

# Untitled

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```
logitGD <- function(y, x, optim.method = "GDI", eps = 10e-4,
                    max.iter = 100, alpha = function(t){1/t}, beta_0 = c(0,0)){
  stopifnot(length(y) == length(x) & optim.method %in% c("GDI", "GDII", "SGDI")
            & is.numeric(c(max.iter, eps, x)) & all(c(eps, max.iter) > 0) &
            is.function(alpha))

  iter <- 0
  err <- list()
  err[[iter+1]] <- eps+1
  w_old <- beta_0

  res <- list()
  while(iter < max.iter && (abs(err[[ifelse(iter==0,1,iter)]]) > eps)){

    iter <- iter + 1
    if (optim.method == "GDI"){
      w_new <- w_old + alpha(iter)*updateWeightsGDI(y, x, w_old)
    }
    if (optim.method == "GDII"){
      w_new <- w_old + as.vector(inverseHessianGDII(x, w_old)%*%
                                updateWeightsGDI(y, x, w_old))
    }
    if (optim.method == "SGDI"){
      w_new <- w_old + alpha(iter)*updateWeightsSGDI(y[iter], x[iter], w_old)
    }
    res[[iter]] <- w_new
    err[[iter]] <- sqrt(sum((w_new - w_old)^2))

    w_old <- w_new

  }
  return(list(steps = c(list(beta_0),res), errors = c(list(c(0,0)),err)))
}

updateWeightsGDI <- function(y, x, w_old){
  (1/length(y))*c(sum(y-p(w_old, x)), sum(x*(y-p(w_old, x))))
  #c(sum(y-p(w_old, x)), sum(x*(y-p(w_old, x))))
}

updateWeightsSGDI <- function(y_i, x_i, w_old){
  c(y_i-p(w_old, x_i), x_i*(y_i-p(w_old, x_i)))
}

p <- function(w_old, x_i){
  1/(1+exp(-w_old[1]-w_old[2]*x_i))
}

inverseHessianGDII <- function(x, w_old){
```

```

solve(
  matrix(c(
    sum(p(w_old, x)*(1-p(w_old, x))),
    sum(x*p(w_old, x)*(1-p(w_old, x))),
    sum(x*p(w_old, x)*(1-p(w_old, x))),
    sum(x*x*p(w_old, x)*(1-p(w_old, x)))
  ),
  nrow = 2 )
)
}

```

```

# wstępna inicjalizacja parametrów
eps = 1e-5 # warunek stopu.

n = length(data) # data jest listą ramek danych.

diff = eps + 1 # różnice w oszacowaniach parametrów
# między kolejnymi krokami.

learningRates = function(x) 1/x # długości kroku algorytmu.

beta_old = numeric(0, length = k) # punkt startowy długości k,
# gdzie k to liczba zmiennych
# objaśniających w modelu.

max.iter = 500 # maksymalna liczba kroków.
ż

# estymacja
i = 1 # iterator kroku algorytmu.
while(i <= max.iter | diff < eps) do
  iter = ifelse(i mod n == 0, n, i mod n) # wybierz kolejny podzbiór batch.
  batch = data[[iter]]
  beta_new = beta_old - learningRates(i) * U_Batch(batch)
  # U_Batch to częściowa funkcja
  # log-wiarogdności dla zaobserwowanego
  # zbioru `batch`
  diff = euclidean_dist(beta_new, beta_old) # odległość euklidesowa
  beta_old = beta_new
  i = i + 1
end while
return beta_new

```

```

coxphSGD <- function(formula, data, learningRates = function(x){1/x},
  beta_0 = 0, epsilon = 1e-5, max.iter = 500 ) {
  checkArguments(formula, data, learningRates,
    beta_0, epsilon) -> beta_start # check arguments
  n <- length(data)
  diff <- epsilon + 1
  i <- 1
  beta_new <- list() # steps are saved in a list so that they can
  beta_old <- beta_start # be tracked in the future
  # estimate
  while(i <= max.iter & diff > epsilon) {

```

```

    beta_new[[i]] <- coxphSGD_batch(formula = formula, beta = beta_old,
                                   learningRate = learningRates(i), data = data[[ifelse(i%%n==0,n,i%%n)]])

    diff <- sqrt(sum((beta_new[[i]] - beta_old)^2))
    beta_old <- beta_new[[i]]
    i <- i + 1
  }
  # return results
  list(Call = match.call(), epsilon = epsilon, learningRates = learningRates,
        steps = i, coefficients = c(list(beta_start), beta_new))
}

coxphSGD_batch <- function(formula, data, learningRate, beta){
  # collect times, status, variables and reorder samples
  # to make the algorithm more clear to read and track
  batchData <- prepareBatch(formula = formula, data = data)

  # calculate the log-likelihood for this batch sample
  partial_sum <- list()

  for(k in 1:nrow(batchData)) {
    # risk set for current time/observation
    risk_set <- batchData %>% filter(times >= batchData$times[k])

    nominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      element * exp(element * beta)
    }) %>% rowSums()

    denominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      exp(element * beta)
    }) %>% rowSums()

    partial_sum[[k]] <-
      batchData[k, "event"] * (batchData[k, -c(1,2)] - nominator/denominator)
  }
  do.call(rbind, partial_sum) %>%
    colSums() -> U_batch

  return(beta + learningRate * U_batch)
}

checkArguments <- function(formula, data, learningRates,
                           beta_0, epsilon) {
  assert_that(is.list(data) & length(data) > 0)
  assert_that(length(unique(unlist(lapply(data, ncol)))) == 1)
  # + check names and types for every variables
  assert_that(is.function(learningRates))
  assert_that(is.numeric(epsilon))
  assert_that(is.numeric(beta_0))

