

Get started

Example dataset

This is a basic example which shows you how to run crest with randomly generated data:

```
library(crestr)
## loading example data
data(crest_ex)
data(crest_ex_pse)
data(crest_ex_selection)
```

Let's first have a look at the data. We have 20 fossil samples from which 7 taxa have been identified. The data are already expressed in percentages.

```
## the first 6 samples
head(crest_ex)
#>      Age Taxon1 Taxon2 Taxon3 Taxon4 Taxon5 Taxon6 Taxon7
#> Sample_1  1     0     0    45     1    22    32     1
#> Sample_2  2     0     0    50     0    23    27     0
#> Sample_3  3     0     0    49     0    25    26     0
#> Sample_4  4     0     0    37     0    27    36     0
#> Sample_5  5     0     3    36     3    18    40     0
#> Sample_6  6     2     2    25     0    21    50     0
```

```
## the structure of the data frame
str(crest_ex)
#> 'data.frame':    20 obs. of  8 variables:
#>  $ Age      : int  1 2 3 4 5 6 7 8 9 10 ...
#>  $ Taxon1: int  0 0 0 0 0 2 3 5 10 15 ...
#>  $ Taxon2: int  0 0 0 0 3 2 5 5 12 8 ...
#>  $ Taxon3: int  45 50 49 37 36 25 18 17 10 12 ...
#>  $ Taxon4: int  1 0 0 0 3 0 0 6 15 14 ...
#>  $ Taxon5: int  22 23 25 27 18 21 21 20 16 13 ...
#>  $ Taxon6: int  32 27 26 36 40 50 53 47 37 38 ...
#>  $ Taxon7: int  1 0 0 0 0 0 0 0 0 0 ...
```

For each reconstruction, a proxy-species equivalency ('pse') table must be provided. Here, with the 7 fake taxa, it looks like:

```
crest_ex_pse
#>   Level      Family      Genus Species ProxyName
#> 1     3 Randomaceae Randomus  Taxon1   Taxon1
#> 2     3 Randomaceae Randomus  Taxon2   Taxon2
#> 3     3 Randomaceae Randomus  Taxon3   Taxon3
#> 4     3 Randomaceae Randomus  Taxon4   Taxon4
#> 5     3 Randomaceae Randomus  Taxon5   Taxon5
#> 6     3 Randomaceae Randomus  Taxon6   Taxon6
#> 7     3 Randomaceae Randomus  Taxon7   Taxon7
```

Finally, one can specify which taxa should be used to reconstruct each variable:

```
crest_ex_selection
#>      bio1 bio12
#> Taxon1    1    1
#> Taxon2    1    0
#> Taxon3    1    0
#> Taxon4    0    1
#> Taxon5    0    1
#> Taxon6    0    0
#> Taxon7    1    1
```

