

fitcorridor vignette v1.0.0

Tristan Nuñez

2022-07-12

This vignette accompanies the article “A statistical framework for predicting migration corridors” by Nuñez, T., Hurley, M., Graves, T. Ortega, A. Sawyer, H., Fattebert, J., Merkle, J., and Kauffman, M., accepted for publication in *Methods in Ecology and Evolution*, and the fitcorridor code to go with it.

The fitcorridor code fits cost-distance models to animal movement tracks.

The fitcorridor model fitting code will be updated in the future (including conversion to R package format). Check the github page for the latest version at github.com/tristannunez/fitcorridor.

Getting Started

Review the manuscript, which outlines the calculations and algorithms involved in fitting cost-distance models to movement tracks; Figure 1 and Sections 2.2 through 2.8 of the Methods section are particularly relevant.

Prerequisites

The code requires the following R packages be installed: gdistance, parallel, rgdal, ggplot2, ggspatial, and rgeos. Make sure they are installed before proceeding.

Let's fit a cost-distance model!

We'll begin by fitting a cost distance model to a set of simulated movement tracks. The model we will fit is $conductance = e^{\beta \cdot HumanFootprint}$. For each movement track, the code will find the value of β that maximizes the likelihood of the data given the model. It will also find the optimal value of λ , the rate parameter of the exponential distribution used to model the probability of deviations from the least cost path (see Methods Section 2.4 in the manuscript). $1/\lambda$ is the mean residual cost distance of the fitted distribution, allowing us to directly assess how far on average an animal deviates from the modeled least cost path in cost distance units.

Setting up

First, make sure your working directory is the fitcorridor folder:

```
getwd()
#> [1] "C:/Users/Tristan/Desktop/github/fitcorridor"
```

Source the R file containing the functions.

```
source("./fitcorridor_functions.R")
```

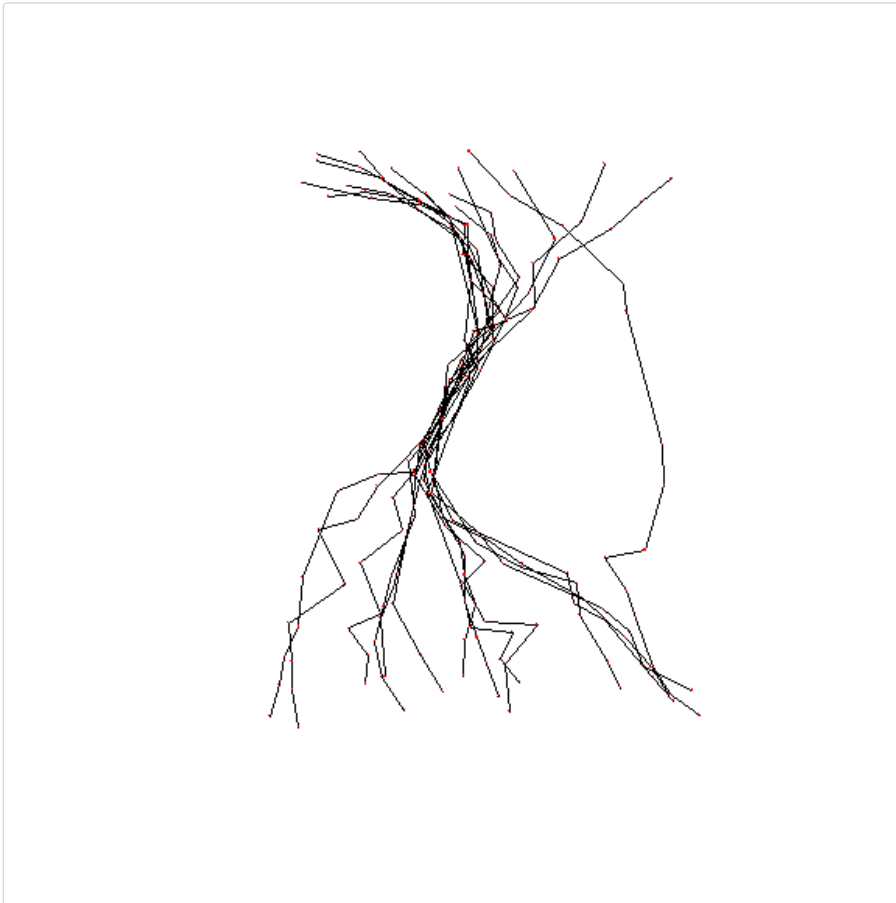
Read in the animal movement tracks. In this case, we will be using a set of 15 tracks simulated from a human footprint surface.

```
tracks<-readOGR("./data/tracks/HF_sim_tracks.shp", stringsAsFactors = F)
#> OGR data source with driver: ESRI Shapefile
#> Source: "C:/Users/Tristan/Desktop/github/fitcorridor/data/tracks/HF_sim_tracks.shp", Layer:
    "HF_sim_tracks"
#> with 208 features
#> It has 4 fields
# Set the coordinate reference system
mycrs <- "+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs +towgs84=0,0,0"
crs(tracks) <- mycrs
# turn the tracks into SpatialLinesDataFrame just for plotting
tracks$id <- tracks$trackid # TrackSPDFtoTrackSPLLines requires an $id column
```

```

tracks.as.lines <- TrackSPDFtoTrackSPLFLines(tracks)
plot(tracks.as.lines)
plot(tracks, add=T, col="red", pch=".", cex=1.2)

