

Initialization of Numerical Optimization in R

Advertising the {ino} Package

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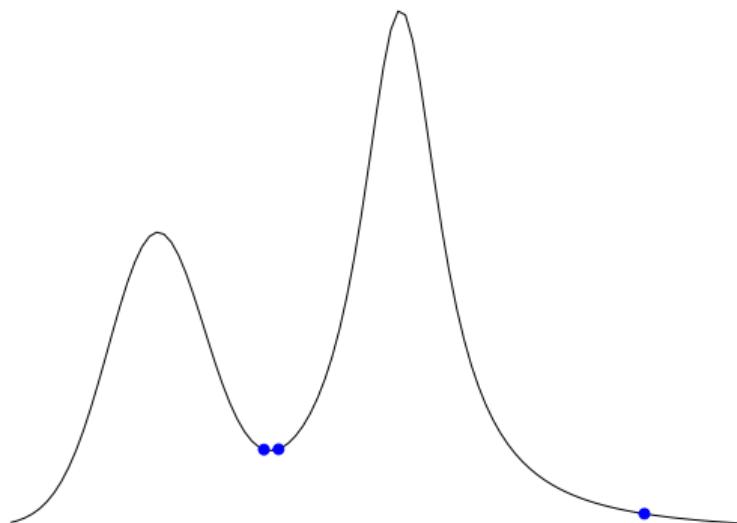
Outline

- 1** What does initialization of numerical optimization mean?
- 2** Why should we as statisticians care?
- 3** We implemented the `{ino}` toolbox in R
- 4** Three package demonstrations
- 5** Takeaways and outlook

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Numerical optimization of f means iteratively adjusting x to find the *globally* best $f(x)$.
And most algorithms need to start at some user-defined **initial value x_0** .



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Depending on x_0 , the optimization

- works fine 😊
- does not work 😞



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And most algorithms need to start at some user-defined **initial value x_0** .

Depending on x_0 , the optimization

- works fine 😊
- does not work 😞
- takes an eternity 😴

The Ackley function is a challenging test for optimizers:

$$f(x, y) = -20 \exp\left(-0.2\sqrt{(x^2 + y^2)/2}\right) - \exp\left(\frac{\cos(2\pi x) + \cos(2\pi y)}{2}\right) + 20 + \exp(1)$$

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We seek to globally optimize log-likelihood functions:

- Probit model

$$f(\boldsymbol{\theta} = (\beta, \Sigma) | X, y) = \sum_{n,j} 1(y_n = j) \log \Phi_{0, \Delta_j \Sigma \Delta'_j}(-\Delta_j X_n \beta)$$

- Hidden Markov model

$$f(\boldsymbol{\theta} = (\Gamma, \mu, \sigma, \delta) | X, N) = \log \delta P(x_1 | \mu, \sigma, N) \Gamma P(x_2 | \mu, \sigma, N) \cdots \Gamma P(x_T | \mu, \sigma, N) \mathbf{1}'$$

- Gaussian mixture model (two classes)

$$f(\boldsymbol{\theta} = (\pi, \mu, \sigma) | X) = \sum_n \log \left(\pi \phi_{\mu_1, \sigma_1^2}(x_n) + (1 - \pi) \phi_{\mu_2, \sigma_2^2}(x_n) \right)$$

We seek to globally optimize log-likelihood functions:

- Probit model

$$f(\boldsymbol{\theta} = (\beta, \Sigma) \mid \textcolor{blue}{X}, \textcolor{blue}{y}) = \sum_{n,j} 1(y_n = j) \log \Phi_{0, \Delta_j \Sigma \Delta'_j}(-\Delta_j \mathbf{X}_n \beta)$$

- Hidden Markov model

$$f(\boldsymbol{\theta} = (\Gamma, \mu, \sigma, \delta) \mid \textcolor{blue}{X}, N) = \log \delta P(x_1 \mid \mu, \sigma, N) \Gamma P(x_2 \mid \mu, \sigma, N) \cdots \Gamma P(x_T \mid \mu, \sigma, N) \mathbf{1}'$$

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They depend on observed data, which yields ideas for initialization strategies.

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The {ino} package

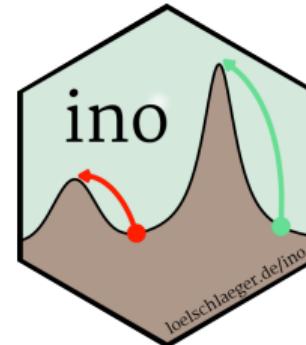
An R package to compare

1. any optimizer for any real-valued function
2. different initialization strategies

Designed to be user-friendly

1. only a single R6 object
2. every user input is validated
3. detailed function documentation and vignettes

And some more convenience, like parallel optimization, progress bar, standardized outputs of optimizers, time limit for long optimizations, trace of optimization path, plots, etc.



```
ackley <- TestFunctions::TF_ackley
ackley(c(0, 0))
```

```
## [1] 4.440892e-16
```

```
ackley <- TestFunctions::TF_ackley
ackley(c(0, 0))

## [1] 4.440892e-16

Nop$new(f = ackley, npar = 2)$
  set_optimizer(optimizer_nlm())$ 
  initialize_fixed(list(c(1, 4), c(1, 3), c(3, 3)))$ 
  optimize()$ 
  summary(c("value", "parameter", "initial"), digits = 2)

##   value parameter initial
## 1  2.58  0.95, 0.00    1, 4
## 2  0.00      0, 0    1, 3
## 3  6.56  1.97, 1.97    3, 3
```

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Speed up probit likelihood maximization

First package demonstration: fitting a probit model.

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- connects covariates X_n to discrete choices y_n
- via latent utilities U_n that are defined as
 1. a linear function $V_n = X_n\beta$
 2. plus a Gaussian error ε_n

$$U_n = V_n + \varepsilon_n$$

$$V_n = X_n\beta$$

$$\varepsilon_n \sim N(0, \Sigma)$$

$$y_n = \arg \max U_n$$

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The probit likelihood sums multiple Gaussian CDFs.

