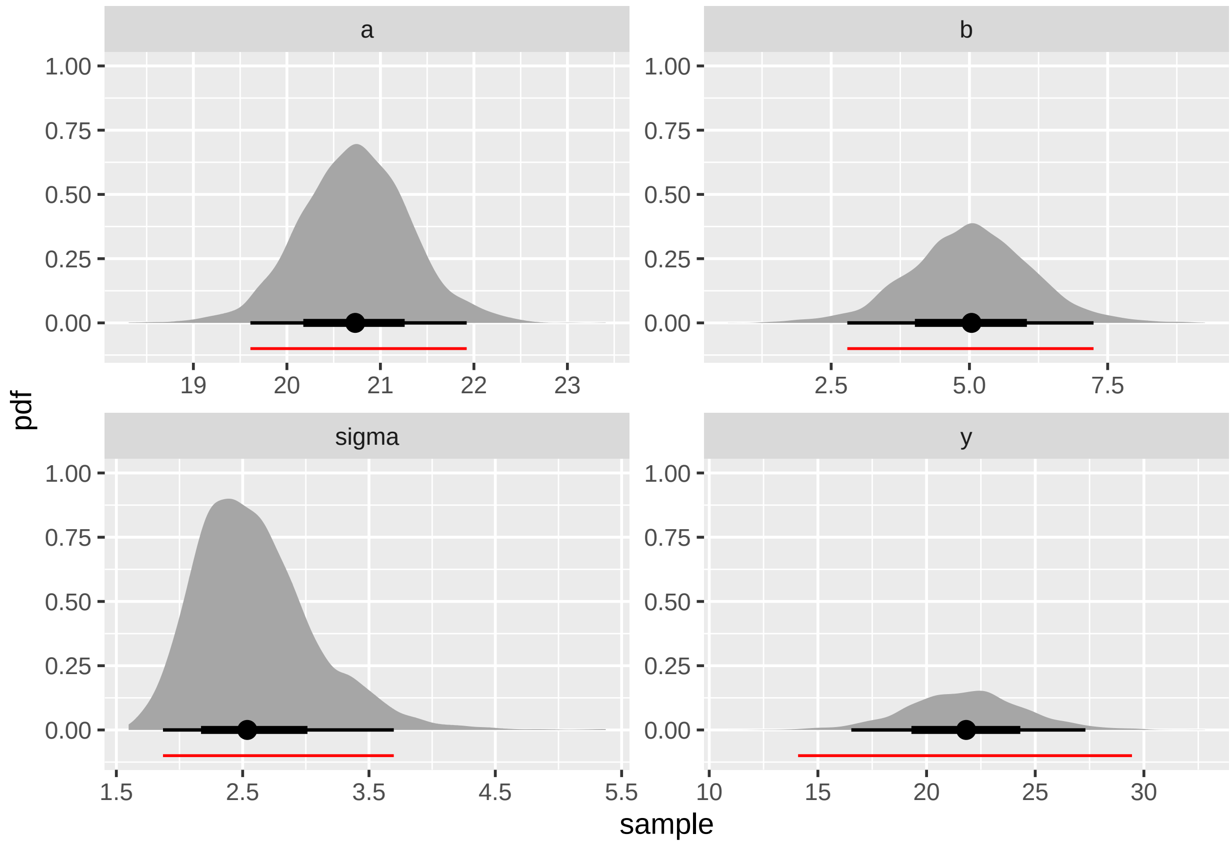
```
a <- quantile(mcmc_sample[,"a"],probs = c(0.025,0.975))
b <- quantile(mcmc_sample[,"b"],probs = c(0.025,0.975))
sigma <- quantile(mcmc_sample[,"sigma"],probs = c(0.025,0.975))
x <- 60
y <- c(min(a)+min(b*(x-50)/50) + qnorm(0.05,0,max(sigma)),
           max(a)+max(b*(x-50)/50) + qnorm(0.95,0,max(sigma)))

df_int <- data.frame(quantity = c('a','b','sigma','y'), lower = c(a[1],b[1],sigma[1],y[1]), upper = c(a

df_inputoutput <- data.frame(sample = c(mcmc_sample[,'a'],mcmc_sample[,'b'],mcmc_sample[,'sigma'],y_mc)

ggplot(df_inputoutput,aes(x = sample)) +
 stat_halfeye() +
```

```
  geom_segment(data = df_int, aes(x = lower, xend = upper, y = -0.1, yend = -0.1), col = 'red') +
  facet_wrap(~quantity, scales = "free") +
  ylab('pdf')
```



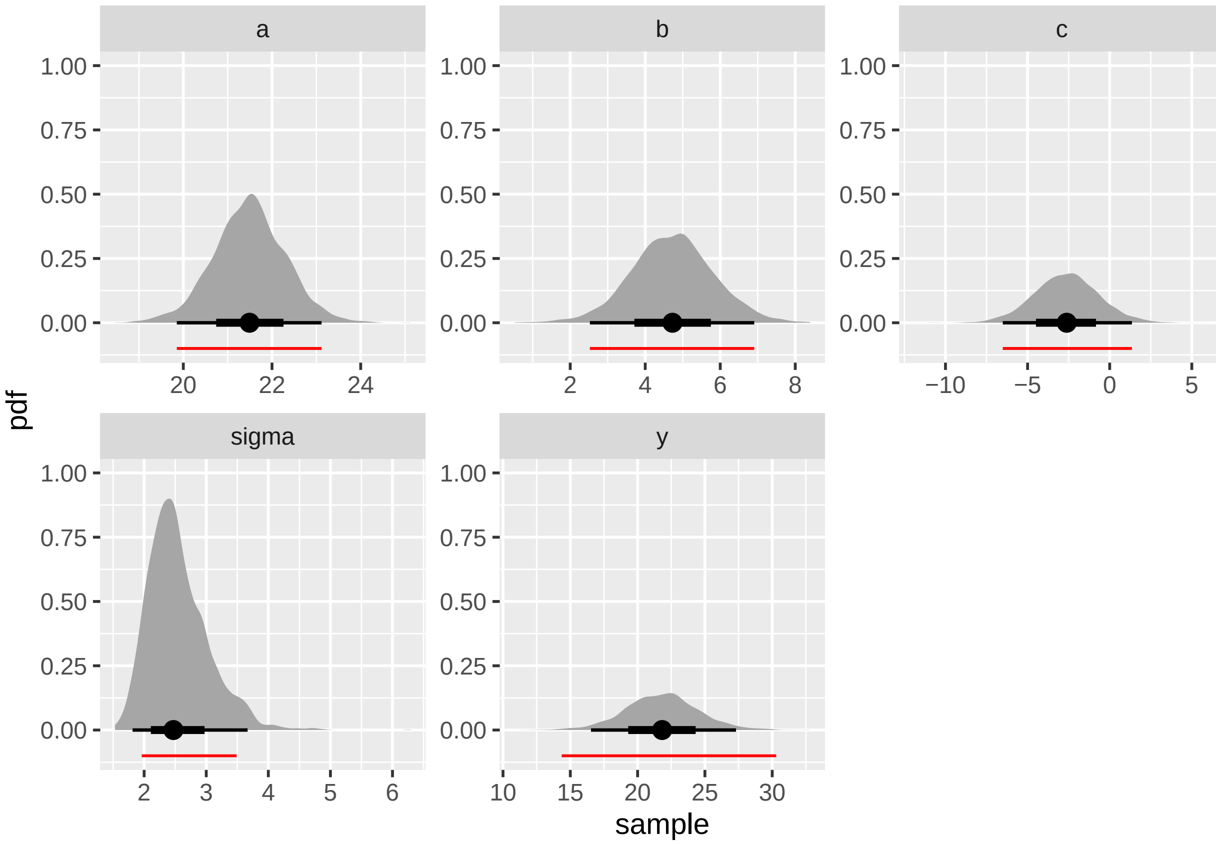
Interval analysis of the model with a squared term

```
a <- quantile(mcmc_sample_sq[,"a"],probs = c(0.025,0.975))