```

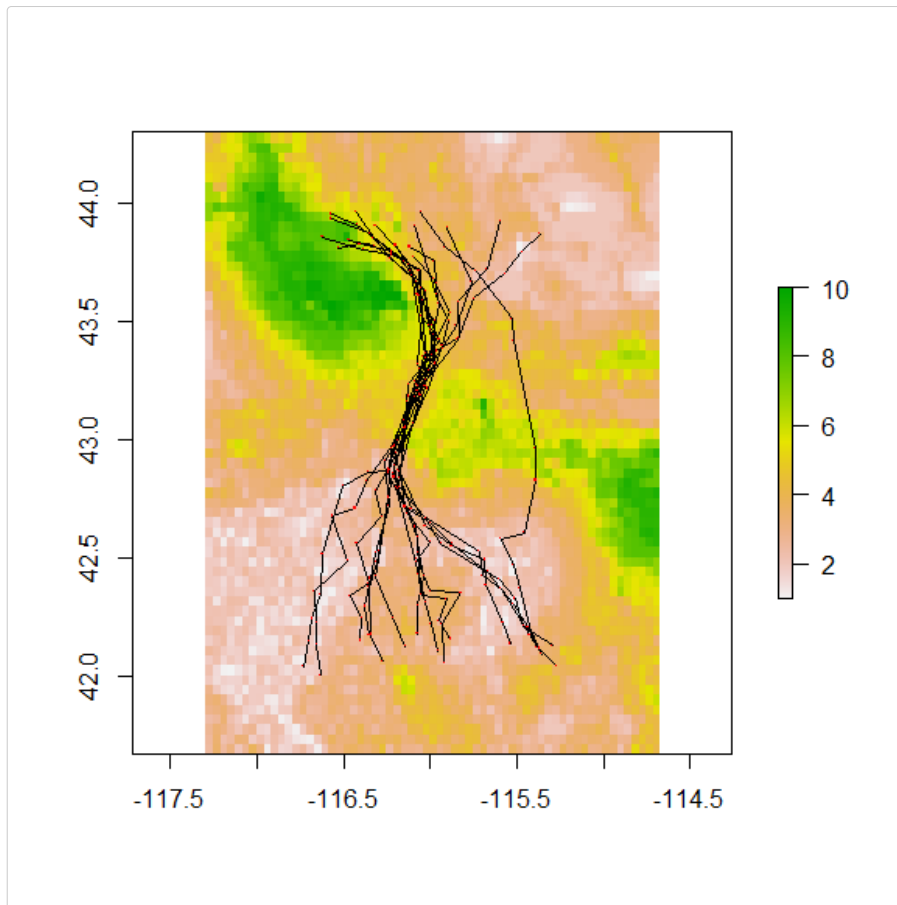


Read in the environmental covariates. Here, we will read in the human footprint surface previously used to simulate the movement tracks. This data is from Leu et al. 2008 (<https://doi.org/10.1890/07-0480.1>, <http://sagemap.wr.usgs.gov/>), cropped to the Boise, ID area.

```

# Higher values represent more human influence
covars <- brick("./data/covariates/HF.tif")
# specify the Coordinate Reference System
crs(covars) <- mycrs
# assign names to layers
names(covars) <- c("HF") # if more than one layer, use this format: c("HF", "DEM")
# plot to check
plot(covars)
plot(tracks.as.lines, add=T, cex=.75)
plot(tracks, add=T, pch=".", col="red", cex=1.2)

```



The simulated tracks, which move between randomly selected start and end points in the upper and lower quarter of the human footprint raster, avoid areas of high human footprint. This is because they were simulated using a β value of -1.

