

End-member modelling analysis

The R-package EMMAgeo

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The R-package
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A universal modelling protocol
○○○○○○○○

Validation
○○○○○○

Future perspectives
○○○○○○

End-member modelling analysis

The R-package EMMAgeo

Michael Dietze

GFZ German Research Centre for Geosciences, Section 5.1 Geomorphology

EMMAgeo - on CRAN



CRAN - Package EMMAgeo - Mozilla Firefox

CRAN - Package EMMAgeo

cran.r-project.org/web/packages/EMMAgeo/index.html

EMMAgeo: End-member modelling algorithm and supporting functions for grain-size analysis

This package provides a set of functions for convenient end-member modelling analysis of grain-size data (EMMAgeo).

Version: 0.9.1

Depends: R (\geq 3.0.1), [GPARotation](#), [limSolve](#), [shape](#)

Published: 2013-10-14

Author: Michael Dietze, Elisabeth Dietze

Maintainer: Michael Dietze <micha.dietze at mailbox.tu-dresden.de>

License: [GPL-3](#)

NeedsCompilation: no

Materials: [NEWS](#)

CRAN checks: [EMMAgeo results](#)

Downloads:

Reference manual: [EMMAgeo.pdf](#)

Package source: [EMMAgeo_0.9.1.tar.gz](#)

MacOS X binary: [EMMAgeo_0.9.1.tgz](#)

Windows binary: [EMMAgeo_0.9.1.zip](#)

Old sources: [EMMAgeo archive](#)

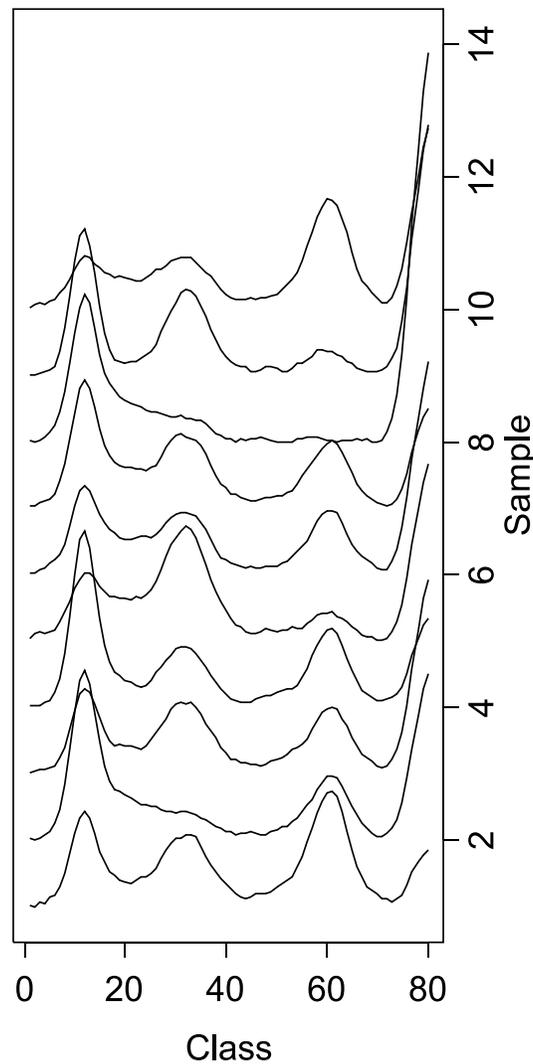
EMMAgeo - package overview

Functions

```

convert.units()
interpolate.classes()
check.data()
test.lw()
test.L()
test.parameters()
EMMA()
test.robustness()
robust.EM()
residual.EM()
Mqs.uncertainty()
create.EM()
mix.EM()
    
```

Example data set



Documentation (& Tutorial)

Package ‘EMMAgeo’
October 14, 2013

Type Package
Title End-member modelling algorithm and supporting functions for grain-size analysis
Version 0.9.1
Date 2013-10-14
Author Michael Dietze, Elisabeth Dietze
Maintainer Michael Dietze <micha.dietze@mailbox.tu-dresden.de>
Description This package provides a set of functions for convenient end-member modelling analysis of grain-size data (EMMAgeo).
License GPL-3
Depends R (>= 3.0.1), GPArotation, limSolve, shape
NeedsCompilation no
Repository CRAN
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R topics documented:

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Rescale data matrix X to constant sum c.

```
X <- X / apply(X, 1, sum) * c
```

Weight transformation after Miesch (1970).

```
qts <- function(X, lw) quantile(X, c(lw, 1-lw), type = 5)
ls <- t(apply(X, 2, qts, lw = lw))
W <- t((t(X) - ls[,1]) / (ls[,2] - ls[,1]))
```

Similarity matrix calculation (major product).

```
A <- t(W) %*% W
```

Eigen space extraction.

```
EIG <- eigen(A)
V <- EIG$vectors[,order(seq(ncol(A), 1, -1))]
Vf <- V[,order(seq(ncol(A), 1, -1))]
L <- EIG$values[order(seq(ncol(A), 1, -1))]
Lv <- cumsum(sort(L / sum(L), decreasing = TRUE))
```

Varimax rotation of the eigen vector matrix Vf.

```
Vr <- do.call(rotation, list(Vf[,1:q]))
```

Extract and sort (decreasing) factor loadings and write them to matrix Vq.
Rescale (Vqr) and normalise (Vqn) the factor loadings column-wise.

```
Vq <- Vr$loadings[,order(seq(q, 1, -1))]
Vqr <- t(t(Vq) / apply(Vq, 2, sum)) * c
Vqr <- t(Vqr)
Vqn <- t((Vqr - apply(Vqr, 1, min)) / (
  apply(Vqr, 1, max) - apply(Vqr, 1, min)))
```

Calculate factor scores matrix (Mq) by non-negative least square fitting of Vqn and transposed row-wise weight-transformed data W.

```
Mq <- matrix(nrow = nrow(X), ncol = q)
for (i in 1:nrow(X)) {Mq[i,] = nnls(Vqn, as.vector(t(W[i,])))$X}
```

Model the dataset (Wm) as the minor product

```
Wm <- Mq %*% t(Vqn)
```

Rescale the factor loadings matrix Vqn to Vqsn.

```
s <- (c - sum(ls[,1])) / apply(Vqn * unname(ls[,2] - ls[,1]), 2, sum)
Vqs <- Vqn
for(i in 1:q) {Vqs[,i] <- t(s[i] * t(Vqn[,i]) * (ls[,2] - ls[,1]) + ls[,1])}
Vqsn <- t(t(Vqs) / apply(Vqs, 2, sum)) * c
```

Rescale factor scores (Mq) to matrix Mqs and calculate variance explained by scores.

```
Mqs <- t(t(Mq) / s) / apply(t(t(Mq) / s), 1, sum)
Mqs.var <- diag(var(Mqs)) / sum(diag(var(Mqs))) * 100
```

Evaluate measures of model goodness.

```
Em <- as.vector(apply(X - Xm, 1, mean))
En <- as.vector(apply(X - Xm, 2, mean))
Rm <- diag(cor(t(X), t(Xm))^2)
Rn <- diag(cor(X, Xm)^2)
```

Rescale data matrix X to constant sum c.

```
X <- X / apply(X, 1, sum) * c
```

Weight transformation after Miesch (1970).

```
qts <- function(X, lw) quantile(X, c(lw, 1-lw), type = 5)
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W <- t((t(X) - ls[,1]) / (ls[,2] - ls[,1]))
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Vf <- V[,order(seq(ncol(A), 1, -1))]
L <- EIG$values[order(seq(ncol(A), 1, -1))]
LV <- cumsum(sort(L / sum(L), decreasing = TRUE))
```

Principal component analysis

Varimax rotation of the eigen vector matrix Vf.

```
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Rescale (Vqr) and normalise (Vqn) the factor loadings column-wise.

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Vqr <- t(t(Vq) / apply(Vq, 2, sum)) * c
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Rescale factor scores (Mq) to matrix Mqs and calculate variance explained by scores.

```
Mqs <- t(t(Mq) / s) / apply(t(t(Mq) / s), 1, sum)
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Vf <- V[,order(seq(ncol(A), 1, -1))]
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Factor analysis

Rescale the factor loadings matrix Vqn to Vqsn.