b <- quantile(mcmc_sample_sq[,"b"],probs = c(0.025,0.975))
c <- quantile(mcmc_sample_sq[,"c"],probs = c(0.025,0.975))
sigma <- quantile(mcmc_sample[,"sigma"],probs = c(0.05,0.95))
x <- 60
y <- c(min(a)+min(b*(x-50)/50) +min(c*(x-50)/50 *(x-50)/50) + qnorm(0.05,0,max(sigma)),
           max(a)+max(b*(x-50)/50) +max(c*(x-50)/50 *(x-50)/50) + qnorm(0.95,0,max(sigma)))

df_int <- data.frame(quantity = c('a','b','c','sigma','y'), lower = c(a[1],b[1],c[1],sigma[1],y[1]), upp

df_inputoutput <- data.frame(sample = c(mcmc_sample_sq[,'a'],mcmc_sample_sq[,'b'],mcmc_sample_sq[,'c'],m

ggplot(df_inputoutput,aes(x = sample)) +
 stat_halfeye() +
  geom_segment(data = df_int, aes(x = lower, xend = upper, y = -0.1, yend = -0.1), col = 'red') +
  facet_wrap(~quantity, scales = "free") +
  ylab('pdf')
```



a
b
c
sigma
y
pdf
sample
1.00
0.75
0.50
0.25
0.00
20
22
24
2
4
6
8
−10
−5
0
5
2
3
4
5
6
10
15
20
25
30