Running the model fitting code

Now that we have read in the inputs, we can fit the cost distance model $conductance = e^{\beta \cdot HumanFootprint}$ to the movement tracks. We do this using the `FitSingleModel` function:

```
FitSingleModel(
  tracks = tracks,
  covars = covars,
  model.to.fit = "iso(HF)",
  neighbors = 8,
  covar.aggregate = 1,
  covar.standardize = c(1),
  param.factor = c(1),
  startval.string = c(-5, 0),
  dataset = "SimHerd1",
  out.folder.path = "./fittedmods/",
  n.inside.cores = 4,
  Lt.tiff = T
)
#> Warning in .local(x, ...): all fact(s) were 1, nothing to aggregate
```

This takes around ten minutes on a PC laptop (Intel(R) i7 CPU @ 2.90GHz with 4 cores). Disregard the “In `.local(x, ...)`: all fact(s) were 1, nothing to aggregate” warning. Let’s explore each of the arguments for the `FitSingleModel` function:

tracks

A `SpatialPointsDataFrame`. The dataframe needs to have a ‘trackid’ column with a unique id for each movement

track. Must have the same coordinate reference system as `covars`. The movement track needs to be a directed movement, so that it is consistent with the assumptions of cost distance modeling, particularly that the animal is acting to minimize its movement costs (or maximize its movement benefits) as it moves between the start and end of the track. For example, any loops (a track doubling back on itself) would violate this assumption and inflate the amount of variance in the model fit.

covars

A Raster* object. Must have the same crs as `tracks`. Must have the same names (use `names(covars)` to check) as the variable names in `model.to.fit`; for example, if `model.to.fit` is "iso(HF)+iso(DEM)," then HF and DEM should be the names of layers found in `covars` (the order of the variables in the model do not need to be in the same order as the order of the variables in `covars`). `covars` must have an extent not just larger than `tracks`, but sufficiently large that the spatial likelihood surfaces generated in modeling approach zero at their boundaries. This is established with trial and error, but using an extent 1.3 to 1.5 times larger than the extent of `tracks` is a good starting point.

model.to.fit

A character string. Specifies the variables to be included in the model as well as the type of cost-distance calculation to be used. `iso()` results in an isotropic cost distance calculation, and `aniso()` results in an anisotropic (stepwise difference) cost distance calculation. For example, if we use "HF" and "DEM" as variable names for Human Footprint and Elevation, respectively, then the model $e^{\beta_1 \cdot \text{HumanFootprint} + \beta_2 \cdot \text{Elevation}_{diff}}$ would be specified as "iso(HF)+aniso(DEM)". Note there are no spaces and "+" is used to separate terms, and that the variable names must be the same as the names of the layers in the `covars` Raster* object. See the manuscript for descriptions and uses of isotropic and anisotropic calculations.

neighbors

The number of directions in which cells are connected (4 (rook's case), 8 (queen's case), 16 (knight and one-cell queen moves), or other), see `?raster::adjacent`.

covar.aggregate

A positive integer. Controls how `covar` is spatially aggregated to speed computation by reducing resolution. It is the aggregation factor expressed as number of cells in each direction (horizontally and vertically). This is passed to the "fact" argument of `raster::aggregate()`, see documentation of that function for more details. A value of 1 will keep the original resolution of `covar`, but will throw this warning: "In `.local(x, ...)` : all fact(s) were 1, nothing to aggregate".

covar.standardize

A numeric vector with the same length as the number of terms in `model.to.fit` (the terms are separated by "+"). Specifies for each term in `model.to.fit` whether that variable should be standardized by the `raster::scale()` function; a value of 1 will standardize, whereas a value of 0 will not standardize the variable. As currently implemented, the code only scales, but does not center the variable (see `raster::scale()` for details. Generally, isotropic variables are scaled and anisotropic variables are not scaled, in order to aid in model fitting convergence.

param.factor

A numeric vector with the same length as the number of terms in `model.to.fit`. This factor multiplies the β coefficient. A value of 1 has no effect; for isotropic variables, use 1. For unstandardized anisotropic variables, try 10 or 100 for elevation (in meters), and 100 or 1000 for variables with Julian day units, such as snow-off date.