- ⇒ Optimization is time-consuming.
⇒ Good initial values can save time in comparison to random initialization.

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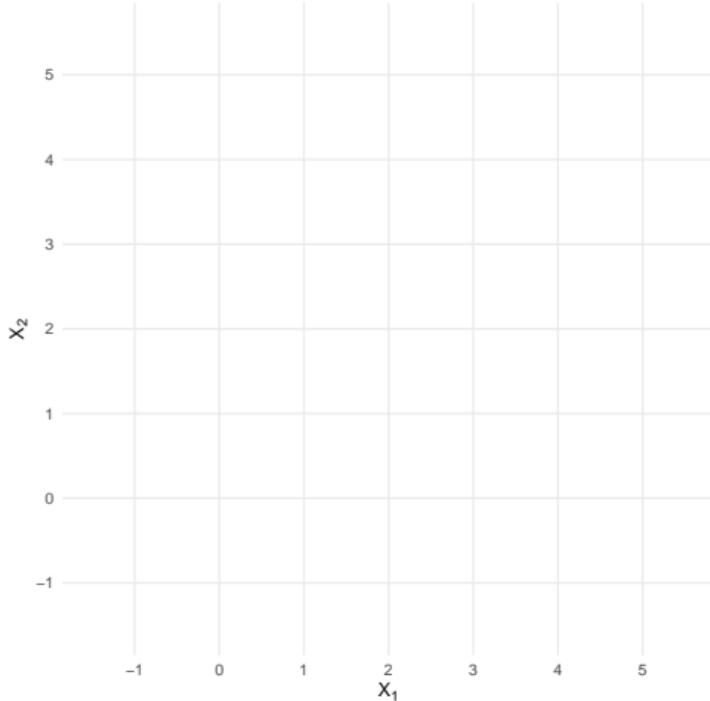
$$y_n = \arg \max U_n$$

The probit likelihood sums multiple Gaussian CDFs.

- ⇒ Optimization is time-consuming.
- ⇒ Good initial values can save time in comparison to random initialization.

We developed an initialization strategy that can be tested via `{ino}`.

Speed up probit likelihood maximization

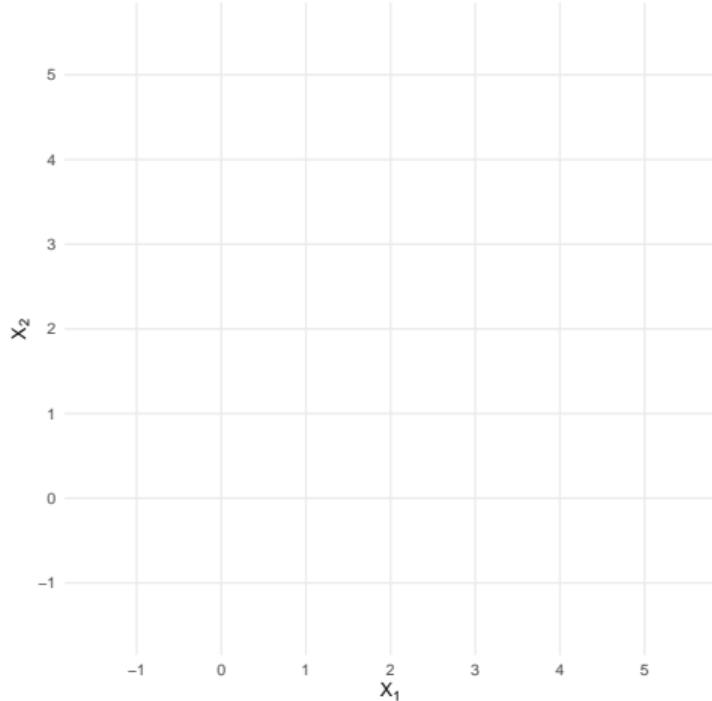


Assume

$$\begin{pmatrix} V_1 \\ V_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix}$$

(such a definition is typical for alternative-varying X with alternative-specific β , e.g., travel time)

Speed up probit likelihood maximization



Assume

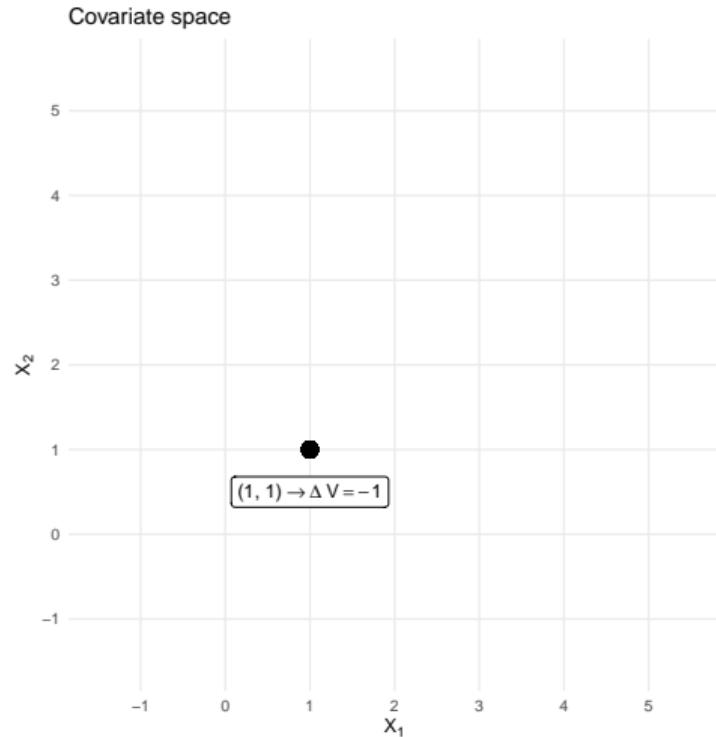
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Let

$$\begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix} = \begin{pmatrix} 1 \\ 2 \end{pmatrix}$$