  # check length of the start parameter
  if (length(beta_0) == 1) {
    beta_0 <- rep(beta_0, as.character(formula)[3] %>%

```

```

        strsplit("\\\\+") %>%
        unlist %>%
        length)
    }
    return(beta_0)
}

```

```

x <- runif(1000)
z <- 2 + 3*x
pr <- 1/(1+exp(-z))
y <- rbinom(1000,1,pr)

```

```

logitGD(y, x, optim.method = "GDI", eps = 10e-5, max.iter = 500)$steps -> GDI
logitGD(y, x, optim.method = "GDII", eps = 10e-5, max.iter = 500)$steps -> GDII

```

```

ind <- sample(length(y))
logitGD(y[ind], x[ind], optim.method = "SGDI",
        max.iter = 500, eps = 10e-5)$steps -> SGDI.1
ind2 <- sample(length(y))
logitGD(y[ind2], x[ind2], optim.method = "SGDI",
        max.iter = 500, eps = 10e-5)$steps -> SGDI.2
ind3 <- sample(length(y))
logitGD(y[ind3], x[ind3], optim.method = "SGDI",
        max.iter = 500, eps = 10e-5)$steps -> SGDI.3
ind4 <- sample(length(y))
logitGD(y[ind4], x[ind4], optim.method = "SGDI",
        max.iter = 500, eps = 10e-5)$steps -> SGDI.4
ind5 <- sample(length(y))
logitGD(y[ind5], x[ind5], optim.method = "SGDI",
        max.iter = 500, eps = 10e-5)$steps -> SGDI.5

```

```

do.call(rbind, c(GDI, GDII, SGDI.1, SGDI.2, SGDI.3, SGDI.4, SGDI.5)) -> coeffs
unlist(lapply(list(GDI, GDII, SGDI.1, SGDI.2, SGDI.3, SGDI.4, SGDI.5), length)) -> algorithm
data2viz <- cbind(as.data.frame(coeffs),
                 algorithm = unlist(mapply(rep, c("GDI", "GDII", "SGDI.1", "SGDI.2", "SGDI.3", "SGDI.4", "SGDI.5"))
names(data2viz)[1:2] <- c("Intercept", "X")
library(ggplot2); library(ggthemes)
ggplot(data2viz) +
  geom_point(aes(x = X, y = Intercept, col = algorithm)) +
  geom_line(aes(x = X, y = Intercept, col = algorithm,
               group = algorithm)) +
  theme_tufte(base_size = 20)

```

logitGD() asda graphSGD()

```

graphSGD(c(0,0), y, x)
graphSGD(c(3.1,2.1), y, x)
graphSGD(c(4,3), y, x)
graphSGD(c(1,2), y, x)

```

```

dataCox <- function(N, lambda, rho, x, beta, censRate){

  # real Weibull times
  u <- runif(N)
  Treal <- (- log(u) / (lambda * exp(x %*% beta)))^(1 / rho)

  # censoring times
  Censoring <- rexp(N, censRate)

  # follow-up times and event indicators
  time <- pmin(Treal, Censoring)
  status <- as.numeric(Treal <= Censoring)

  # data set
  data.frame(id=1:N, time=time, status=status, x=x)
}

x <- matrix(sample(0:1, size = 40, replace = TRUE), ncol = 2)

head(dataCox(20, 3, 2, x, beta = c(2,3), 5))

```

	id	time	status	x.1	x.2
1	1	0.07852976	1	0	0
2	2	0.10314559	0	0	1
3	3	0.04471293	1	0	1
4	4	0.03496663	1	1	1
5	5	0.14461568	0	0	1
6	6	0.09745620	1	1	0

```

graphSGD(c(0,0), y, x, 4561);graphSGD(c(0,0), y, x, 456)
graphSGD(c(2,1), y, x, 4561);graphSGD(c(2,1), y, x, 456);
graphSGD(c(1,0), y, x, 4561);graphSGD(c(1,0), y, x, 456);
graphSGD(c(2.1,3.1), y, x, 4561)graphSGD(c(2.1,3.1), y, x, 456)

```

```

x <- matrix(sample(0:1, size = 20000, replace = TRUE), ncol = 2)
dCox <- dataCox(10^4, lambda = 3, rho = 2, x, beta = c(1,3), censRate = 5)
vizCoxSGD(dCox)

```

```

coxphSGD <- function(formula, data, learningRates = function(x){1/x},
                     beta_0 = 0, epsilon = 1e-5, max.iter = 500 ) {
  checkArguments(formula, data, learningRates,
                 beta_0, epsilon) -> beta_start # check arguments
  n <- length(data)
  diff <- epsilon + 1
  i <- 1
  beta_new <- list() # steps are saved in a list so that they can
  beta_old <- beta_start # be traced in the future
  # estimate
  while(i <= max.iter & diff > epsilon) {
    beta_new[[i]] <- coxphSGD_batch(formula = formula, beta = beta_old,
                                   learningRate = learningRates(i), data = data[[ifelse(i%%n==0,n,i%%n)]]) %>%
    unlist
    diff <- sqrt(sum((beta_new[[i]] - beta_old)^2))
    beta_old <- beta_new[[i]]
    i <- i + 1 ; cat("\r iteration: ", i, "\r")
  } # return results
  list(Call = match.call(), epsilon = epsilon, learningRates = learningRates,
       steps = i, coefficients = c(list(beta_start), beta_new))
}

coxphSGD_batch <- function(formula, data, learningRate, beta){
  # collect times, status, variables and reorder samples
  # to make the algorithm more clear to read and track
  batchData <- prepareBatch(formula = formula, data = data)
  # calculate the log-likelihood for this batch sample
  partial_sum <- list()
  foreach(k = 1:nrow(batchData)) %do% {
    # risk set for current time/observation
    risk_set <- batchData %>% filter(times >= batchData$times[k])

    nominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      element * exp(element * beta)
    }) %>% rowSums()

    denominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      exp(element * beta)
    }) %>% rowSums()

    partial_sum[[k]] <-
      batchData[k, "event"] * (batchData[k, -c(1,2)] - nominator/denominator)
  }
  do.call(rbind, partial_sum) %>%
  colSums() -> U_batch

  return(beta + learningRate * U_batch)
}

prepareBatch <- function(formula, data) {
  # Parameter identification as in `survival::coxph()`.
  Call <- match.call()
  indx <- match(c("formula", "data"),

```