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Vqs <- Vqn
for(i in 1:q) {Vqs[,i] <- t(s[i] * t(Vqn[,i]) * (ls[,2] - ls[,1]) + ls[,1])}
Vqsn <- t(t(Vqs) / apply(Vqs, 2, sum)) * c
```

Rescale factor scores (Mq) to matrix Mqs and calculate variance explained by scores.

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Mqs <- t(t(Mq) / s) / apply(t(t(Mq) / s), 1, sum)
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```

Rescale data matrix X to constant sum c.	<pre>X <- X / apply(X, 1, sum) * c</pre>
Weight transformation after Miesch (1970).	<pre>qts <- function(X, lw) quantile(X, c(lw, 1-lw), type = 5) ls <- t(apply(X, 2, qts, lw = lw)) W <- t((t(X) - ls[,1]) / (ls[,2] - ls[,1]))</pre>
Similarity matrix calculation (major product).	<pre>A <- t(W) %** W</pre>
Eigen space extraction.	<pre>EIG <- eigen(A) V <- EIG\$vectors[,order(seq(ncol(A), 1, -1))] Vf <- V[,order(seq(ncol(A), 1, -1))] L <- EIG\$values[order(seq(ncol(A), 1, -1))] LV <- cumsum(sort(L / sum(L), decreasing = TRUE))</pre>
Varimax rotation of the eigen vector matrix Vf.	<pre>Vr <- do.call(rotation, list(Vf[,1:q]))</pre>
Extract and sort (decreasing) factor loadings and write them to matrix Vq. Rescale (Vqr) and normalise (Vqn) the factor loadings column-wise.	<pre>Vq <- Vr\$loadings[,order(seq(q, 1, -1))] Vqr <- t(t(Vq) / apply(Vq, 2, sum)) * c Vqr <- t(Vqr) Vqn <- t((Vqr - apply(Vqr, 1, min)) / (apply(Vqr, 1, max) - apply(Vqr, 1, min)))</pre>
Calculate factor scores matrix (Mq) by non-negative least square fitting of Vqn and transposed row-wise weight-transformed data W.	<pre>Mq <- matrix(nrow = nrow(X), ncol = q) for (i in 1:nrow(X)) {Mq[i,] = nnls(Vqn, as.vector(t(W[i,])))\$X}</pre>
Model the dataset (Wm) as the minor product	<pre>Wm <- Mq %** t(Vqn)</pre>
Rescale the factor loadings matrix Vqn to Vqsn.	<pre>s <- (c - sum(ls[,1])) / apply(Vqn * unname(ls[,2] - ls[,1]), 2, sum) Vqs <- Vqn for(i in 1:q) {Vqs[,i] <- t(s[i] * t(Vqn[,i]) * (ls[,2] - ls[,1]) + ls[,1])} Vqsn <- t(t(Vqs) / apply(Vqs, 2, sum)) * c</pre>
Rescale factor scores (Mq) to matrix Mqs and calculate variance explained by scores.	<pre>Mqs <- t(t(Mq) / s) / apply(t(t(Mq) / s) / c, 1, sum) Mqs.var <- diag(var(Mqs)) / sum(diag(var(Mqs))) * 100</pre>
Evaluate measures of model goodness.	<pre>Em <- as.vector(apply(X - Xm, 1, mean)) En <- as.vector(apply(X - Xm, 2, mean)) Rm <- diag(cor(t(X), t(Xm))^2) Rn <- diag(cor(X, Xm)^2)</pre>

Principal component analysis

Factor analysis

End-member modelling analysis

EMMAgeo - package overview

Functions

```

convert.units()
interpolate.classes()
check.data()
test.lw()
test.L()
test.parameters()
EMMA()
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robust.EM()
residual.EM()
Mqs.uncertainty()
create.EM()
mix.EM()
    
```

convert.units()

```

phi <- -2:5

mu <- convert.units(phi = phi)

mu

[1] 4000.00 2000.00 1000.00 500.00 250.00 125.00 62.50 31.25

convert.units(mu = mu)

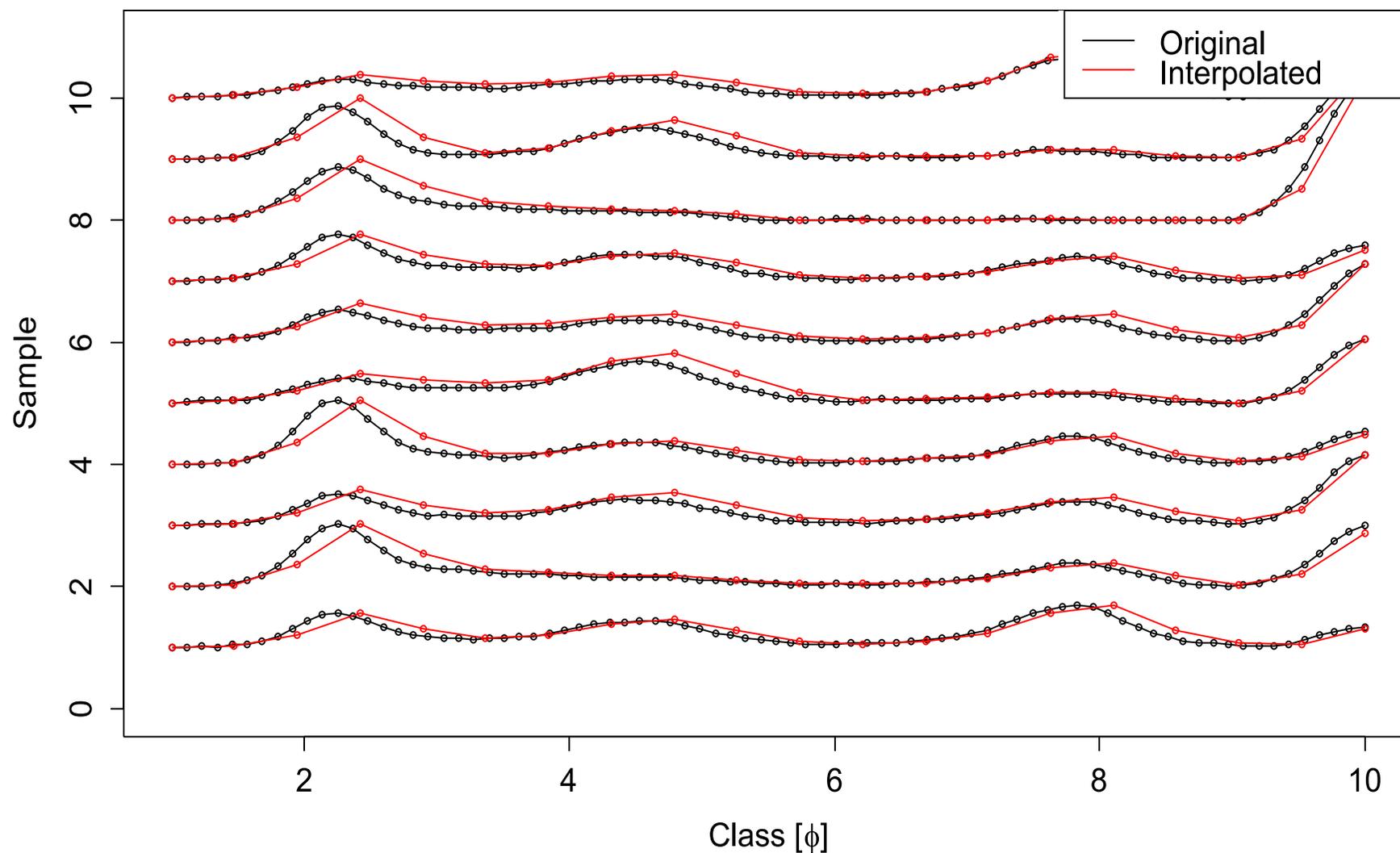
[1] -2 -1 0 1 2 3 4 5
    
```

EMMAgeo - package overview

Functions

- convert.units()
- interpolate.classes()**
- check.data()
- test.lw()
- test.L()
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- robust.EM()
- residual.EM()
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- create.EM()
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interpolate.classes()



EMMAgeo - package overview

Functions

- convert.units()
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check.data()

```
check.data(X = X.artificial, q = 6,
           lw = seq(0, 0.2, 0.01), c = 1)

[1] "Data matrix passed test... OK"
[2] "End-member vector passed test... OK"
[3] "Weight transformation limit vector
    passed test... OK"
[4] "Scaling parameter passed test... OK"
[5] "NA-test passed... OK"
[6] "Test for zero-only values passed... OK"
[7] "Maximum weight transformation limit
    value passed test... OK"
[8] "All samples sum up to constant sum... OK"
```

Input data must:

- be free of NA-values
- be of numeric data type
- contain no zero-only columns
- sum to constant value
- within stable limits (I_w)

EMMAgeo - package overview

Functions

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residual.EM()  
Mqs.uncertainty()  
create.EM()  
mix.EM()
```

test.lw()

```
lw <- seq(from = 0, to = 0.5, by = 0.02)
```

```
test.lw(X = X.artificial, lw = lw)
```

```
$step  
[1] 12
```

```
$lw.max  
[1] 0.22
```

