

Data examples

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Code to reproduce results from Köhler, Rügamer and Schmid 2024:

<https://arxiv.org/abs/2407.18650>

For an updated version of the ONAM package, see

https://github.com/Koehlibert/ONAM_R

Install package:

```
install.packages("devtools")
library(devtools)
devtools::install_github("Koehlibert/ONAM")
```

If this is the first time using keras or tensorflow in R, you need to run `keras::install_keras()`. `## Fit model on Chesapeake Bay watershed biotic integrity dataset`

```
library(keras)
```

```
## Warning: Paket 'keras' wurde unter R Version 4.2.3 erstellt
```

```
library(ONAM)
```

```
##
```

```
## Attache Paket: 'ONAM'
```

```
## Das folgende Objekt ist maskiert 'package:stats':
```

```
##
```

```
##      decompose
```

```
#define model formula
```

```
BIBIformula <-
```

```
Prediction ~ deep_model(Latitude) + deep_model(Longitude) +
  deep_model(BioregUpstream2) + deep_model(AreaSqKM) +
  deep_model(dep_so4_2011) + deep_model(elevation) +
  deep_model(hydrogroup_d4) + deep_model(percent_sandy) +
  deep_model(surfcoarse) + deep_model(deg_barr_all_local) +
  deep_model(upstream.total_precip) + deep_model(Agriculture) +
  deep_model(Development) + deep_model(Forest) + deep_model(Openwater) +
  deep_model(Barren) + deep_model(Grass) + deep_model(Woodywetland) +
  deep_model(Herbwetland) +
  deep_model(Development, elevation) +
  deep_model(Agriculture, elevation) +
  deep_model(Agriculture, Development) +
  deep_model(
    Latitude,
    Longitude,
    BioregUpstream2,
    AreaSqKM,
```

```

    dep_so4_2011,
    elevation,
    hydrogroup_d4,
    percent_sandy,
    surfcoarse,
    deg_barr_all_local,
    Openwater,
    Barren,
    upstream.total_precip,
    Agriculture,
    Development,
    Forest,
    Grass,
    Woodywetland,
    Herbwetland
  )
#load data
library(readxl)

```

Warning: Paket 'readxl' wurde unter R Version 4.2.3 erstellt

```

trainData <- read_xlsx("BIBITrain.xlsx")
trainData <- as.matrix(trainData)
#Specify model architecture in a named list where the name corresponds to the model name in the model f
list_of_deep_models_BIBI <- list(deep_model = ONAM:::get_submodel)
categorical_features <- c("BioregUpstream2")
#Fit PHONAM model
BIBIExpl <-
  onam(
    BIBIformula,
    list_of_deep_models_BIBI,
    categorical_features = categorical_features,
    trainData,
    n_ensemble = 10,
    progresstext = FALSE,
    verbose = 0
  )

```