```

        names(Call), nomatch = 0)
if (indx[1] == 0)
  stop("A formula argument is required")
temp <- Call[c(1, indx)]
temp[[1]] <- as.name("model.frame")

mf <- eval(temp, parent.frame())
Y <- model.extract(mf, "response")

if (!inherits(Y, "Surv"))
  stop("Response must be a survival object")
type <- attr(Y, "type")

if (type != "right" && type != "counting")
  stop(paste("Cox model doesn't support \"", type, "\" survival data",
    sep = ""))

# collect times, status, variables and reorder samples
# to make the algorithm more clear to read and track
cbind(event = unclass(Y)[,2], # 1 indicates event, 0 indicates cens
      times = unclass(Y)[,1],
      mf[, -1]) %>%
  arrange(times)
}

```

```

simulateCoxSGD(dCox, learningRates = function(x){1/(100*sqrt(x))},
  max.iter = 10, epsilon = 1e-5, beta_0 = c(2,2))

```

```

logitGD <- function(y, x, optim.method = "GDI", eps = 10e-4,
  max.iter = 100, alpha = function(t){1/t}, beta_0 = c(0,0)){
  stopifnot(length(y) == length(x) & optim.method %in% c("GDI", "GDII", "SGDI")
    & is.numeric(c(max.iter, eps, x)) & all(c(eps, max.iter) > 0) &
    is.function(alpha))

  iter <- 0
  err <- list()
  err[[iter+1]] <- eps+1
  w_old <- beta_0

  res <- list()
  while(iter < max.iter && (abs(err[[ifelse(iter==0,1,iter)]]) > eps)){

    iter <- iter + 1
    if (optim.method == "GDI"){
      w_new <- w_old + alpha(iter)*updateWeightsGDI(y, x, w_old)
    }
    if (optim.method == "GDII"){
      w_new <- w_old + as.vector(inverseHessianGDII(x, w_old)%*%
        updateWeightsGDI(y, x, w_old))
    }
    if (optim.method == "SGDI"){
      w_new <- w_old + alpha(iter)*updateWeightsSGDI(y[iter], x[iter], w_old)
    }
    res[[iter]] <- w_new
  }
}

```

```

err[[iter]] <- sqrt(sum((w_new - w_old)^2))

w_old <- w_new

}
return(list(steps = c(list(beta_0),res), errors = c(list(c(0,0)),err)))
}

updateWeightsGDI <- function(y, x, w_old){
  #(1/length(y))*c(sum(y-p(w_old, x)), sum(x*(y-p(w_old, x))))
  c(sum(y-p(w_old, x)), sum(x*(y-p(w_old, x))))
}

updateWeightsSGDI <- function(y_i, x_i, w_old){
  c(y_i-p(w_old, x_i), x_i*(y_i-p(w_old, x_i)))
}

p <- function(w_old, x_i){
  1/(1+exp(-w_old[1]-w_old[2]*x_i))
}

inverseHessianGDII <- function(x, w_old){
  solve(
    matrix(c(
      sum(p(w_old, x)*(1-p(w_old, x))),
      sum(x*p(w_old, x)*(1-p(w_old, x))),
      sum(x*p(w_old, x)*(1-p(w_old, x))),
      sum(x*x*p(w_old, x)*(1-p(w_old, x)))
    ),
    nrow = 2 )
  )
}

set.seed(1283)
x <- runif(10000)
z <- 2 + 3*x
pr <- 1/(1+exp(-z))
y <- rbinom(10000,1,pr)

global_loglog <- function(beta1, beta2, xX, yY){
  sum(yY*(beta1+beta2*xX)-log(1+exp(beta1+beta2*xX)))
}

calculate_outer <- function(x, y){
  ## contours
  outer_res <- outer(seq(0.4, length = 100),
    seq(0.5, length = 100),
    Vectorize( function(beta1,beta2){
      global_loglog(beta1, beta2, xX = x, yY = y)
    } )
  )
}

```



```

outer_res_melted <- melt(outer_res)

outer_res_melted$Var1 <- as.factor(outer_res_melted$Var1)
levels(outer_res_melted$Var1) <- as.character(seq(0,4, length = 100))
outer_res_melted$Var2 <- as.factor(outer_res_melted$Var2)
levels(outer_res_melted$Var2) <- as.character(seq(0,5, length = 100))
outer_res_melted$Var1 <- as.numeric(as.character(outer_res_melted$Var1))
outer_res_melted$Var2 <- as.numeric(as.character(outer_res_melted$Var2))
return(outer_res_melted)
}

library(ggplot2); library(ggthemes); library(reshape2)
graphSGD <- function(beta, y, x, seed = 4561, outerBounds = calculate_outer(x,y)){
  set.seed(seed)

  beta <- rev(beta)

  logitGD(y, x, optim.method = "GDI", beta_0 = beta,
    eps = 10e-4, max.iter = 10000,
    alpha = function(t){1/(1000*sqrt(t))})$steps -> GDI.S