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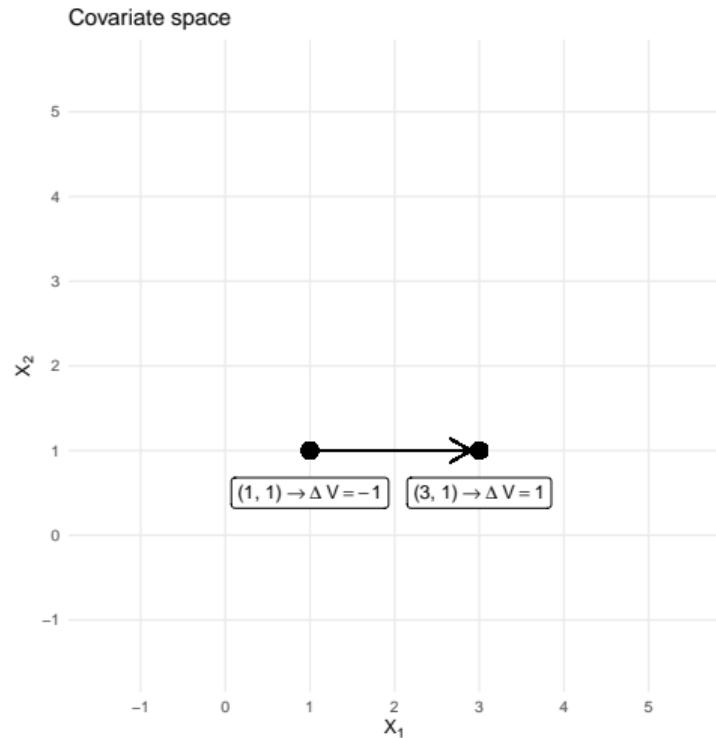
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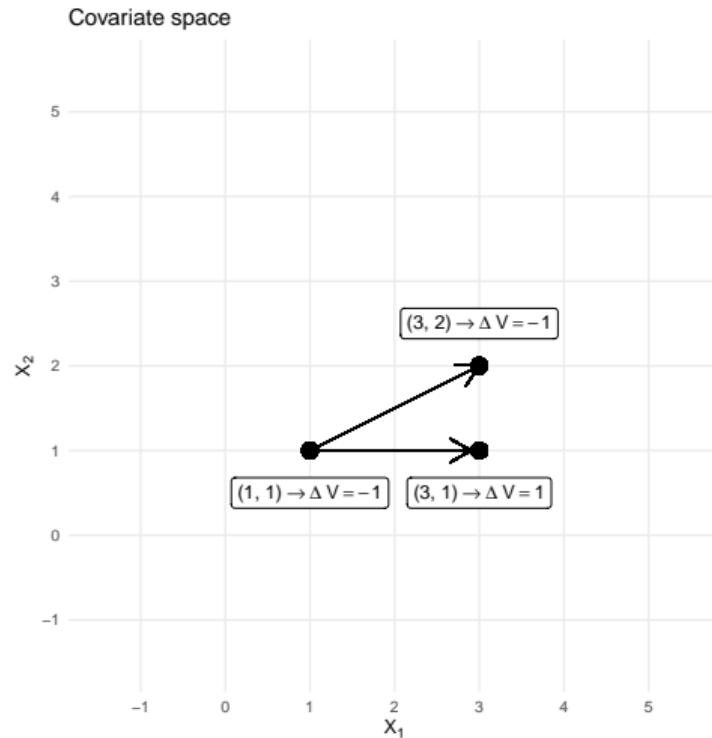
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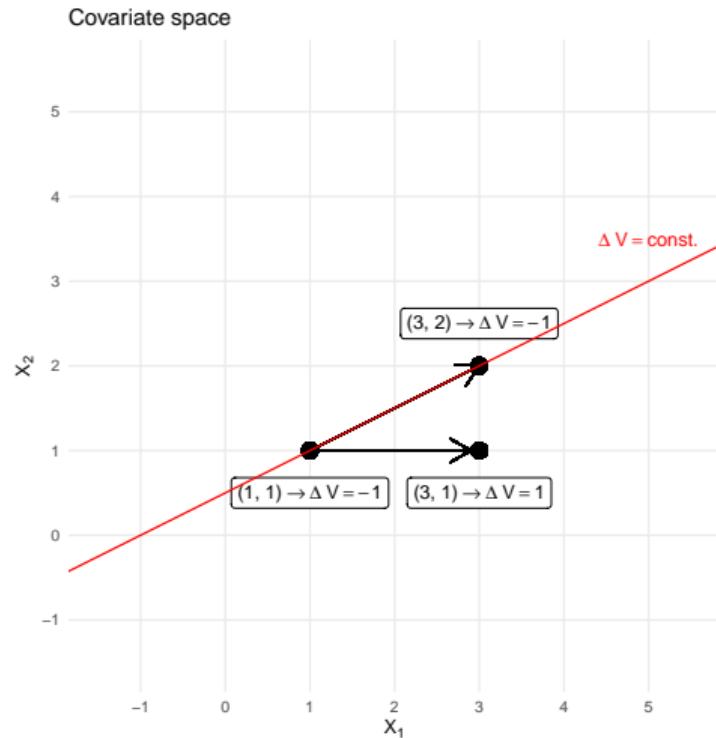
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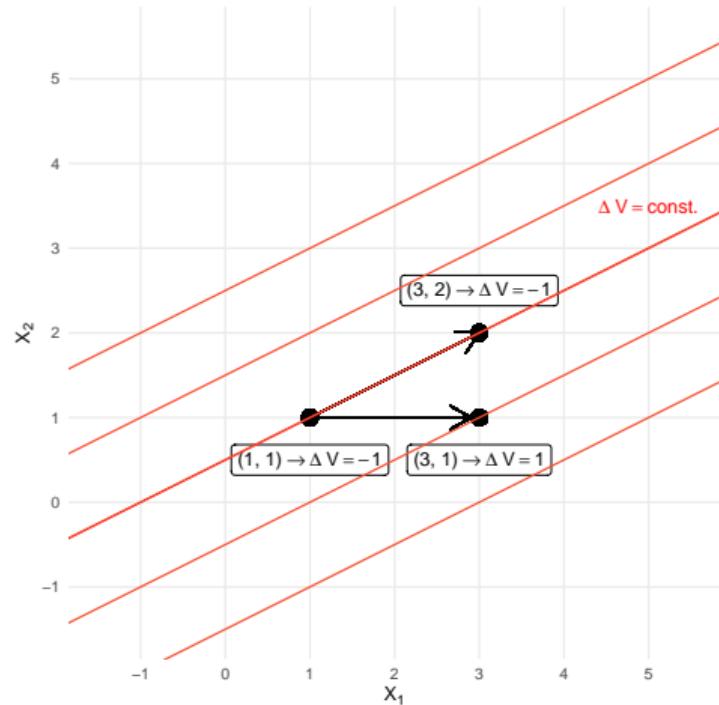
We find the direction