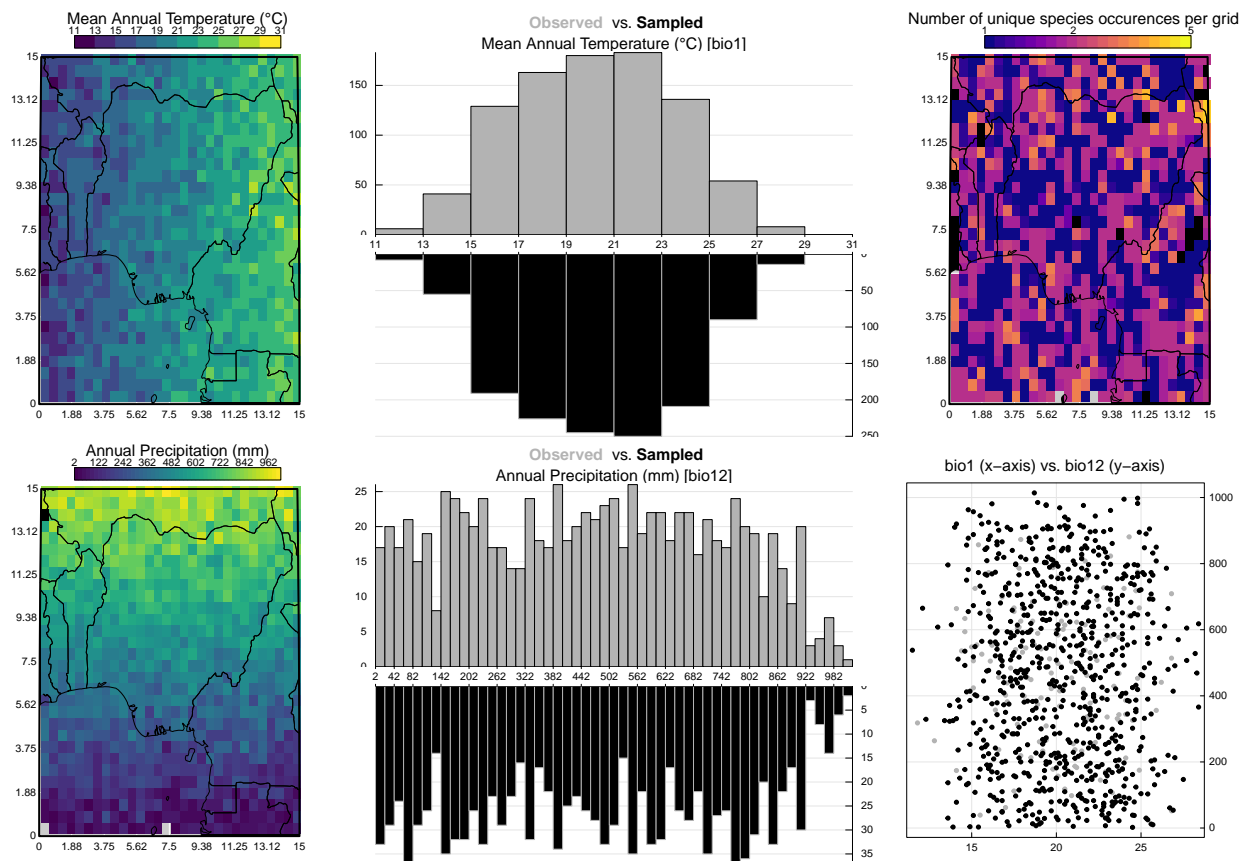
Application

To illustrate the process, we will reconstruct bio1 (mean annual temperature) and bio12 (annual precipitation) from these fake data. The description of the different parameters is available in the first **vignette**.

```
recons <- crest(
  df = crest_ex, pse = crest_ex_pse, taxaType = 0,
  climate = c("bio1", "bio12"), bin_width = c(2, 20),
  shape = c("normal", "lognormal"),
  selectedTaxa = crest_ex_selection, dbname = "crest_example"
)
```