startval.string

A numeric vector that specifies the starting value for each parameter (including `log(lambda)`) for the optimization routine. `startval.string` is one element longer than the number of terms in `model.to.fit`. The first element of the vector is the start value for `log(lambda)`, and typically a value between -5 and -10 works well for this. The remaining elements correspond to the model terms (in order), and 0 (no effect) generally works well for these.

dataset

A character string that names the output folder. It can be the name of the animal herd, population, or individual

that the tracks in `tracks` come from, or any other useful descriptor.

out.folder.path

A character string that names the folder where outputs from running the model should be written. Note that the folder name should be enclosed by `./` and `/`, as in `"/fittedmods/"`

n.inside.cores

A positive integer specifying how many cores are used in the parallel computing portion of the model fitting process. Should be less than the number of available cores and less than the number of movement tracks in `tracks`. See the help for `parallel::makeCluster()`.

Lt.tiff

Logical. If TRUE, the spatial likelihood surfaces for each track (L_t) and for all tracks in `tracks` (L_h) will be written out as GeoTiffs, as well as a plot of L_h .

Exploring the model outputs

Check the `"/fittedmods/SimHerd1/iso(HF)"` folder to explore the results! First, we can look in the output folder for this dataset and model to see the contents:

```
dir("./fittedmods/SimHerd1/iso(HF)")
#> [1] "AIC_etc.csv"      "beta_hs_w_95CIs.csv" "beta_ts.csv"
#> [4] "betas_boxplot.png" "indivtrackfits"      "L_h.png"
#> [7] "Lh_raster.tif"    "Likprofiles"         "Lt_rasterstack.tif"
```

AIC_etc.csv

The first CSV file `AIC_etc.csv` contains information about the model fit including AIC, the negative log likelihood, and estimates of $\log(\lambda)$ at the herd level.

```
knitr::kable(read.csv("./fittedmods/SimHerd1/iso(HF)/AIC_etc.csv"))
```

nll_h	loglambda.mean	loglambda.sd	alltrackconverge	AIC	AICc	k	ntracks	model	dataset	resolution
1035.675	-7.121744	0.6535592	1	2075.35	2076.35	2	15	iso(HF)	SimHerd1	0.0416667

- `nll_h` is the negative log likelihood of the herd (ie., $-\log(l_h)$ from the manuscript)
- `loglambda.mean` and `loglambda.sd` are the mean and standard deviation of the estimates of $\log(\lambda)$ for each track
- `alltrackconverge` is a Boolean: 1 if the optimization converged in the `optim()` function for all tracks; 0 if not
- `AIC` is the AIC of the model, and can be used to compare this model to the fits of other models.
- `AICc` is the AICc of the model
- `k` is the number of parameters in the model (number of model terms + 1 for λ)
- `ntracks` is the number of individual movement tracks
- `model` is the model that was run
- `dataset` is the name assigned to the collection of tracks (corresponds to herd in the manuscript)
- `resolution` is the cell size in the units of the coordinate reference system. Assumes square pixels
- `neighbors` is the number of neighbors used in the analysis

beta_hs_w_95CIs.csv

```
knitr::kable(read.csv("./fittedmods/SimHerd1/iso(HF)/beta_hs_w_95CIs.csv"))
```

loglambda	HF	descr
-6.7909977	-0.8893714	upper95CI_SEMmethod
-7.1217443	-1.0399086	beta_h
-7.4524909	-1.1904459	lower95CI_SEMmethod
1.0000000	1.0000000	signif95CI_SEMmethod
0.6535592	0.2974634	stddev.of.beta_ts
-7.9802359	-1.2312035	lower95CI_mean_of_hessian_method
-6.2632527	-0.8486138	upper95CI_mean_of_hessian_method
0.1687483	0.0768047	std.err.mean

beta_hs_w_95CIs.csv contains information about the fitted coefficients – this is where to look to assess the effect of environmental covariates on your movement tracks. Each column of beta_hs_w_95CIs.csv corresponds to a parameter (in this case only log(lambda) and 'HF', as our model includes only these two parameters), except for the column 'descr', which describes the quantity reported in each of the rows.