$$\overrightarrow{\begin{pmatrix} 1 \\ 0.5 \end{pmatrix}} = \overrightarrow{\begin{pmatrix} 1/\beta_1 \\ 1/\beta_2 \end{pmatrix}}$$

in which $\Delta V = V_1 - V_2 = \text{const.}$

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Covariate space



Assume

$$\begin{pmatrix} V_1 \\ V_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix}$$

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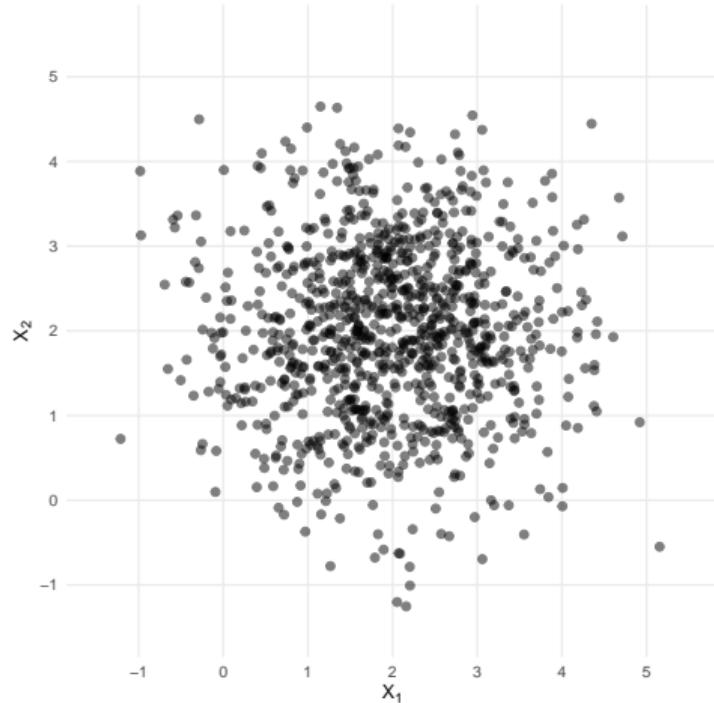
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Speed up probit likelihood maximization

Simulated data with N = 1000



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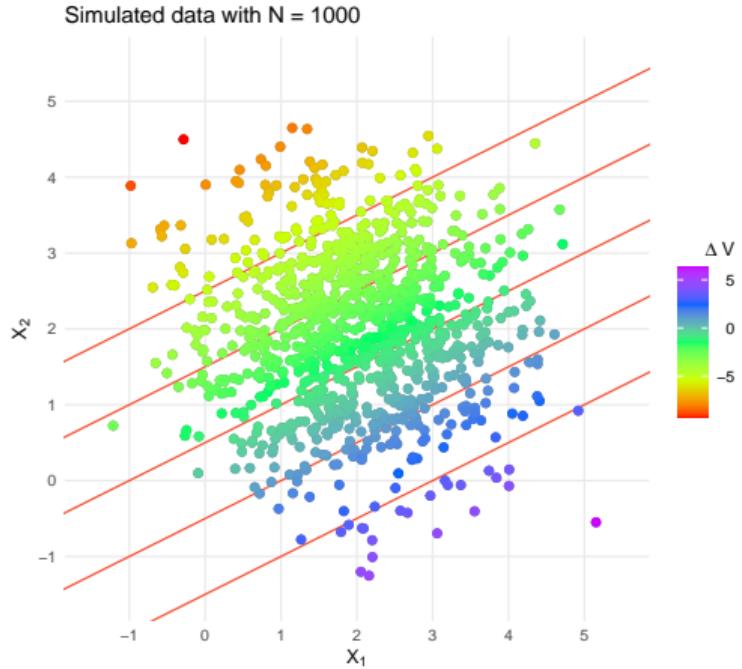
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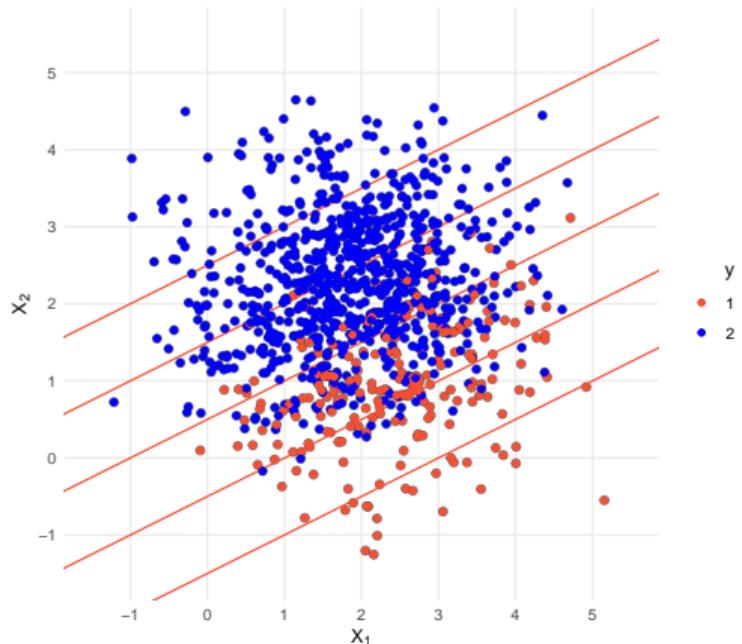
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Speed up probit likelihood maximization