  logitGD(y, x, optim.method = "GDII", beta_0 = beta,
    eps = 10e-4, max.iter = 5000)$steps -> GDII

  ind2 <- sample(length(y))
  logitGD(y[ind2], x[ind2], optim.method = "SGDI", beta_0 = beta,
    max.iter = 10000, eps = 10e-4,
    alpha = function(t){1/sqrt(t)})$steps -> SGDI.1.S
  ind3 <- sample(length(y))
  logitGD(y[ind3], x[ind3], optim.method = "SGDI", beta_0 = beta,
    max.iter = 10000, eps = 10e-4,
    alpha = function(t){5/sqrt(t)})$steps -> SGDI.5.S
  ind4 <- sample(length(y))
  logitGD(y[ind4], x[ind4], optim.method = "SGDI", beta_0 = beta,
    max.iter = 10000, eps = 10e-4,
    alpha = function(t){6/sqrt(t)})$steps -> SGDI.6.S

  do.call(rbind, c(GDI.S, GDII, SGDI.1.S, SGDI.5.S, SGDI.6.S)) -> coeffs
  unlist(lapply(list(GDI.S, GDII, SGDI.1.S, SGDI.5.S, SGDI.6.S),
    length)) -> algorithm
  data2viz <- cbind(as.data.frame(coeffs),
    algorithm = unlist(mapply(rep,
      c(paste("GDI", length(GDI.S), "steps"),
        paste("GDII", length(GDII), "steps"),
        paste("SGDI.1", length(SGDI.1.S), "steps"),
        paste("SGDI.5", length(SGDI.5.S), "steps"),
        paste("SGDI.6", length(SGDI.6.S), "steps")),
      algorithm)))
  names(data2viz)[1:2] <- c("Intercept", "X")
  data2viz$algorithm <- factor(data2viz$algorithm, levels = rev(levels(data2viz$algorithm)))

```

```

beta[2] -> XX
beta[1] -> YY

ggplot()+
  geom_path(aes(x = data2viz$X,
               y = data2viz$Intercept,
               col = data2viz$algorithm,
               group = data2viz$algorithm), size = 1) +
  geom_point(aes(as.vector(round(coefficients(glm(y~x,
                                                family = 'binomial')), 2)[2]),
                 as.vector(round(coefficients(glm(y~x,
                                                family = 'binomial')), 2)[1])),
             col = "black", size = 4, shape = 15) +
  geom_point(aes(x=XX, y=YY),
             col = "black", size = 4, shape = 17) +
  theme_bw(base_size = 20) +
  theme(panel.border = element_blank(),
        legend.key = element_blank()) +
  scale_colour_brewer(palette="Set1", name = 'Algorithm') +
  xlab('X') +
  ylab('Intercept') -> pl_g

return(pl_g)
}

full_cox_loglik <- function(beta1, beta2, x1, x2, censored){
  sum(rev(censored)*(beta1*rev(x1) + beta2*rev(x2) -
                    log(cumsum(exp(beta1*rev(x1) + beta2*rev(x2))))))
}

calculate_outer_cox <- function(x1, x2, censored){
  ## contours
  outer_res <- outer(seq(-1,3, length = 100),
                    seq(0,4, length = 100),
                    Vectorize( function(beta1,beta2){
                      full_cox_loglik(beta1, beta2, x1 = x1, x2 = x2, censored = censored)
                    } )
  )
  outer_res_melted <- melt(outer_res)
  outer_res_melted$Var1 <- as.factor(outer_res_melted$Var1)
  levels(outer_res_melted$Var1) <- as.character(seq(-1,3, length = 100))
  outer_res_melted$Var2 <- as.factor(outer_res_melted$Var2)
  levels(outer_res_melted$Var2) <- as.character(seq(0,4, length = 100))
  outer_res_melted$Var1 <- as.numeric(as.character(outer_res_melted$Var1))
  outer_res_melted$Var2 <- as.numeric(as.character(outer_res_melted$Var2))
  return(outer_res_melted)
}

simulateCoxSGD <- function(dCox = dCox, learningRates = function(x){1/x},
                          epsilon = 1e-03, beta_0 = c(0,0), max.iter = 100){

  sample(1:90, size = 10^4, replace = TRUE) -> group

```

```

split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*90) -> estimates

sample(1:60, size = 10^4, replace = TRUE) -> group
split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*60) -> estimates2

sample(1:120, size = 10^4, replace = TRUE) -> group
split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*120) -> estimates3

sample(1:200, size = 10^4, replace = TRUE) -> group
split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*200) -> estimates4

sample(1:30, size = 10^4, replace = TRUE) -> group
split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*30) -> estimates5

sample(1:10, size = 10^4, replace = TRUE) -> group
split(dCox, group) -> dCox_splitted
coxphSGD(Surv(time, status)~x.1+x.2, data = dCox_splitted,
  epsilon = epsilon, learningRates = learningRates,
  beta_0 = beta_0, max.iter = max.iter*10) -> estimates6

t(simplify2array(estimates$coefficients)) %>%
  as.data.frame() -> df1
t(simplify2array(estimates2$coefficients)) %>%
  as.data.frame() -> df2
t(simplify2array(estimates3$coefficients)) %>%
  as.data.frame() -> df3
t(simplify2array(estimates4$coefficients)) %>%
  as.data.frame() -> df4
t(simplify2array(estimates5$coefficients)) %>%
  as.data.frame() -> df5
t(simplify2array(estimates6$coefficients)) %>%
  as.data.frame() -> df6

df1 %>%
  mutate(version = paste("90 batches,", nrow(df1), " steps")) %>%
  bind_rows(df2 %>%

```