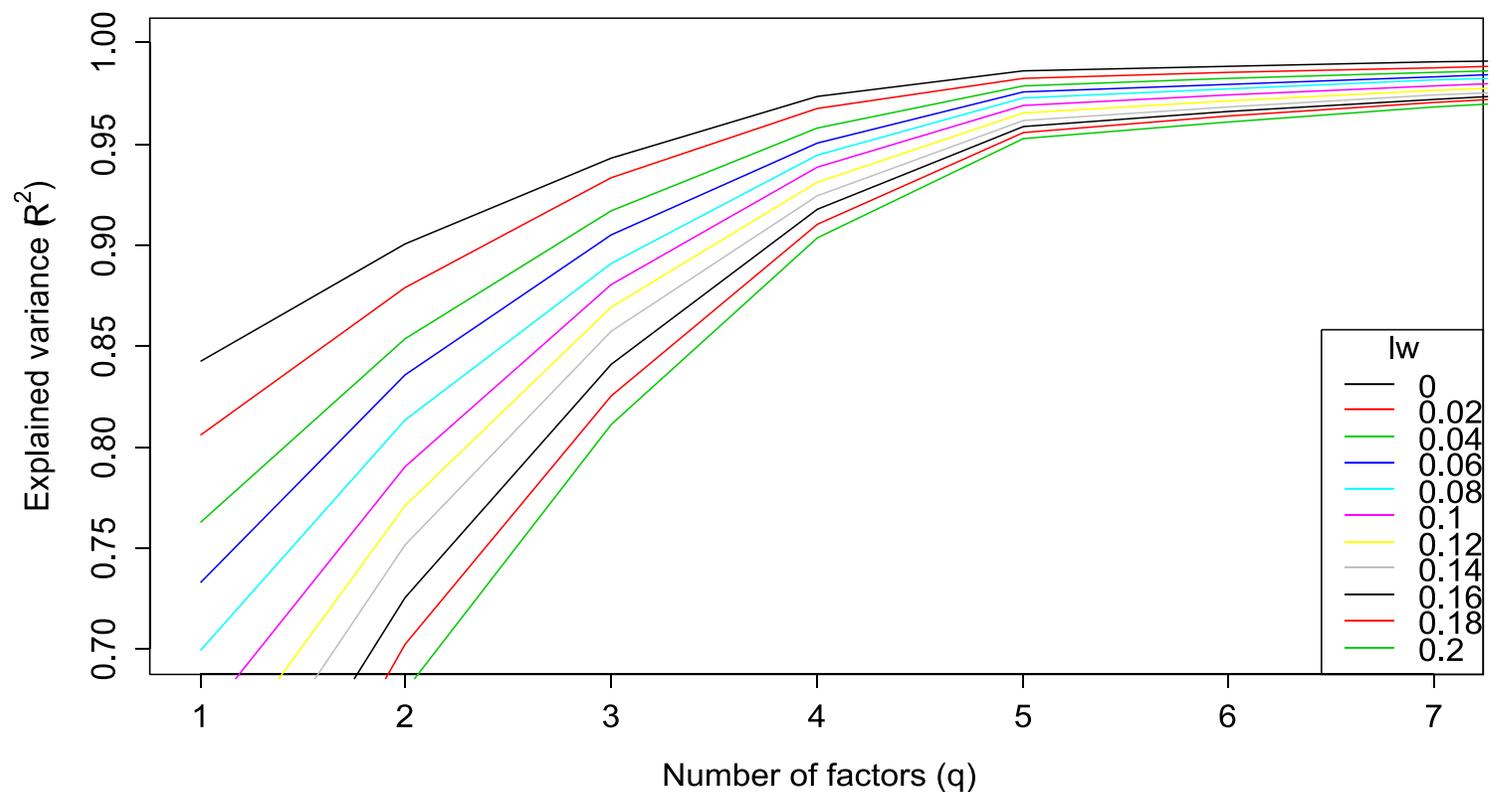
Weight transformation limits must be below a critical value from which on no similarity matrix can be computed any more. The function returns the last possible value for l_w .

EMMAgeo - package overview

Functions

- convert.units()
- interpolate.classes()
- check.data()
- test.lw()
- test.L()**
- test.parameters()
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- robust.EM()
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- create.EM()
- mix.EM()

test.L()



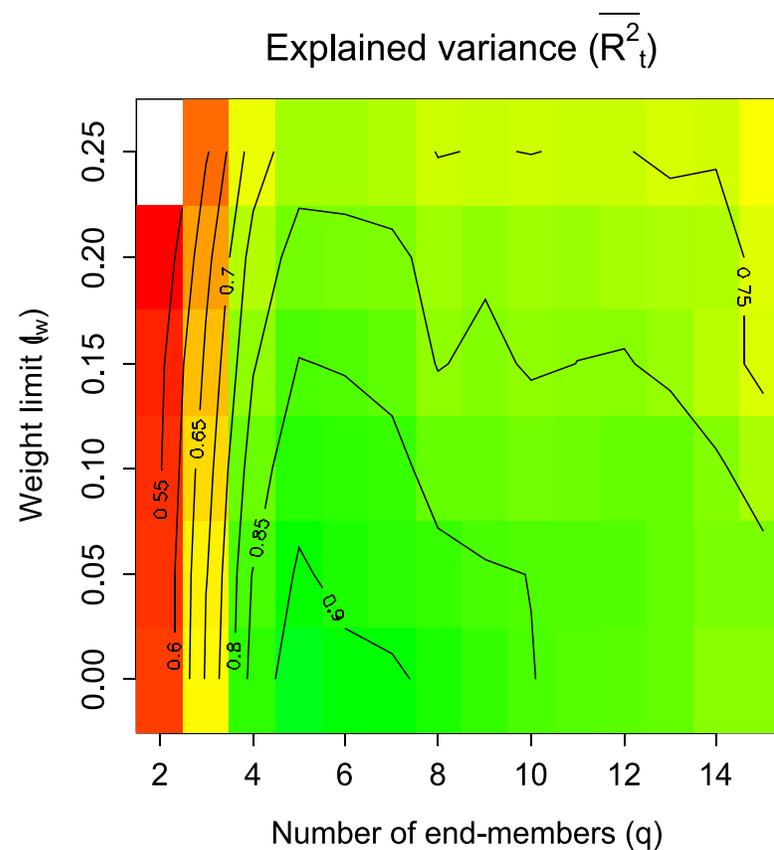
```
L$q.min  
[1] 4 4 4 4 5 5 5 5 5 5 5
```

EMMAgeo - package overview

Functions

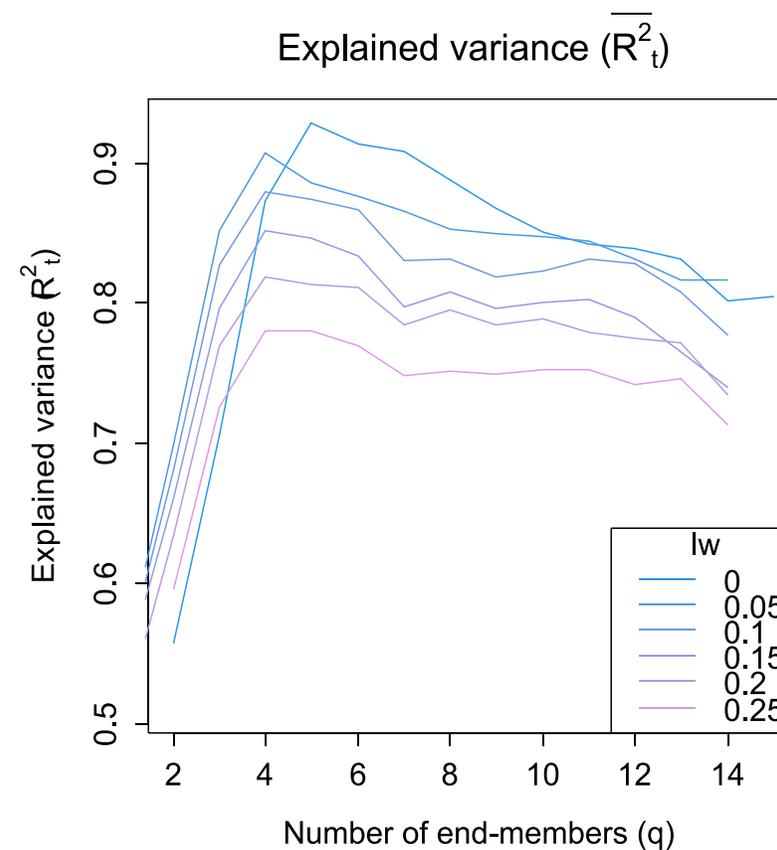
- convert.units()
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- check.data()
- test.lw()
- test.L()
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test.parameters()