Simulated data with $N = 1000$

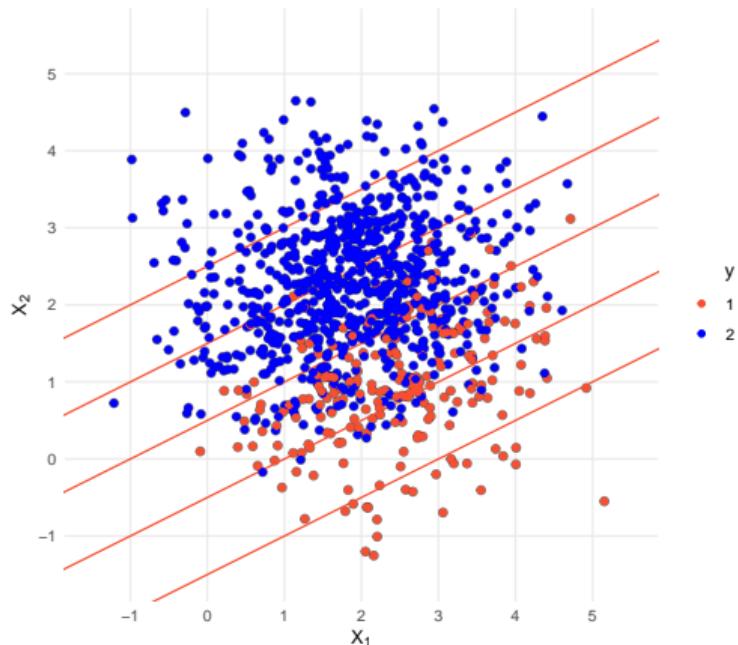


We do not observe ΔV

(depends on the unknown β)
but we observe the choices y .

Speed up probit likelihood maximization

Simulated data with $N = 1000$



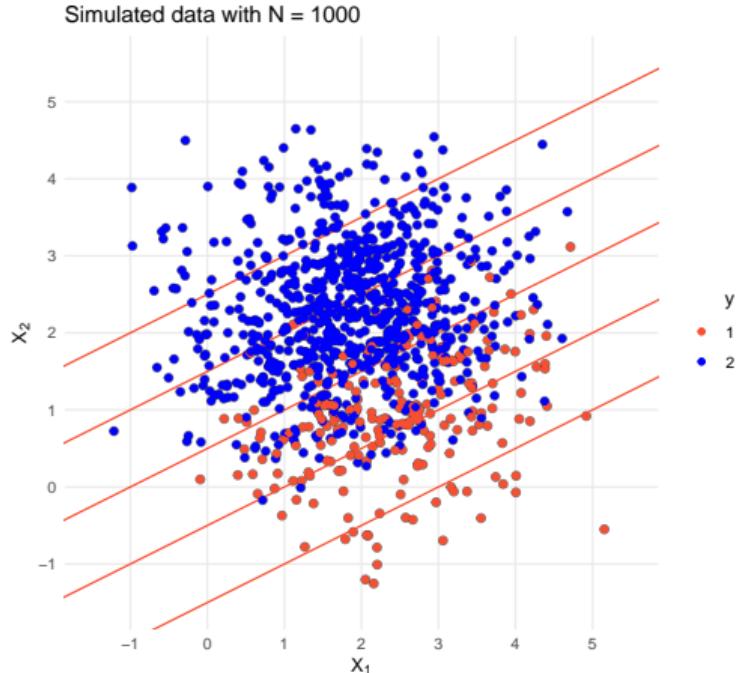
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They are disturbed by the error-term ε .

(here I used $\Sigma = \begin{pmatrix} 2 & 1 \\ 1 & 2 \end{pmatrix}$)

Speed up probit likelihood maximization



We do not observe ΔV

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They are disturbed by the error-term ε .

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But we can still identify

$$\overrightarrow{\begin{pmatrix} 1/\beta_1 \\ 1/\beta_2 \end{pmatrix}}$$

as the kernel of $\text{Cor}(X, y)$.

(constant choice probability in this direction)