```

        mutate(version = paste("60 batches,", nrow(df2), " steps")))) %>%
bind_rows(df3 %>%
        mutate(version = paste("120 batches,", nrow(df3), " steps")))) %>%
bind_rows(df4 %>%
        mutate(version = paste("200 batches,", nrow(df4), " steps")))) %>%
bind_rows(df5 %>%
        mutate(version = paste("30 batches,", nrow(df5), " steps")))) %>%
bind_rows(df6 %>%
        mutate(version = paste("10 batches,", nrow(df6), " steps")))) -> d2ggplot

return(list(d2ggplot = d2ggplot, est1 = estimates, est2 = estimates2,
          est3 = estimates3, est4 = estimates4, est5 = estimates5))
}

simulateCoxSGD(dCox, learningRates = function(x){1/(100*sqrt(x))},
              max.iter = 10, epsilon = 1e-5) -> d2ggplot

d2ggplot -> backpack
d2ggplot <- d2ggplot$d2ggplot
beta_0 = c(0,0)
solution = c(1,3)

pdf(file = "b_0_0_iter_10_e-5_100sqrt_878.pdf", width = 10, height = 10)
ggplot() +
  stat_contour(aes(x=outerCox$Var1,
                  y=outerCox$Var2,
                  z=outerCox$value),
              bins = 40, alpha = 0.25) +
  geom_path(aes(d2ggplot$V1, d2ggplot$V2, group = d2ggplot$version,
                colour = d2ggplot$version), size = 1) +
  theme_bw(base_size = 20) +
  theme(panel.border = element_blank(),
        legend.key = element_blank(), legend.position = "top") +
  scale_colour_brewer(palette="Dark2", name = 'Algorithm \n & Steps') +
  geom_point(aes(x = beta_0[1], y = beta_0[2]), col = "black", size = 4, shape = 17) +
  geom_point(aes(x = solution[1], y = solution[2]), col = "black", size = 4, shape = 15) +
  geom_point(aes(x = summary(coxph(Surv(time, status)~x.1+x.2, data = dCox))$coeff[1,1],
                    y = summary(coxph(Surv(time, status)~x.1+x.2, data = dCox))$coeff[2,1]),
              col = "black", size = 4, shape = 13) +
  xlab("X1") + ylab("X2") +
  guides(col = guide_legend(ncol = 3))
dev.off()

```

```

extractSurvival <- function(cohorts){

  survivalData <- list()
  for(i in cohorts){
    get(paste0(i, ".clinical"), envir = .GlobalEnv) %>%
      select(patient.bcr_patient_barcode,
             patient.vital_status,
             patient.days_to_last_followup,
             patient.days_to_death ) %>%
      mutate(bcr_patient_barcode = toupper(patient.bcr_patient_barcode),
             patient.vital_status = ifelse(patient.vital_status %>%

```

```

                                as.character() == "dead", 1, 0),
    barcode = patient.bcr_patient_barcode %>%
                                as.character(),
    times = ifelse( !is.na(patient.days_to_last_followup),
    patient.days_to_last_followup %>%
                                as.character() %>%
                                as.numeric(),
    patient.days_to_death %>%
                                as.character() %>%
                                as.numeric() )
                                ) %>%
filter(!is.na(times)) -> survivalData[[i]]

}
do.call(rbind,survivalData) %>%
  select(bcr_patient_barcode, patient.vital_status, times) %>%
  unique

}

extractMutations <- function(cohorts, prc){
  mutationsData <- list()
  for(i in cohorts){
    get(paste0(i, ".mutations"), envir = .GlobalEnv) %>%
      select(Hugo_Symbol, bcr_patient_barcode) %>%
      filter(nchar(bcr_patient_barcode)==15) %>%
      filter(substr(bcr_patient_barcode, 14, 15)=="01") %>%
      unique -> mutationsData[[i]]
  }
  do.call(rbind,mutationsData) %>% unique -> mutationsData

mutationsData %>%
  group_by(Hugo_Symbol) %>%
  summarise(count = n()) %>%
  arrange(desc(count)) %>%
  mutate(count_prc = count/length(unique(mutationsData$bcr_patient_barcode))) %>%
  filter_(paste0("count_prc > ",prc)) %>%
  select(Hugo_Symbol) %>%
  unlist -> topGenes

mutationsData %>%
  filter(Hugo_Symbol %in% topGenes) -> mutationsData_top

mutationsData_top %>%
  dplyr::group_by(bcr_patient_barcode) %>%
  dplyr::summarise(count = n()) %>%
  group_by(count) %>%
  summarise(total = n()) %>%
  arrange(desc(count))
#

```

```

# mutationsData_top %>%
#   spread(Hugo_Symbol, bcr_patient_barcode) -> mutationsData_top_sp

as.data.table(mutationsData_top) -> mutationsData_top_DT
dcast.data.table(mutationsData_top_DT, bcr_patient_barcode ~ Hugo_Symbol , fill = 0) %>%
  as.data.frame -> mutationsData_top_dcasted

mutationsData_top_dcasted[,-1][mutationsData_top_dcasted[,-1] != "0"] <- 1

mutationsData_top_dcasted -> result
names(result) <- gsub(names(result), pattern = "-", replacement = "")
result
}

extractCohortIntersection <- function(){

  data(package = "RTCGA.mutations")$results[,3] %>%
    gsub(".mutations", "", x = .) -> mutations_data
  data(package = "RTCGA.clinical")$results[,3] %>%
    gsub(".clinical", "", x = .) -> clinical_data

  intersect(mutations_data, clinical_data)
}

prepareCoxDataSplit <- function(mutationsData, survivalData, groups, seed = 4561){
  mutationsData %>%
    mutate(bcr_patient_barcode = substr(bcr_patient_barcode,1,12)) %>%
    left_join(survivalData,
              by = "bcr_patient_barcode") -> coxData