TP\$q.max

[1] 5 5 5 5 5 NA



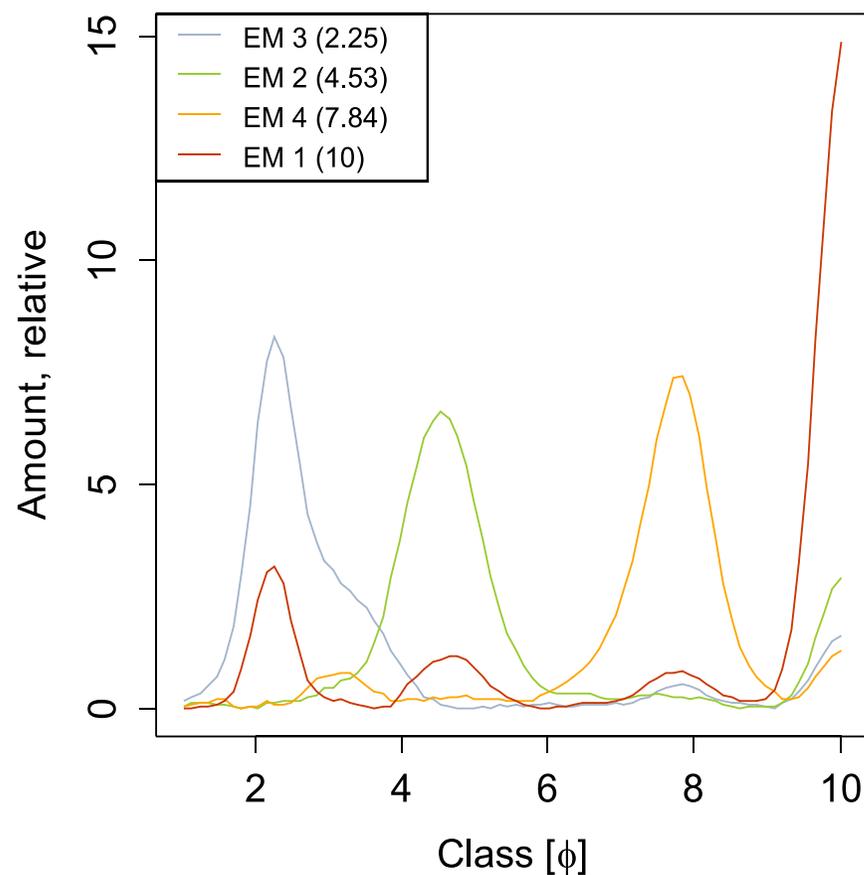
EMMAgeo - package overview

Functions

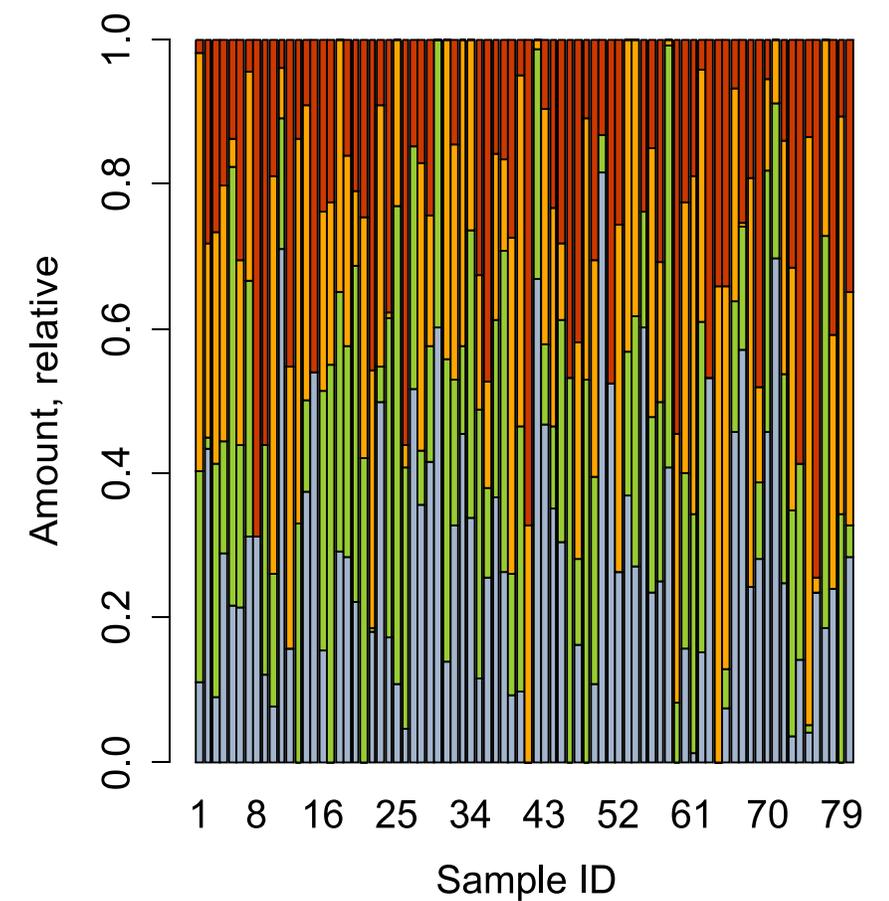
```
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Mqs.uncertainty()  
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```

EMMA()

End-member loadings



End-member scores

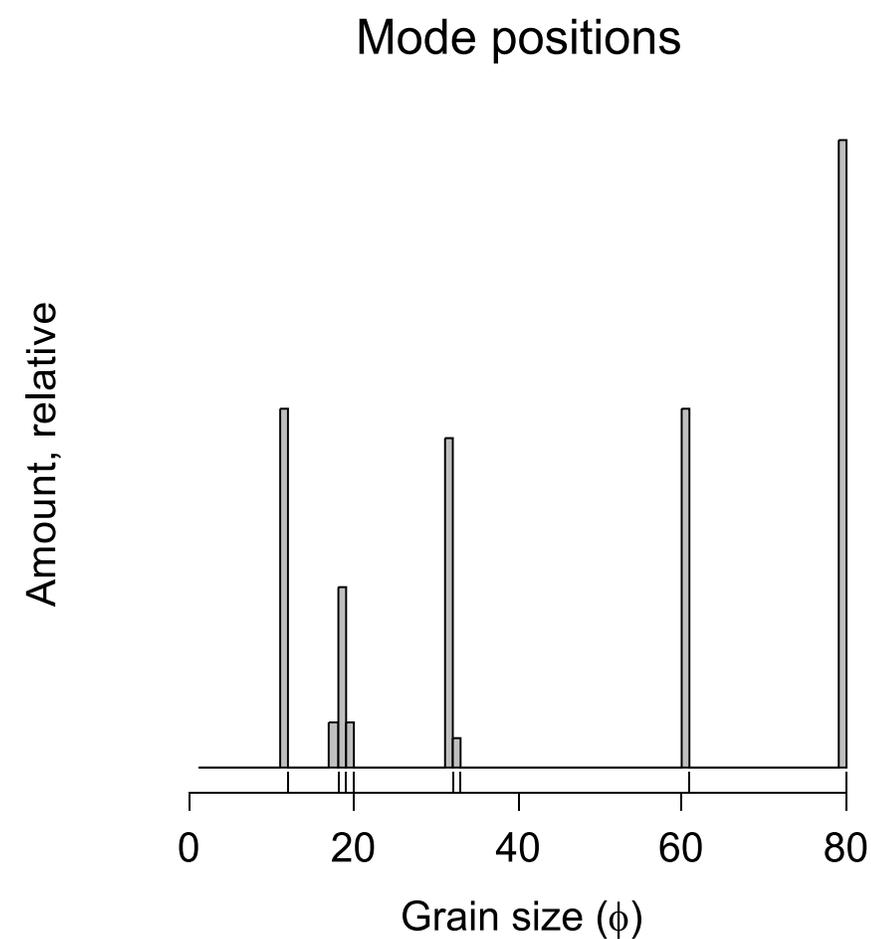
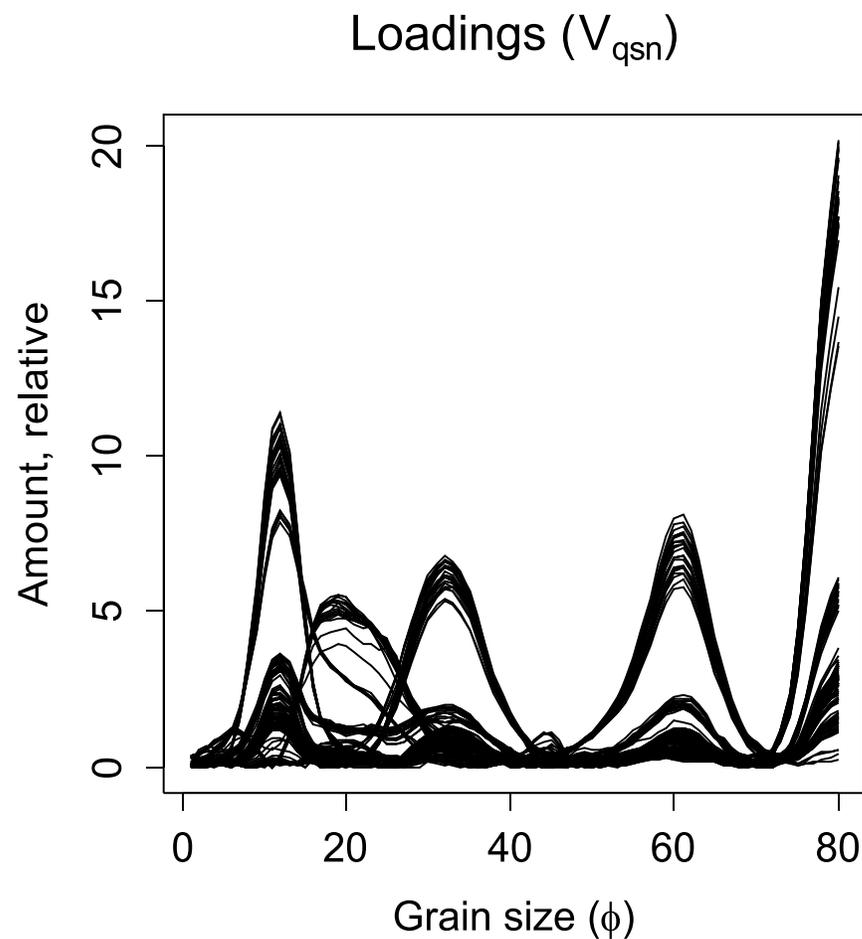


EMMAgeo - package overview

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Mqs.uncertainty()  
create.EM()  
mix.EM()
```

test.robustness()