This strategy can easily be tested with {ino}:

```
beta <- c(1, -1, 2)
Sigma <- matrix(c(2, 1, 0, 1, 2, 1, 0, 1, 2), 3)
J <- nrow(Sigma)
P <- length(beta)

Nop_probit <- Nop$new(f = logLik_probit, npar = 5, fix_beta1 = 1)$
  set_optimizer(optimizer_nlm())

for (i in 1:100) {

  probit_data <- sim_mnp(
    N = 200, J = J, P = P, beta = beta, Sigma = Sigma,
    X = function(n) diag(stats::rnorm(P))
  )
  direction <- find_direction(probit_data, fix_beta1 = 1)

  Nop_probit$  

    argument("set", data = probit_data)$
    initialize_random()$  

    optimize(optimization_label = "random", which_direction = "max")$  

    initialize_fixed(at = c(direction, stats::rnorm(J * (J - 1) / 2)))$  

    optimize(optimization_label = "strategy", which_direction = "max")
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```

</> For the implementations of logLik_probit and sim_mnp see the {ino} probit application vignette. The implementation of find_direction can be provided on request.

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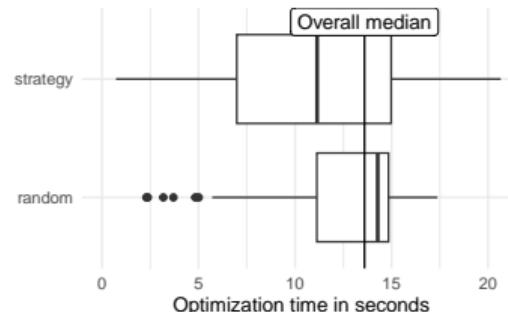
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```

Nop_probit\$plot(group_by = ".optimization_label")



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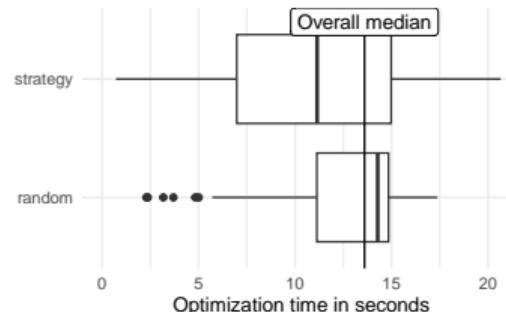
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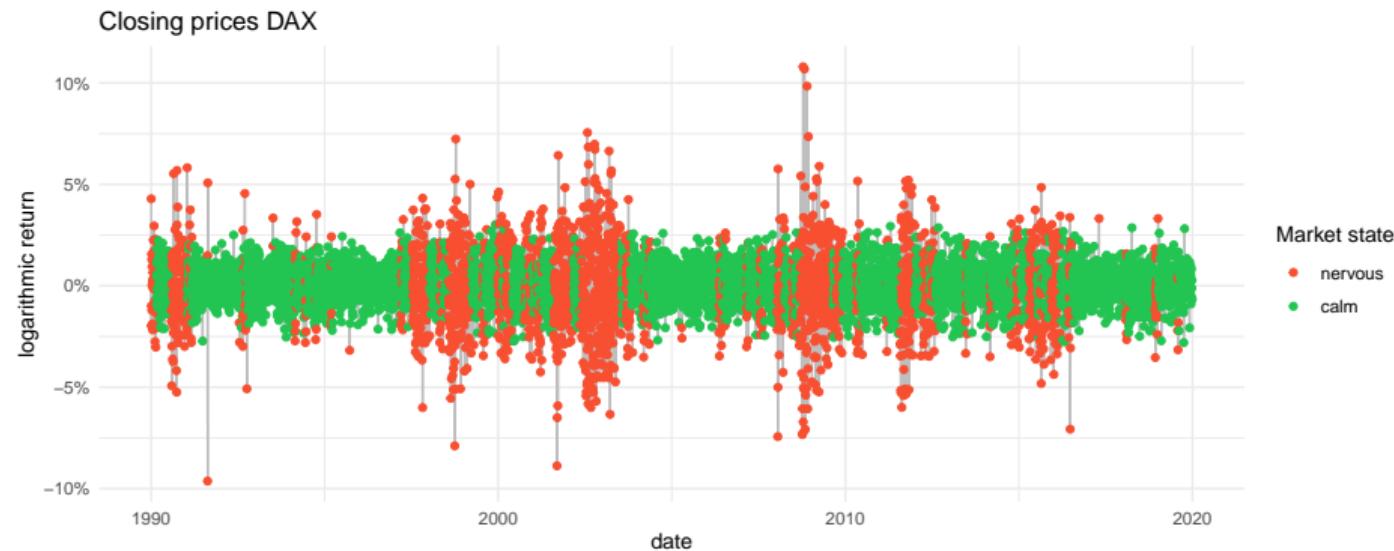
Nop_probit\$plot(group_by = ".optimization_label")



Conclusion: computation time reduced by 1/3
(will be more pronounced for more covariates / observations)

</> For the implementations of logLik_probit and sim_mnp see the {ino} probit application vignette. The implementation of find_direction can be provided on request.

Second package demonstration: fitting a two-state HMM.



HMMs are known to have multiple local optima, let's see how many we can find here:

```
Nop_hmm <- Nop$new(f = logLik_hmm, npar = 6, data = dax$logreturn, N = 2)$  
set_optimizer(optimizer_nlm())$  
initialize_random(runs = 100, seed = 1)$  
optimize(optimization_label = "random", which_direction = "max", reset_initial = FALSE)
```

</> For the implementation of `logLik_hmm` see the `{ino}` HMM application vignette.

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initialize_random(runs = 100, seed = 1)$  
optimize(optimization_label = "random", which_direction = "max", reset_initial = FALSE)
```

Get an overview of the optima:

```
Nop_hmm$optima(digits = 0)
```

```
##   value frequency  
## 1 22446       67  
## 2 21372       32  
## 3 20755        1
```

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HMMs are known to have multiple local optima, let's see how many we can find here:

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```

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```
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```

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## 1 22446      67  
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Get the best parameter:

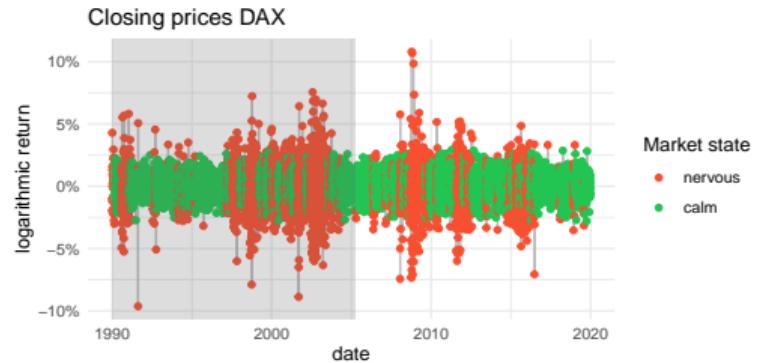
```
Nop_hmm$best("parameter", which_direction = "max",  
digits = 2)
```

```
## [1] -4.52 -3.70  0.00  0.00 -3.86 -4.72  
## attr(,".run_id")  
## [1] 64  
## attr(,"optimizer_label")  
## [1] "stats::nls"
```

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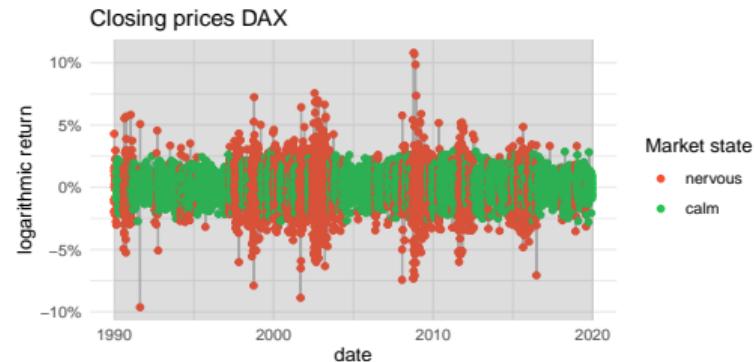
A simple idea to reduce computation time:

1. fit the HMM to the first 50% data



A simple idea to reduce computation time:

1. fit the HMM to the first 50% data
2. use the estimates as initial values for the estimation on the full data set



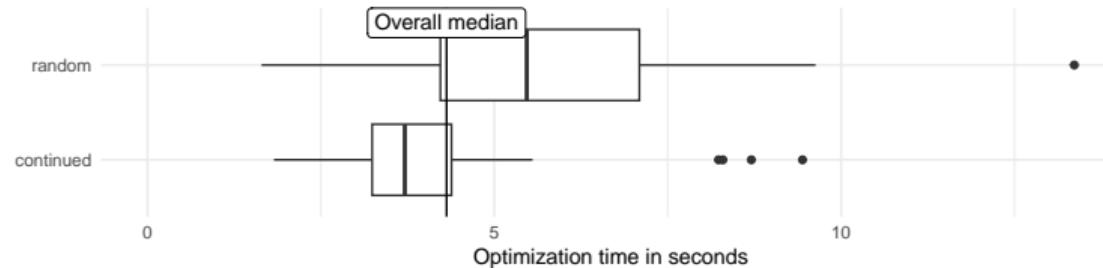
Will adding computation time from 1. and 2. be faster than full data estimation directly?

This idea can easily be tested with {ino}:

```
Nop_hmm$  
  argument("subset", name = "data", how = "first", proportion = 0.5)$  
  optimize(which_direction = "max")$  
  argument("reset", name = "data")$  
  initialize_continue()$  
  optimize(optimization_label = "continued", which_direction = "max")$  
  plot(group_by = ".optimization_label")
```

This idea can easily be tested with {ino}:

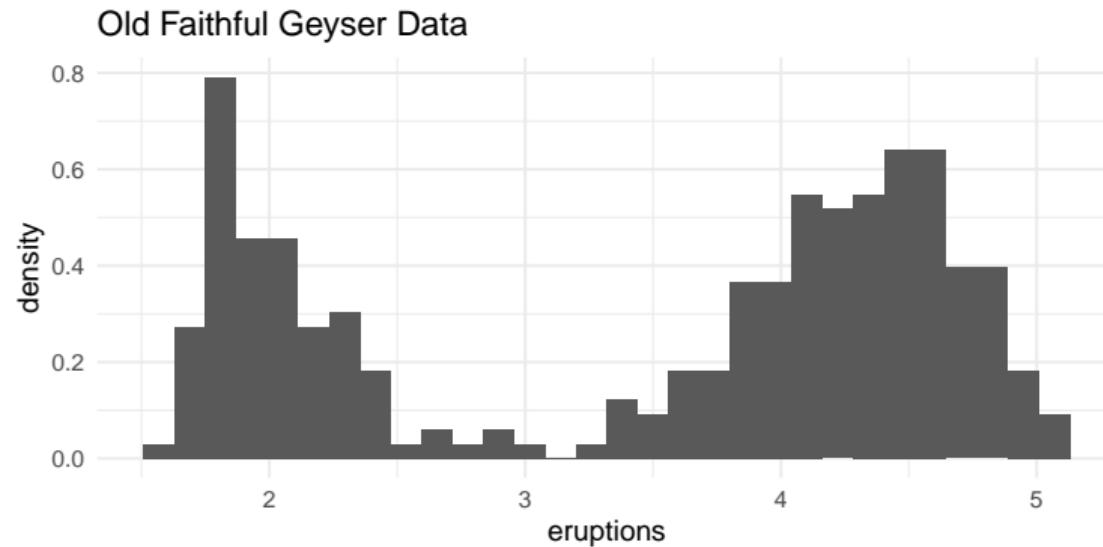
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```



Conclusion: reduces computation time a bit (will probably be more pronounced for more complex models)

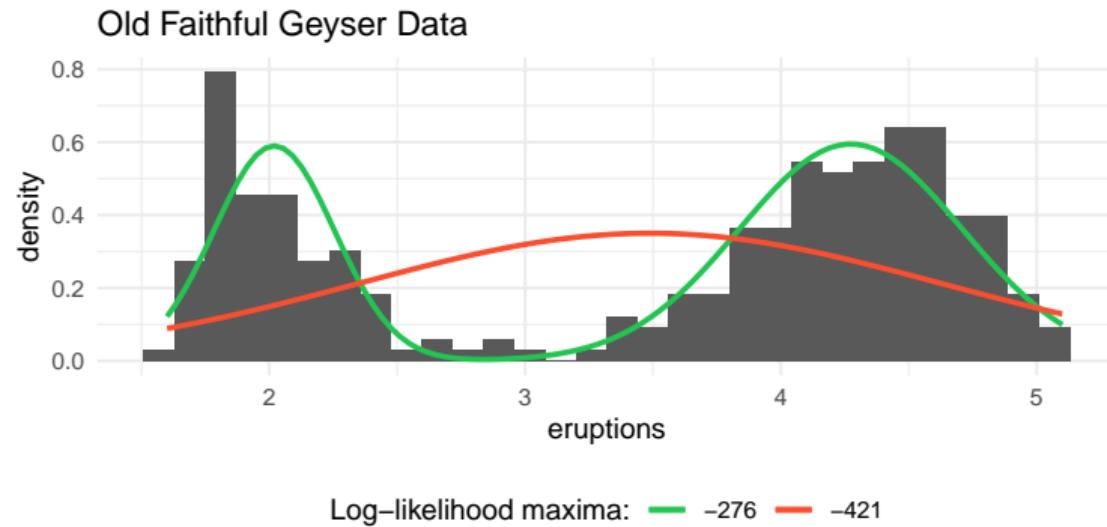
The EM-algorithm for mixture models

Third and final package demonstration: fitting a two-class Gaussian mixture model.



The EM-algorithm for mixture models

Third and final package demonstration: fitting a two-class Gaussian mixture model.



Depending on the initial value, either a **sensible** or a **one-class solution** is estimated.