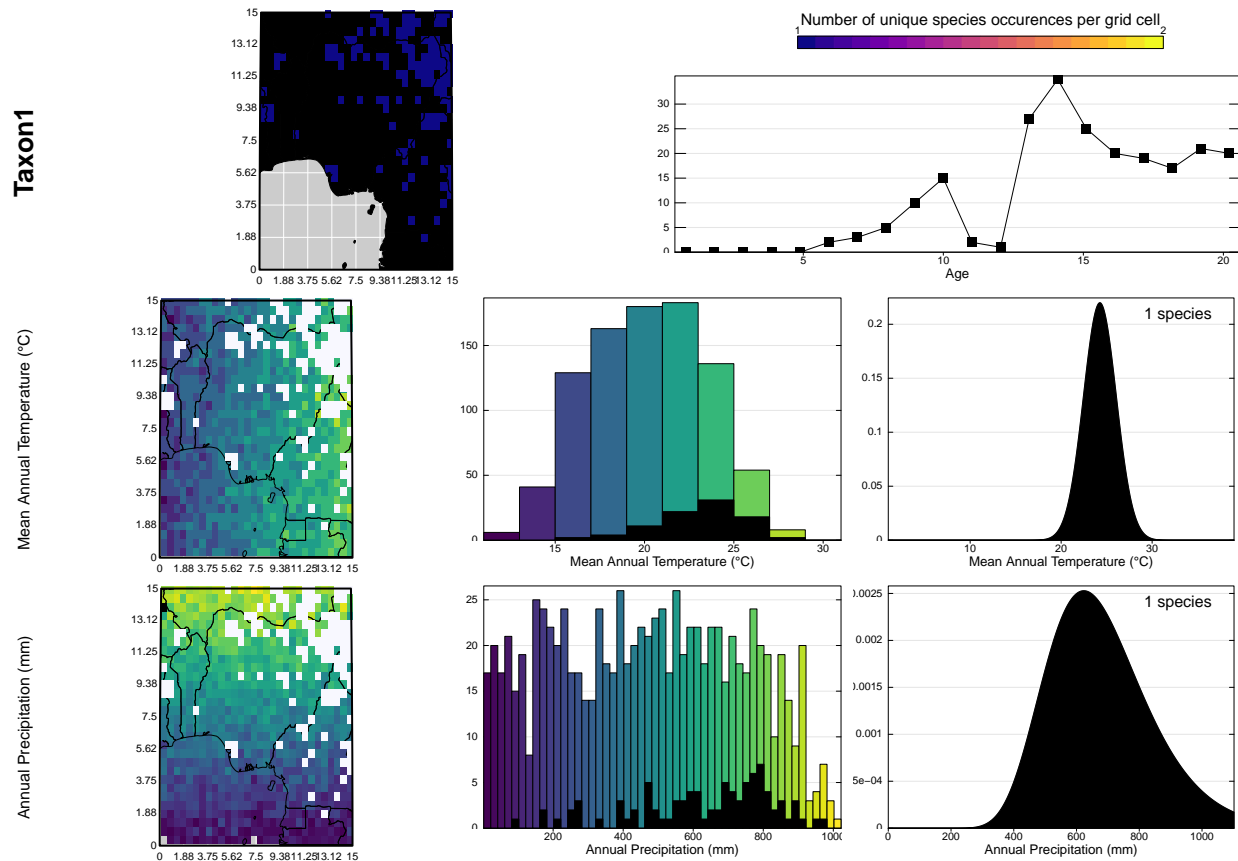
The climate sampled by the data can be assessed graphically using the figure

`plot_climateSpace(recons)`



Graphical tools also exist to assess which taxa should/could be used for each variable

```
plot_taxaCharacteristics(recons, taxanames='Taxon1')
```



Plotting the results

Finally, the results can be visualised using the `plot` function and the reconstructed climate values can be accessed from the nested `recons` object:

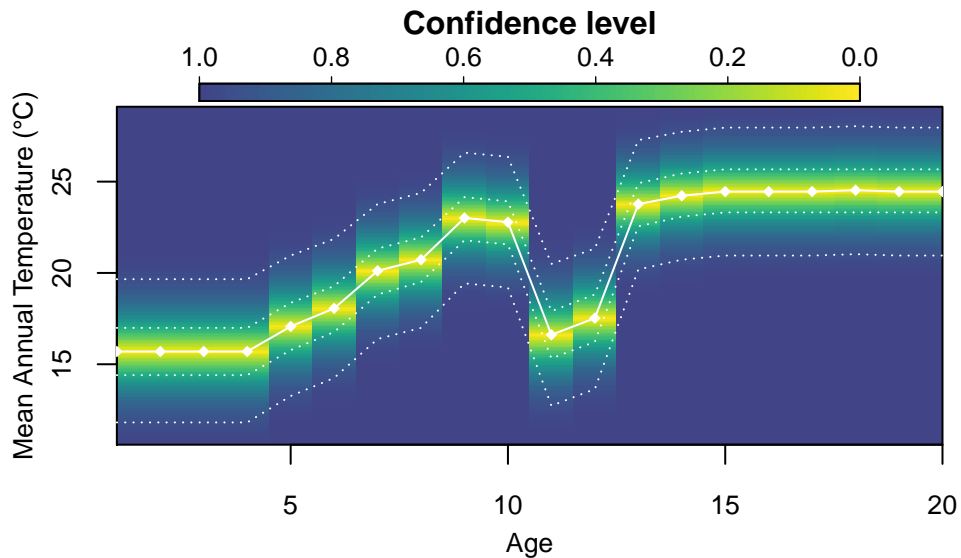
```
names(recons)
#> [1] "inputs"          "parameters"      "modelling"       "reconstructions"
#> [5] "misc"
lapply(recons$reconstructions, names)
#> $bio1
#> [1] "posterior"      "uncertainties" "optima"
#>
#> $bio12
#> [1] "posterior"      "uncertainties" "optima"

head(recons$reconstructions$bio1$optima)
#>   Age optima mean
#> 1   1 15.69739 15.69943
#> 2   2 15.69739 15.69943
#> 3   3 15.69739 15.69943
#> 4   4 15.69739 15.69943
#> 5   5 17.06814 17.08516
```