- upper95CI_SEMmethod is the upper 95% confidence interval calculated using the standard error of the mean of the track estimates
- beta_h is the herd-level estimate of the coefficient for a specific parameter (or the average loglambda value for loglambda). In our example, the estimate of beta_h of -1.0399086 is close to that used to simulate the movement tracks.
- lower95CI_SEMmethod is the lower 95% confidence interval calculated using the standard error of the mean of the track estimates
- stddev.of.beta_ts is the standard deviation of the beta_ts, the track-level coefficient estimates
- lower95CI_mean_of_hessian_method and upper95CI_mean_of_hessian_method are the mean of the respective confidence intervals calculate using the standard error estimated from the Hessian matrix produced by optim()
- std.err.mean is the standard error of the mean used to calculate the confidence interval using the SEM of the track estimates

beta_ts.csv:

```
knitr::kable(head(read.csv("./fittedmods/SimHerd1/iso(HF)/beta_ts.csv"), 6))
```

ICI	est	uCI	SE	vars	trackid	tracknll	model	dataset
-7.472459	-6.813941	-6.1554231	0.3359786	loglambda	1	54.84799	iso(HF)	SimHerd1
-1.255393	-1.120601	-0.9858088	0.0687714	HF	1	54.84799	iso(HF)	SimHerd1
-8.362138	-7.560880	-6.7596217	0.4088052	loglambda	2	68.20966	iso(HF)	SimHerd1
-1.448593	-1.262398	-1.0762034	0.0949972	HF	2	68.20966	iso(HF)	SimHerd1
-7.986016	-7.149631	-6.3132467	0.4267268	loglambda	3	59.53633	iso(HF)	SimHerd1
-1.493356	-1.253544	-1.0137327	0.1223529	HF	3	59.53633	iso(HF)	SimHerd1

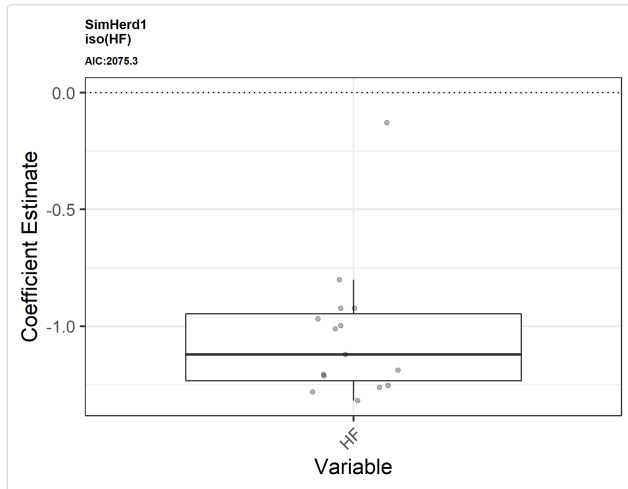
beta_ts.csv provides information about the model fit and the coefficients for each individual track in the tracks (here we just see the first six rows).

- columns ICI, uCI, and SE are the lower and upper 95% CIs and standard error estimated from the Hessian from optim() for that specific track and parameter. optim() often returns NA when the Hessian cannot be calculated
- column est is the beta_t estimate (or loglambda estimate) for the track in column "trackid" and for the variable in "vars"
- tracknll is -log(l_t), the negative log likelihood of the track likelihood

betas_boxplot.png

betas_boxplot.png is a boxplot of the fitted β_t values for all the tracks in tracks.

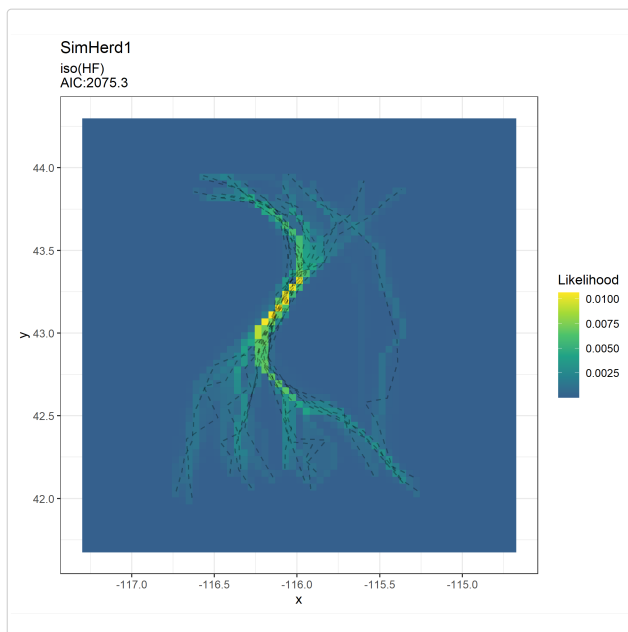
```
knitr::include_graphics("./fittedmods/SimHerd1/iso(HF)/betas_boxplot.png")
```



L_h.png

L_h.png is a plot of the herd-level spatial likelihood surface L_h that combines the track-level likelihoods, as well as the tracks whose endpoints were used to generate the likelihood surface.

```
knitr::include_graphics("./fittedmods/SimHerd1/iso(HF)/L_h.png")
```



Lh_raster

is the raster of L_h in GeoTiff format.