Two popular approaches:

1. Gradient-based optimization
2. EM-algorithm

Which one is faster and will reach **-276** more often than **-421**?

</> For the implementations of `logLik_mixture` and `optimizer_em` see the `{ino}` introductory vignette.

Two popular approaches:

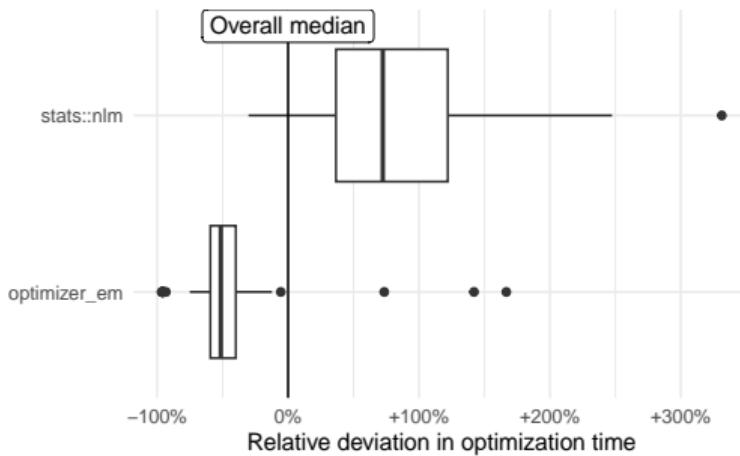
1. Gradient-based optimization
2. EM-algorithm

Which one is faster and will reach **-276** more often than **-421**? Easy comparison with {ino}:

```
Nop_mixture <- Nop$new(  
  f = logLik_mixture, npar = 5, data = faithful$eruptions  
)$  
set_optimizer(optimizer_nlm())$  
set_optimizer(optimizer_em)$  
initialize_random(sampler = function() rnorm(n = 5), runs = 100, seed = 1)$  
optimize(which_direction = "max")
```

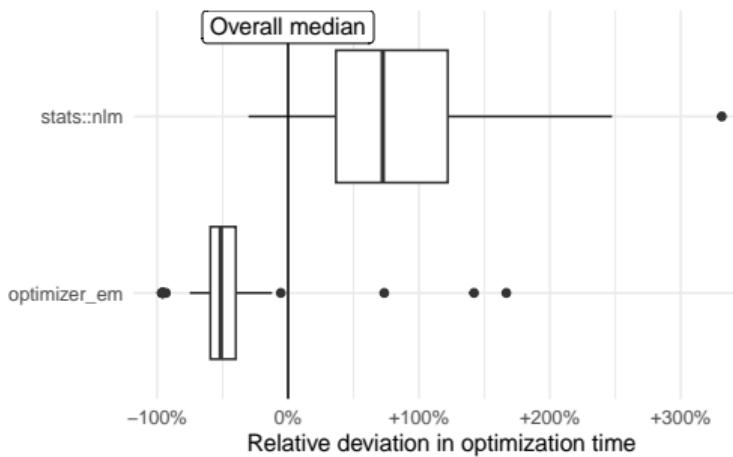
</> For the implementations of logLik_mixture and optimizer_em see the {ino} introductory vignette.

```
Nop_mixture$plot(  
  group_by = ".optimizer_label",  
  relative = TRUE  
)
```



The EM-algorithm for mixture models

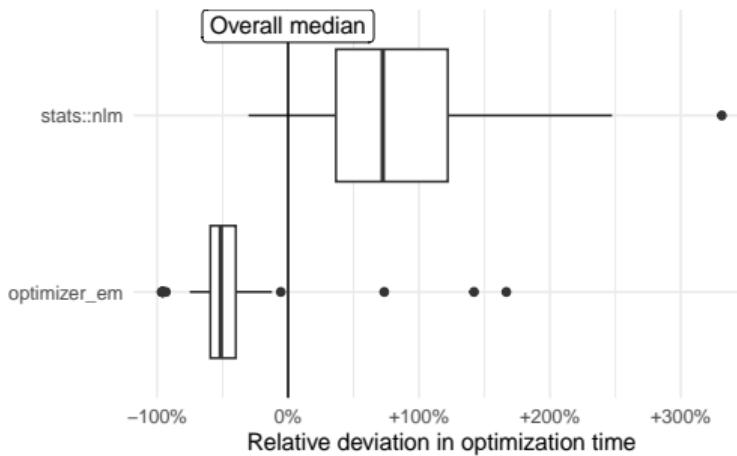
```
Nop_mixture$plot(  
  group_by = ".optimizer_label",  
  relative = TRUE  
)
```



```
Nop_mixture$optima(  
  group_by = ".optimizer_label", digits = 0  
)  
  
## $optimizer_em  
##   value frequency  
## 1  -276      79  
## 2  <NA>      12  
## 3  -421      9  
##  
## $`stats::nlm`  
##   value frequency  
## 1  -421      79  
## 2  -276      20  
## 3  -340      1
```

The EM-algorithm for mixture models

```
Nop_mixture$plot(  
  group_by = ".optimizer_label",  
  relative = TRUE  
)
```



```
Nop_mixture$optima(  
  group_by = ".optimizer_label", digits = 0  
)  
  
## $optimizer_em  
##   value frequency  
## 1  -276      79  
## 2  <NA>      12  
## 3  -421      9  
##  
## $`stats::nlm`  
##   value frequency  
## 1  -421      79  
## 2  -276      20  
## 3  -340      1
```

Conclusion: EM is superior (at least in this example)

Outline

- 1 What does initialization of numerical optimization mean?
- 2 Why should we as statisticians care?
- 3 We implemented the `{ino}` toolbox in R
- 4 Three package demonstrations
- 5 Takeaways and outlook

- Clever initialization in numerical likelihood optimization likely
 1. reduces computation time and
 2. increases the probability of reaching the global optimum
- `{ino}` simplifies comparing initialization strategies and optimization methods
- Test it for your problem and share the outcomes with us!
- Next step: crafting a package manual for the RJournal

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Thanks for your attention! Do you have any questions or comments? 😊

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