  coxData <- coxData[, -c(1,2)]

  coxData %>%
    filter(times > 0) %>%
    filter(!is.na(times)) -> coxData

  apply(coxData[, -c(1092, 1093)], MARGIN = 2, function(x){
    as.numeric(as.character(x))
  }) -> coxData[, -c(1092, 1093)]

  set.seed(seed)
  sample(groups, replace = TRUE, size = 6085) -> groups
  split(coxData, groups) #coxData_split
}

prepareFormulaSGD <- function(coxData){
  as.formula(paste("Surv(times, patient.vital_status) ~ ",
                   paste(names(coxData[[1]])[-c(1092, 1093)],
                         collapse="+"), collapse = ""))
}

```

```
full_cox_loglik_matrix <- function(beta, x, censored){
  order(x$times) -> order2
  x[order2, ] -> xORD
  censored[order2] -> censORD
  sum(censORD*(beta%*%x[, -which(names(x)=='times')] -
    log(cumsum(exp(beta1*rev(x1) + beta2*rev(x2))))))
}

library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(RTCGA.clinical)
```

Loading required package: RTCGA  
 Loading required package: knitr  
 Welcome to the RTCGA (version: 1.2.1).

```
library(RTCGA.mutations)
library(data.table)
```

Attaching package: 'data.table'

The following objects are masked from 'package:dplyr':

between, last

```
library(coxphSGD)
```

Loading required package: survival

Attaching package: 'coxphSGD'

The following object is masked \_by\_ '.GlobalEnv':

dataCox

Do analizy badającej wpływ występowania mutacji genów na czas przeżycia wykorzystano dane kliniczne i dane o występujących u pacjentów mutacjach genetycznych. Starano się wykorzystać dane ze wszystkich 38

dostępnych kohort nowotworowych z badania *The Cancer Genome Atlas* (TCGA), jednak nie dla wszystkich kohort umieszczono w badaniu dane o mutacjach. Część wspólną nazw dla kohort zawierających zarówno dane kliniczne oraz dane o mutacjach wygenerowaną dzięki wywołaniu

```
(extractCohortIntersection() -> cohorts)
```

```
[1] "ACC"      "BLCA"      "BRCA"      "CESC"      "CHOL"      "COAD"
[7] "COADREAD" "DLBC"      "ESCA"      "GBM"      "GBMLGG"    "HNSC"
[13] "KICH"     "KIPAN"     "KIRC"      "KIRP"      "LAML"      "LGG"
[19] "LIHC"     "LUAD"      "LUSC"      "OV"        "PAAD"      "PCPG"
[25] "PRAD"     "READ"      "SARC"      "SKCM"      "STAD"      "STES"
[31] "TGCT"     "THCA"      "UCEC"      "UCS"      "UVM"
```

Następnie dla tak otrzymanych 35 kohort nowotworowych uzyskano dane o statusie pacjenta (śmierć bądź cenzurowanie) oraz jego czasie spędzonym pod obserwacją dzięki funkcji

```
head(extractSurvival(cohorts) -> survivalData)
```

	bcr_patient_barcode	patient.vital_status	times
ACC.1	TCGA-OR-A5J1	1	1355
ACC.2	TCGA-OR-A5J2	1	1677
ACC.3	TCGA-OR-A5J3	0	1942
ACC.4	TCGA-OR-A5J4	1	423
ACC.5	TCGA-OR-A5J5	1	365
ACC.6	TCGA-OR-A5J6	0	2428

Dane o mutacjach występujących wśród tkanek nowotworowych kolejnych pacjentów uzyskano za pomocą

```
extractMutations(cohorts, 0.02) -> mutationsData
```

Using 'bcr\_patient\_barcode' as value column. Use 'value.var' to override

```
mutationsData[1:6, c(1,4,56,100,207,801)]
```

	bcr_patient_barcode	A2ML1	ALMS1	ATP2B2	CNTNAP4	PLEC
1	TCGA-02-0003-01	0	1	0	0	0
2	TCGA-02-0033-01	0	0	0	0	0
3	TCGA-02-0047-01	0	0	0	0	0
4	TCGA-02-0055-01	0	0	0	0	0
5	TCGA-02-2470-01	0	0	0	0	0
6	TCGA-02-2483-01	0	0	1	0	0

gdzie wybrano jedynie te geny, których mutacja dotyczyła co najmniej 2 % pacjentów mających zarówno dane kliniczne jak i dane o występujących mutacjach w genach.

Dla tak otrzymanych dwóch zbiorów danych połączono dla pacjentów informacje kliniczne z informacjami o mutacjach dzięki przypisanym do pacjentów i ich próbek kodów `bcr_patient_barcode`, by ostatecznie podzielić zbiór pacjentów na 100 losowo utworzonych grup.