Lt_rasterstack

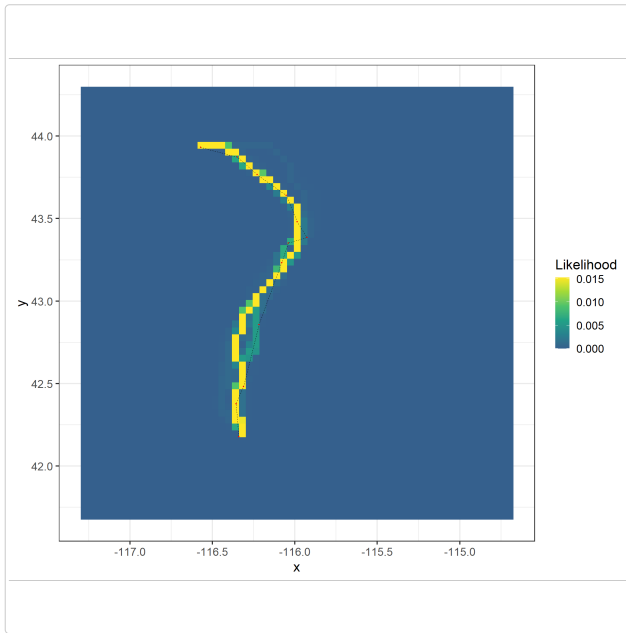
is a raster stack of all of the L_t surfaces, in the order of the tracks in the track shapefile, in GeoTiff format.

/indivtrackfits/

This folder contains plots of the L_t surfaces for each track. Visual inspection can indicate how well the model fits each movement track.

For example:

```
knitr::include_graphics("./fittedmods/SimHerd1/iso(HF)/indivtrackfits/trackplot_1.png")
```

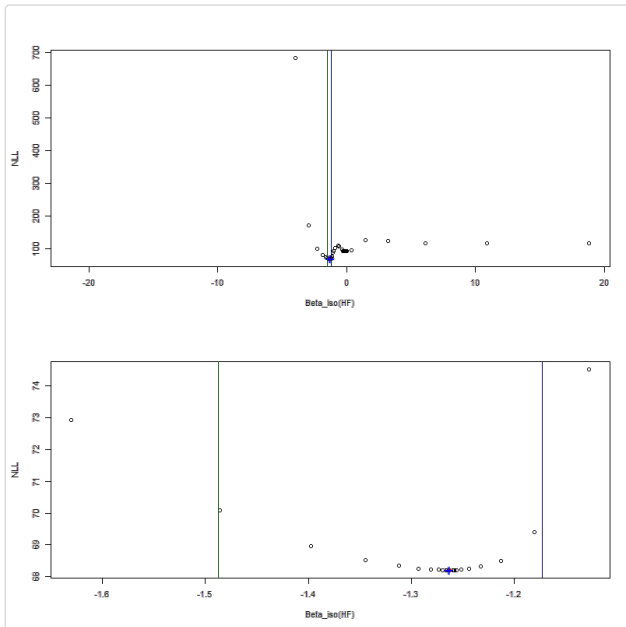


/likprofiles/

This folder contains the likelihood profiles for each track and each parameter.

For example:

```
knitr::include_graphics("./fittedmods/SimHerd1/iso(HF)/likprofiles/likprofile_2_iso(HF).png")
```



The top plot contains all values that were evaluated in the profile. The lower plot is zoomed in to likelihood values within 10 likelihood units of the minimum likelihood. The green and blue lines are the 95% CIs, estimated from the likelihood profile data. The blue "+" is the parameter estimate from `optim()`. The red dot is the estimate in the profile with the lowest negative log likelihood. If in calculating a profile a better set of parameter values (> than 0.1 likelihood units better) is found than was found by `optim()`, the likelihood profile will be recalculated and replotted.

Exploring the likelihood profiles can help determine whether the optimization successfully found a minimum in the negative log likelihood values for a particular variables, and to understand the overall shape of the likelihood surface.