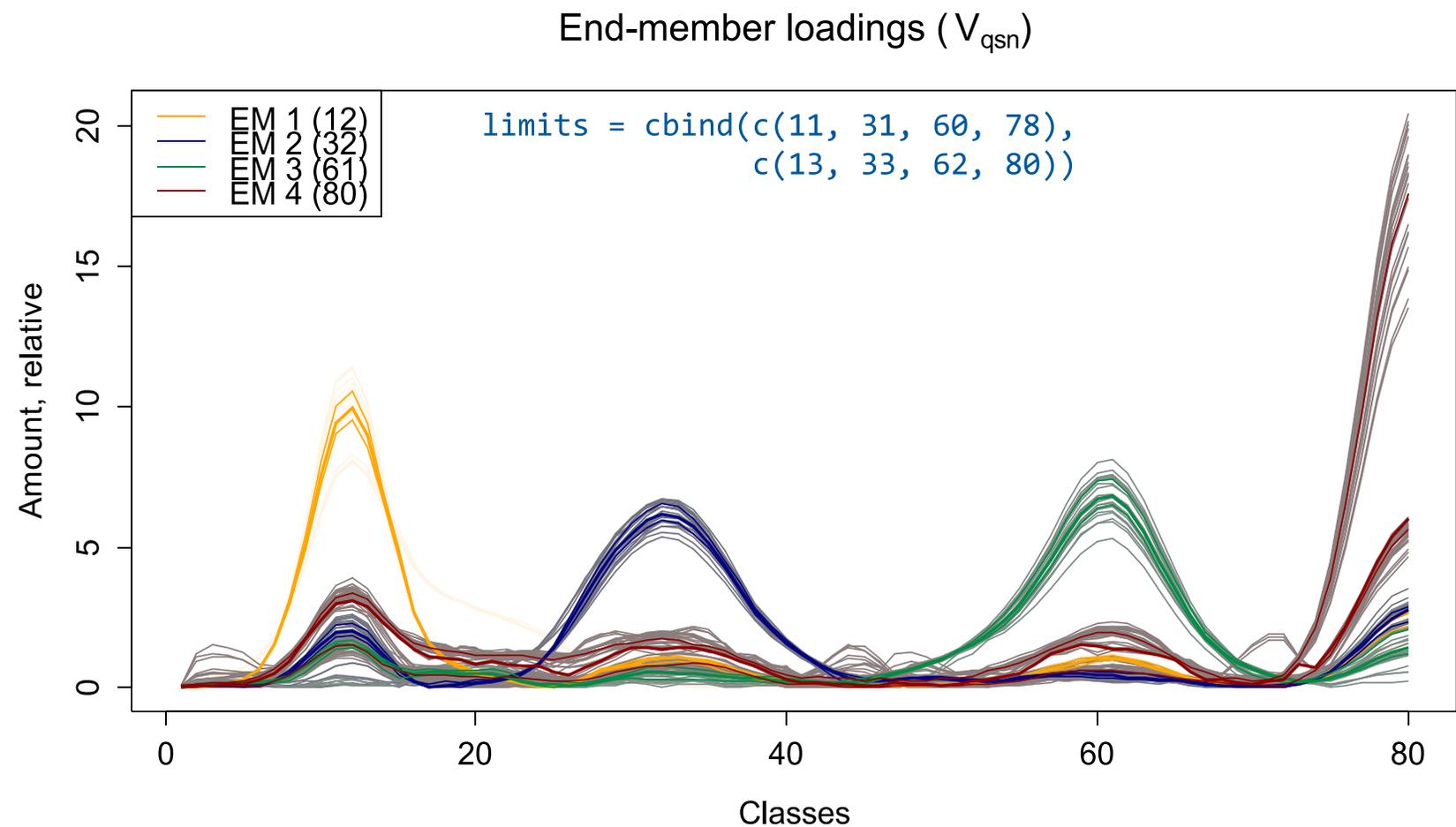


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test.robustness()



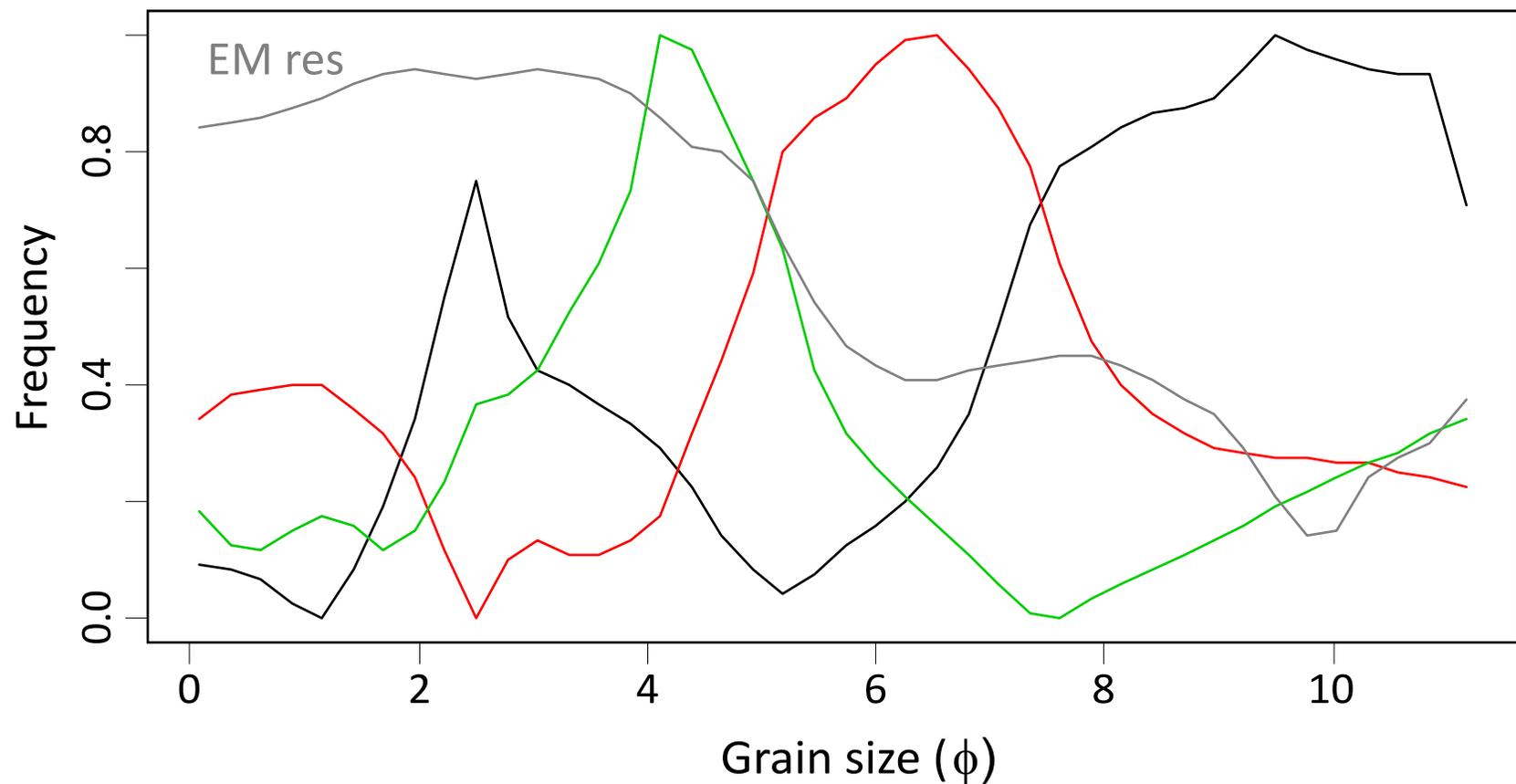
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residual.EM()

End-member loadings (unscaled)