```
set.seed(4561)
prepareCoxDataSplit(mutationsData,survivalData, groups = 100) -> coxData_split
head(coxData_split[[1]][c(1,10), c(210,302,356,898,911,1092:1093)])
```

	COL14A1	DOCK9	FASN	SEMA5A	SHPRH	patient.vital_status	times
81	0	0	0	0	0	1	7
1068	1	0	0	1	0	1	1171

Niezbędną formułę modelu potrzebną do sprezycowania, które geny (a pozostało ich 1091) należy uwzględnić w modelu uzyskano dzięki pomocniczej funkcji

```
prepareFormulaSGD(coxData_split) -> formulaSGD
```

Ostatecznie dla 6085 pacjentów, którzy posiadali informacje o występujących mutacjach, oraz dla których odnotowano komplet i poprawność danych klinicznych dotyczących statusu i obserwowanego czasu przeżycia wyliczono współczynniki modelu proporcjonalnych hazardów Coxa z wykorzystaniem stochastycznego spadku gradientu do estymacji. Model dopasowano wielokrotnie z różnymi ciągami odpowiadającymi za długość kroku algorytmu, dodatkowo badano różną ilość epok w algorytmie. Dla tak powstałych kilku modeli wybrano ten, który dla swoich współczynników dawał największą wartość funkcji częściowej log-wiarogodności dla niewykorzystanej do uczenia próbki, zawierającej 2 ostatnie zaobserwowane podzbiory obserwacji. Dla każdego z ciągów  $1/t$ ,  $1/50 * \sqrt{t}$ ,  $100/5 * \sqrt{100}$  odpowiadających długościom kroków w algorytmie wyznaczono współczynniki modelu dla 5 epok, dzięki czemu możliwe było rozważanie postępu danego wariantu algorytmu również po 1, 2, 3 czy 4 epokach.

```
coxData_split[99:100] -> testCox
coxData_split[1:98] -> trainCox
coxphSGD(formulaSGD, data = trainCox, max.iter = 490) -> model_1_over_t
coxphSGD(formulaSGD, data = trainCox, max.iter = 490,
  learningRates = function(t){1/(50*sqrt(t))}) -> model_1_over_50sqrt_t
coxphSGD(formulaSGD, data = trainCox, max.iter = 490,
  learningRates = function(t){1/(100*sqrt(t))}) -> model_1_over_100sqrt_t
```

Niemożliwe było sprawdzenie założeń modelu dotyczących proporcjonalności hazardu, gdyż zakładano napływającą postać danych (stąd podział danych na 100 grup). Dla takiej postaci pojawiania się danych ciężko także mówić o jakiegokolwiek diagnostyce poprawności dopasowania modelu i dokładności otrzymanych współczynników. Nie stworzono teorii pozwalającej badać istotność statystyczną otrzymanych współczynników w modelu, jednak założono, że współczynniki dostatecznie odległe od 0 można uznać za istotnie wpływające na czas życia pacjenta. Współczynniki dodatnie oznaczają zwiększenie hazardu pacjenta posiadającego mutację w danym genie w stosunku do pacjentów nie posiadających mutacji w danym genie. Współczynniki ujemne oznaczają zmniejszenie hazardu pacjenta posiadającego mutację w danym genie w stosunku do pacjentów nie posiadających mutacji w danym genie. Wzrost proporcji hazardu można otrzymać dla danego genu poprzez obłożenie współczynnika funkcją wykładniczą o wykładniku  $e$ .

Wyniki estymacji dla genów zawierających największe co do modułu współczynniki można znaleźć w Tabeli 1.

```

coxphSGD <- function(formula, data, learningRates = function(x){1/x},
                     beta_0 = 0, epsilon = 1e-5, max.iter = 500 ) {
  checkArguments(formula, data, learningRates,
                 beta_0, epsilon) -> beta_start # check arguments
  n <- length(data)
  diff <- epsilon + 1
  i <- 1
  beta_new <- list() # steps are saved in a list so that they can
  beta_old <- beta_start # be traced in the future
  # estimate
  while(i <= max.iter & diff > epsilon) {
    beta_new[[i]] <- coxphSGD_batch(formula = formula, beta = beta_old,
                                     learningRate = learningRates(i), data = data[[ifelse(i%%n==0,n,i%%n)]]) %>%
    unlist
    diff <- sqrt(sum((beta_new[[i]] - beta_old)^2))
    beta_old <- beta_new[[i]]
    i <- i + 1 ; cat("\r iteration: ", i, "\r")
  } # return results
  list(Call = match.call(), epsilon = epsilon, learningRates = learningRates,
       steps = i, coefficients = c(list(beta_start), beta_new))
}

coxphSGD_batch <- function(formula, data, learningRate, beta){
  # collect times, status, variables and reorder samples
  # to make the algorithm more clear to read and track
  batchData <- prepareBatch(formula = formula, data = data)
  # calculate the log-likelihood for this batch sample
  partial_sum <- list()
  foreach(k = 1:nrow(batchData)) %do% {
    # risk set for current time/observation
    risk_set <- batchData %>% filter(times >= batchData$times[k])

    nominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      element * exp(element * beta)
    }) %>% rowSums()

    denominator <- apply(risk_set[, -c(1,2)], MARGIN = 1, function(element){
      exp(element * beta)
    }) %>% rowSums()

    partial_sum[[k]] <-
      batchData[k, "event"] * (batchData[k, -c(1,2)] - nominator/denominator)
  }
  do.call(rbind, partial_sum) %>%
  colSums() -> U_batch

  return(beta + learningRate * U_batch)
}

coxph_loglik <- function(beta, formula, data) {
  coxph(formula, init=beta, control=list('iter.max'=0), data =data)$loglik[2]
}

```