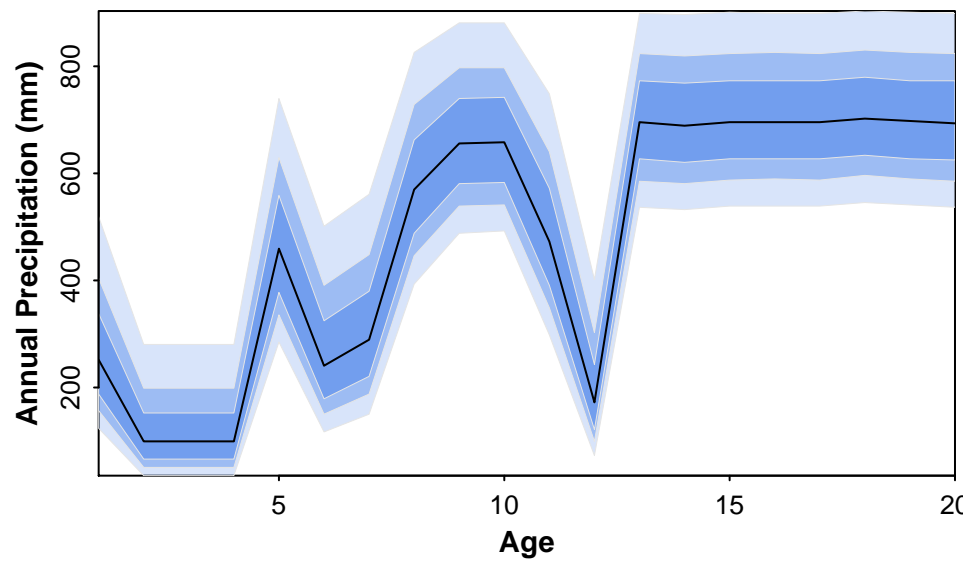
```
#> 6 6 18.05812 18.02322
str(recons$reconstructions$bio1$optima)
#> 'data.frame': 20 obs. of 3 variables:
#> $ Age : int 1 2 3 4 5 6 7 8 9 10 ...
#> $ optima: num 15.7 15.7 15.7 15.7 17.1 ...
#> $ mean : num 15.7 15.7 15.7 15.7 17.1 ...

signif(recons$reconstructions$bio1$posterior[1:6, 1:6], 3)
#> [,1] [,2] [,3] [,4] [,5] [,6]
#> [1,] 1.00e+00 1.08e+00 1.15e+00 1.23e+00 1.30e+00 1.38e+00
#> [2,] 6.69e-13 8.79e-13 1.15e-12 1.51e-12 1.98e-12 2.58e-12
#> [3,] 6.69e-13 8.79e-13 1.15e-12 1.51e-12 1.98e-12 2.58e-12
#> [4,] 6.69e-13 8.79e-13 1.15e-12 1.51e-12 1.98e-12 2.58e-12
#> [5,] 6.69e-13 8.79e-13 1.15e-12 1.51e-12 1.98e-12 2.58e-12
#> [6,] 1.42e-15 1.93e-15 2.62e-15 3.56e-15 4.82e-15 6.52e-15
str(recons$reconstructions$bio1$posterior)
#> num [1:21, 1:500] 1.00 6.69e-13 6.69e-13 6.69e-13 6.69e-13 ...

plot(recons, climate = 'bio1')
```



```
plot(recons, climate = 'bio12', simplify=TRUE, uncertainties=c(0.4, 0.6, 0.8))
```



Exporting the results