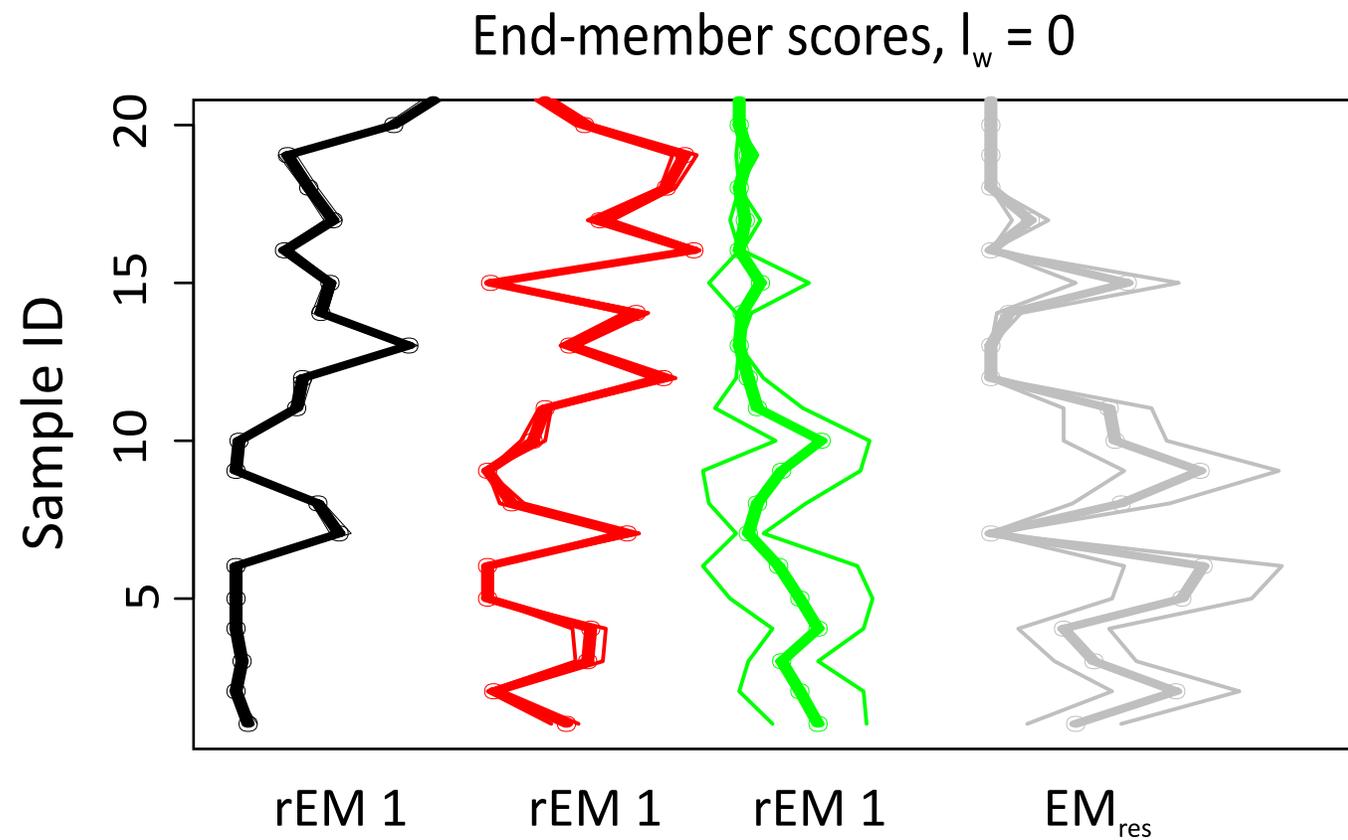


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Mqs.uncertainty()



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create.EM(), mix.EM()

Functions to create and mix user-defined end-members, e.g. for hypothesis testing.

Robust end-member modelling - a protocol suggestion

Protocol steps

1. check the data
2. bracket weight transformation limits
3. bracket numbers of end-members
4. calculate and extract robust end-members
5. run EMMA with optimal parameters
6. evaluate model quality
7. estimate model uncertainty

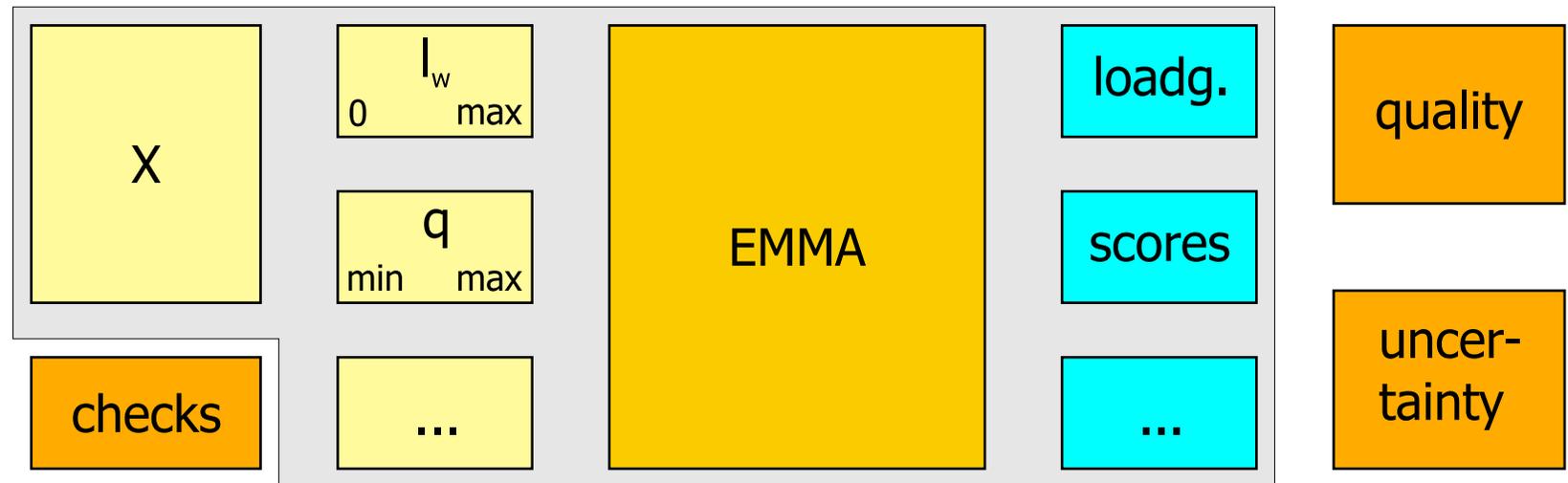
Input data

Model parameters

Model

Model output

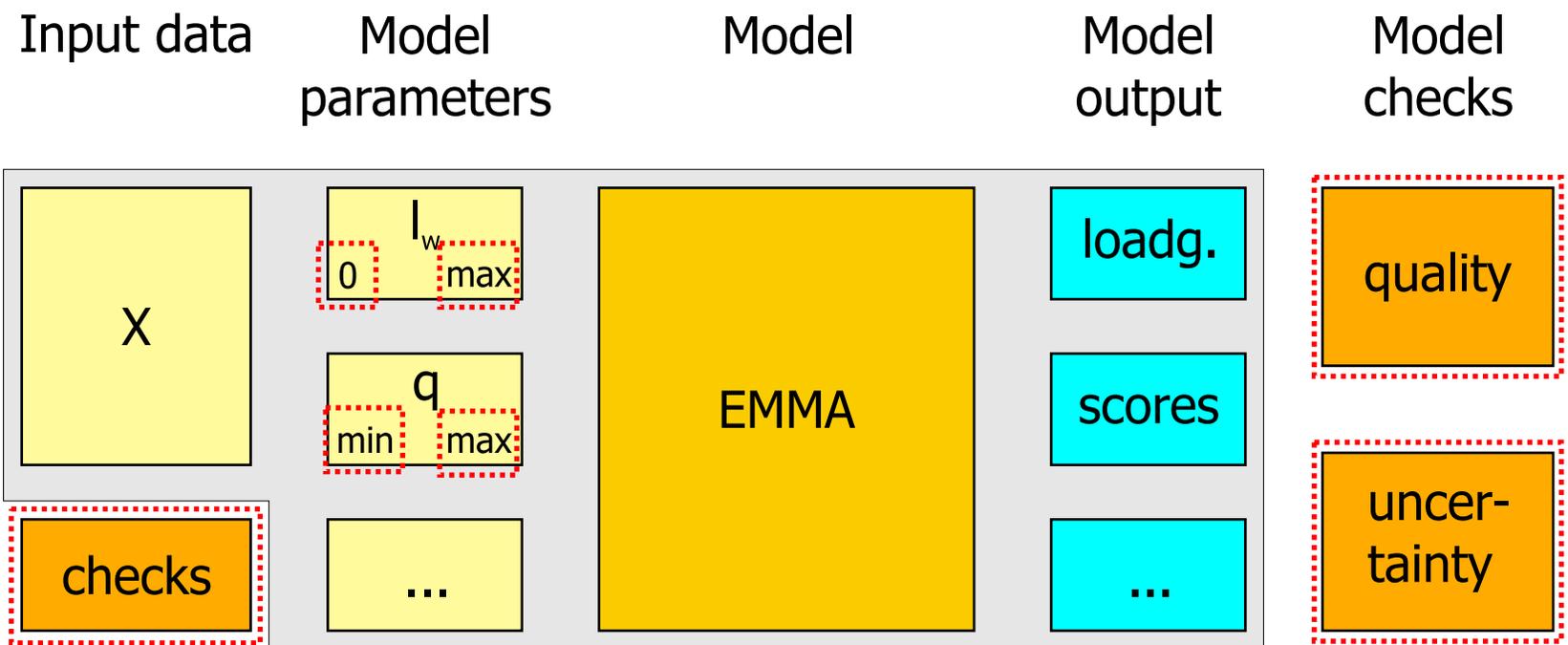
Model checks



Robust end-member modelling - a protocol suggestion

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Protocol is explicitly formulated as R-script and can be run straight forward and adapted if necessary.