```

as.data.frame(t(simplify2array(model_1_over_t$coefficients[-c(1:6)]))) -> x1
as.data.frame(t(simplify2array(model_1_over_50sqrt_t$coefficients[-c(1:6)]))) -> x2
as.data.frame(t(simplify2array(model_1_over_100sqrt_t$coefficients[-c(1:6)]))) -> x3

library(ggplot2)
qplot(1:length(x1$EGFR), x1$EGFR)

data.frame(coef = x1$BRAF,
            iter = 1:length(x1$BRAF)) %>%
  ggplot(aes(x = iter,
             y = coef)) +
  theme_dark() +
  geom_point(col = "white") +
  xlab('Numer iteracji') +
  ylab('Wartość współczynnika') +
  ggtitle('Zmiany wartości współczynnika dla genu BRAF')

data.frame(coef = x1$EGFR,
            iter = 1:length(x1$EGFR)) %>%
  ggplot(aes(x = iter,
             y = coef)) +
  theme_dark() +
  geom_point(col = "white") +
  xlab('Numer iteracji') +
  ylab('Wartość współczynnika') +
  ggtitle('Zmiany wartości współczynnika dla genu EGFR')

library(dplyr)
bind_rows(x1, x2, x3) -> binded

full_cox_loglik_matrix <- function(beta, x, censored){
  order(x$times) -> order2
  x[order2, ] -> xORD
  censored[order2] -> censORD
  sum(censORD*(beta%*%x[, -which(names(x)=='times')] -
              log(cumsum(exp(beta1*rev(x1) + beta2*rev(x2))))))
}

apply(binded, MARGIN = 1, function(x){
  full_cox_loglik_matrix(unlist(x), testCox_binded[, -1092], testCox_binded[,1092])
}) -> logliks_values

logliks_values %>%
  mutate(model = c(rep("model1", 485),
                    rep("model2", 485),
                    rep("model3", 485))) -> d2viz

dim(d2viz)

```

```

library(tidyr)
gather(d2viz, model) -> d2viz_gathered

dim

calculate_outer_cox_3 <- function(dCox){
  ## contours
  outer_res <- outer(seq(-1,3, length = 100),
                    seq(0,4, length = 100),
                    Vectorize( function(beta1,beta2){
                      coxph_loglik(beta=c(beta1,beta2), Surv(time, status)~x.1+x.2-1, dCox)
                    } )
  )
  outer_res_melted <- melt(outer_res)
  outer_res_melted$Var1 <- as.factor(outer_res_melted$Var1)
  levels(outer_res_melted$Var1) <- as.character(seq(-1,3, length = 100))
  outer_res_melted$Var2 <- as.factor(outer_res_melted$Var2)
  levels(outer_res_melted$Var2) <- as.character(seq(0,4, length = 100))
  outer_res_melted$Var1 <- as.numeric(as.character(outer_res_melted$Var1))
  outer_res_melted$Var2 <- as.numeric(as.character(outer_res_melted$Var2))
  return(outer_res_melted)
}
calculate_outer_cox_3(dCox) -> outerCox

```

```

ggplot() +
  stat_contour(aes(x=outerCox$Var1,
                  y=outerCox$Var2,
                  z=outerCox$value),
              bins = 40, alpha = 0.25) +
  geom_path(aes(d2ggplot$V1, d2ggplot$V2, group = d2ggplot$version,
               colour = d2ggplot$version), size = 1) +
  theme_bw(base_size = 20) +
  theme(panel.border = element_blank(),
        legend.key = element_blank(), legend.position = "top") +
  scale_colour_brewer(palette="Dark2", name = 'Algorithm \n & Steps') +
  geom_point(aes(x = beta_0[1], y = beta_0[2]), col = "black", size = 4, shape = 17) +
  geom_point(aes(x = solution[1], y = solution[2]), col = "black", size = 4, shape = 15) +
  geom_point(aes(x = summary(coxph(Surv(time, status)~x.1+x.2, data = dCox))$coeff[1,1],
                  y = summary(coxph(Surv(time, status)~x.1+x.2, data = dCox))$coeff[2,1],
                  col = "black", size = 4, shape = 13) +
  xlab("X1") + ylab("X2") +
  guides(col = guide_legend(ncol = 3))

```

```

source("https://bioconductor.org/biocLite.R")
biocLite("RTCGA")
biocLite("RTCGA.clinical")
biocLite("RTCGA.mutations")
browseVignettes("RTCGA")

```

```

coxphSGD <- function(formula, data, learningRates = function(x){1/x},
                    beta_0 = 0, epsilon = 1e-5, max.iter = 500 ) {
  # check arguments

```

```

checkArguments(formula, data, learningRates,
               beta_0, epsilon) -> beta_start
n <- length(data)
diff <- epsilon + 1
i <- 1
beta_new <- list()      # steps are saved in a list so that they can
beta_old <- beta_start  # be traced in the future
# estimate
while(i <= max.iter & diff > epsilon) {
  beta_new[[i]] <- coxphSGD_batch(formula = formula, beta = beta_old,
    learningRate = learningRates(i), data = data[[ifelse(i%%n==0,n,i%%n)]]) %>%
    unlist
  diff <- sqrt(sum((beta_new[[i]] - beta_old)^2))
  beta_old <- beta_new[[i]]
  i <- i + 1
  cat("\r iteration: ", i, "\r")
}
# return results
list(Call = match.call(), epsilon = epsilon,
      learningRates = learningRates, steps = i,
      coefficients = c(list(beta_start), beta_new))
}

coxphSGD_batch <- function(formula, data, learningRate, beta){
  # collect times, status, variables and reorder samples
  # to make the algorithm more clear to read and track
  batchData <- prepareBatch(formula = formula, data = data)
  # calculate the log-likelihood for this batch sample
  batchData <- batchData %>% arrange(-times)
  # scores occur in nominator and denominator
  scores <- apply(batchData[, -c(1, 2)], 1,
    function(element) exp(element %*% beta) )
  nominator <- apply(batchData[, -c(1, 2)], 2,
    function(element) cumsum(scores*element) )
  denominator <- cumsum(scores)
  # sum over non-censored observations
  partial_sum <- (batchData[, -c(1, 2)] - nominator/denominator)*batchData[, "event"]
  # each column indicates one explanatory variable
  U_batch <- partial_sum %>% colSums()
  return(beta + learningRate * U_batch)
}

installTCGA()

```