Robust end-member modelling - a protocol suggestion



Protocol steps

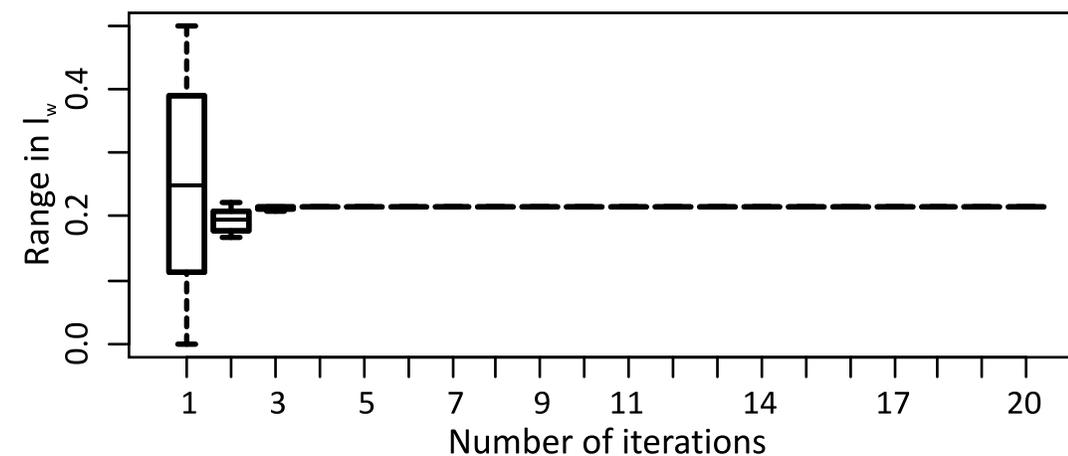
1. check the data
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Functions: test.lw()

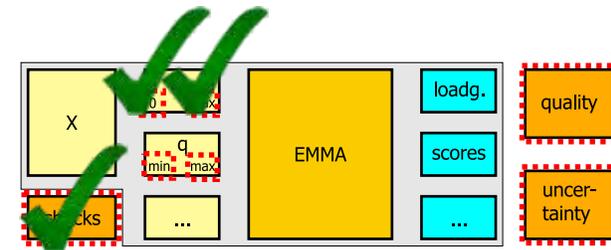
Goal is to find the highest possible weight transformation value l_w . Lower limit is zero, i.e. no weight transformation.

```
for(i in 1:10) {
  if(i == 1) {lw.new <- seq(0,
                          0.5,
                          length = 10)}
  lw <- test.lw(X = X, lw = lw.new)
  lw.new <- seq(lw.new[lw$step],
                lw.new[lw$step + 1],
                length = 10)
}
lw.max <- lw$lw.max
lw.max
```

Approximation progress



Robust end-member modelling - a protocol suggestion



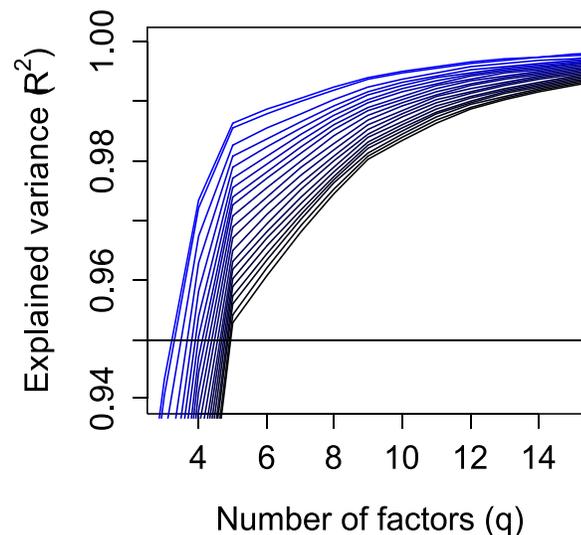
Protocol steps

1. check the data
2. bracket weight transformation limits
3. bracket number of end-members
4. calculate and extract robust end-members
5. run EMMA with optimal parameters
6. evaluate model quality
7. estimate model uncertainty

Functions: test.L(), test.parameters()

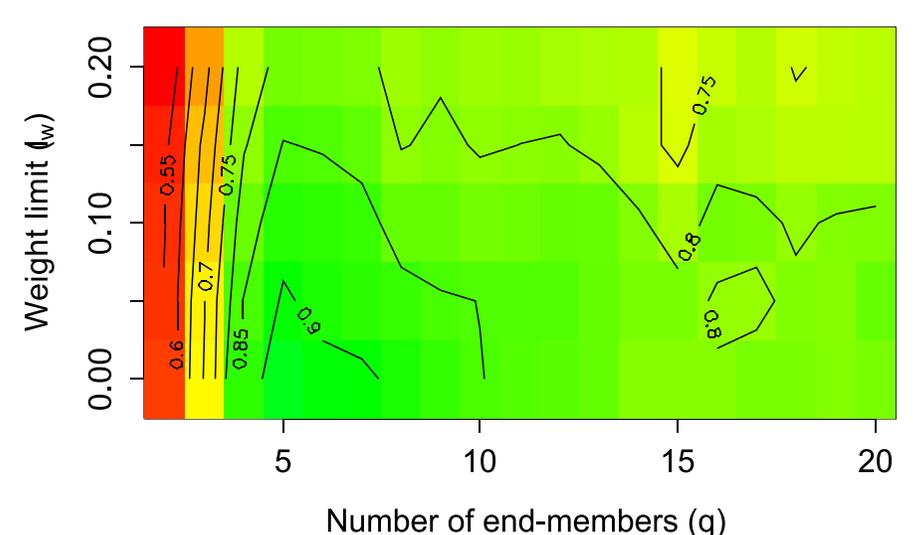
Goal is to find the minimum and maximum number of eigenvectors to adequately model the data set.
 Mathematical definition of "adequate" may differ from geoscientific one.

Variance explained by factors



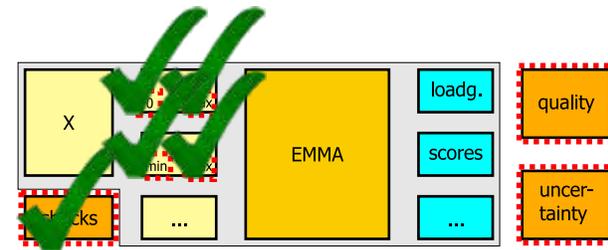
```
q.min <- test.L(X = X, lw = lw)$q.min
q.min
```

Explained variance (R^2)



```
q.max <- test.parameters(X = X, q = q, lw = lw)$q.max
q.max
```

Robust end-member modelling - a protocol suggestion



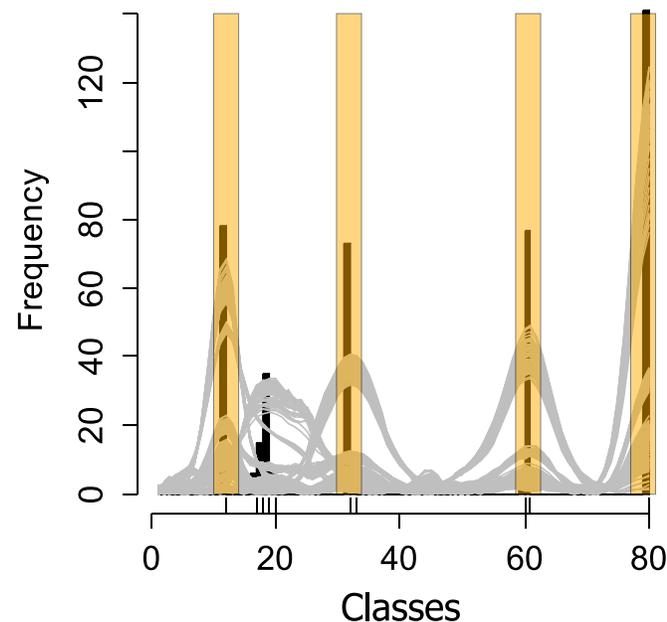
Protocol steps

1. check the data
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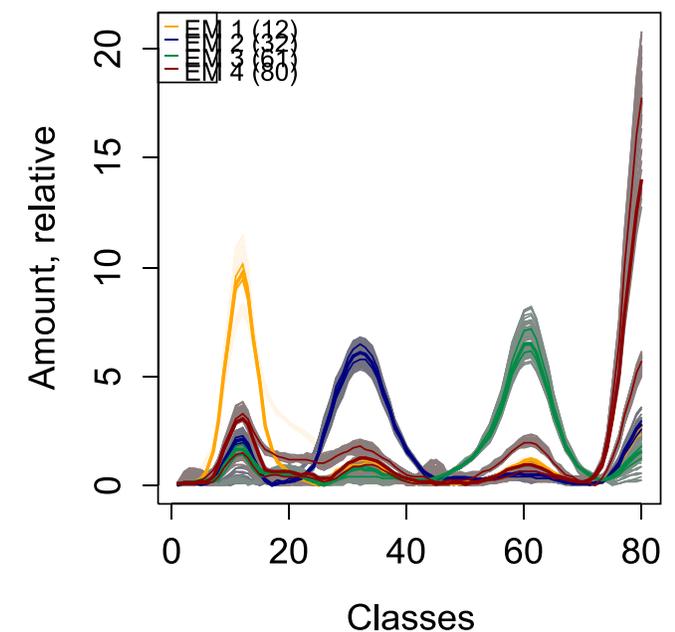
Functions: `test.robustness()`, `robust.EM()`

Several model scenarios are equally likely. Robust end-members persist throughout many scenarios. Goal is to identify and isolate robust end-members.

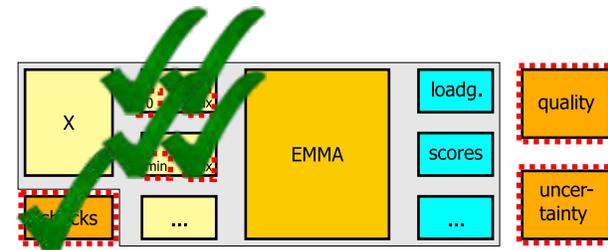
Mode positions of robust end-membe



End-member loadings (V_{qsn})



Robust end-member modelling - a protocol suggestion

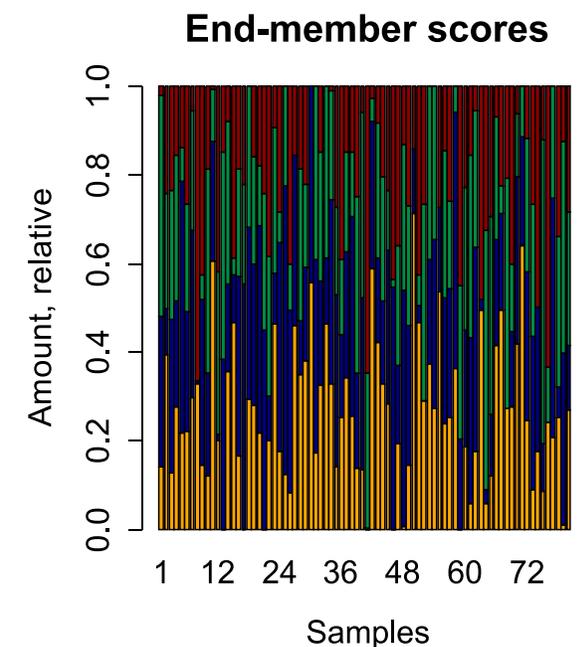
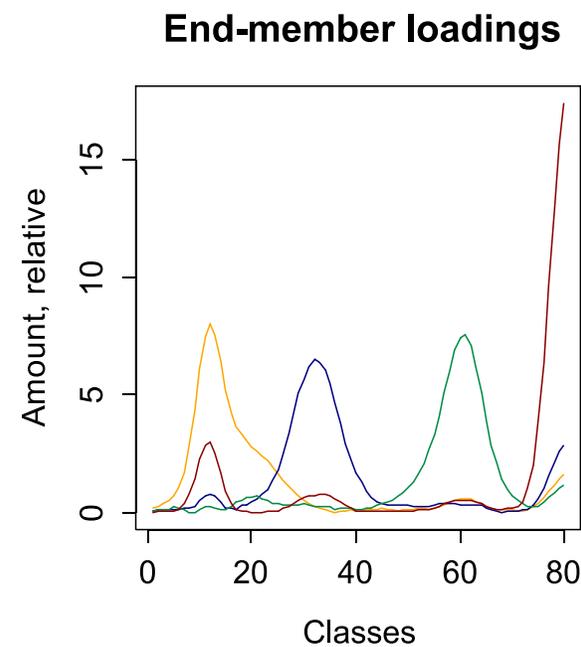
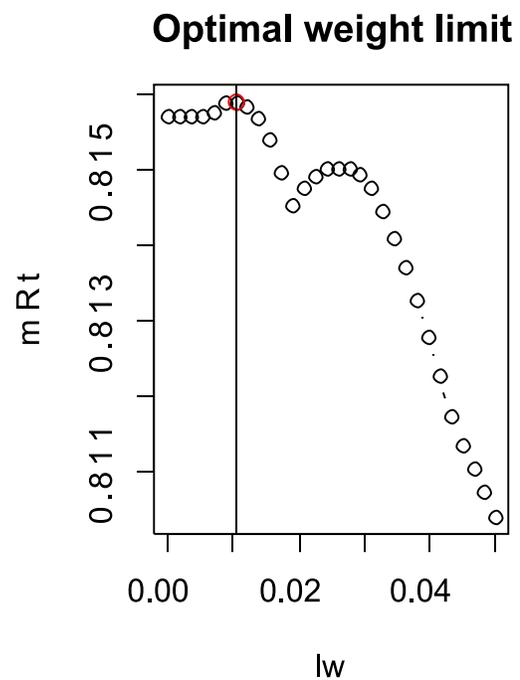


Protocol steps

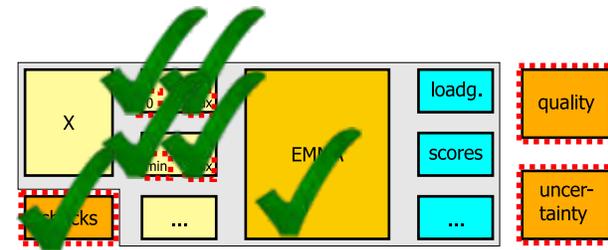
1. check the data
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4. calculate and extract robust end-members
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6. evaluate model quality
7. estimate model uncertainty

Functions: EMMA()

When all parameters are known and optimised, EMMA() can be run.



Robust end-member modelling - a protocol suggestion



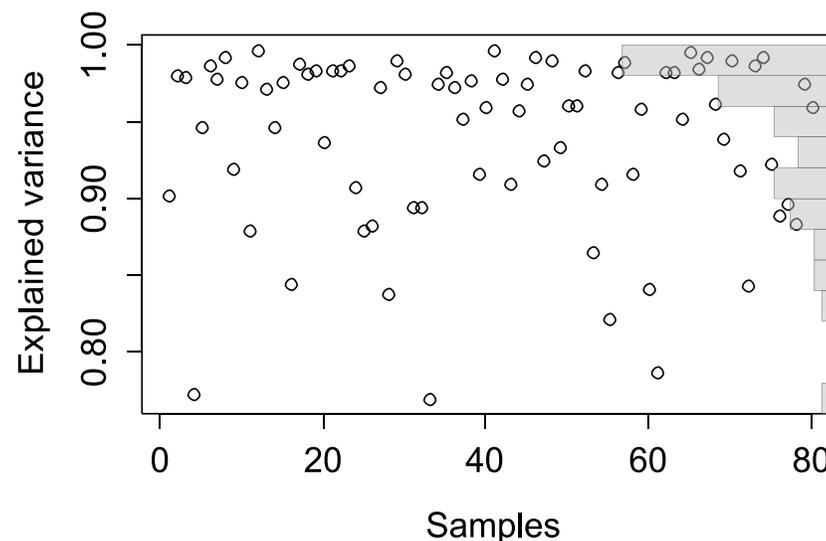
Protocol steps

1. check the data
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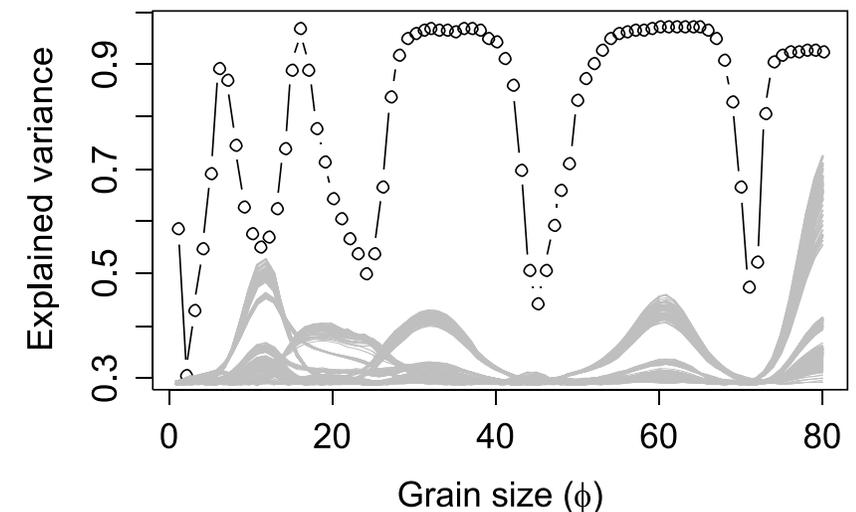
Functions: EMMA()

The quality of the model can be analysed row-wise (sample space) and column-wise (class-wise).

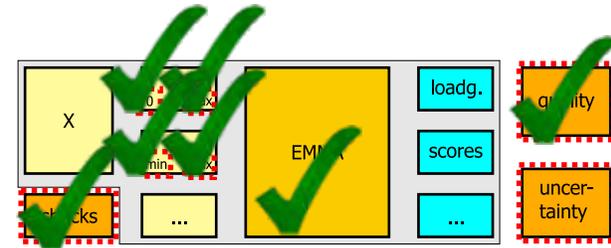
Row-wise model performance



Column-wise model performance



Robust end-member modelling - a protocol suggestion



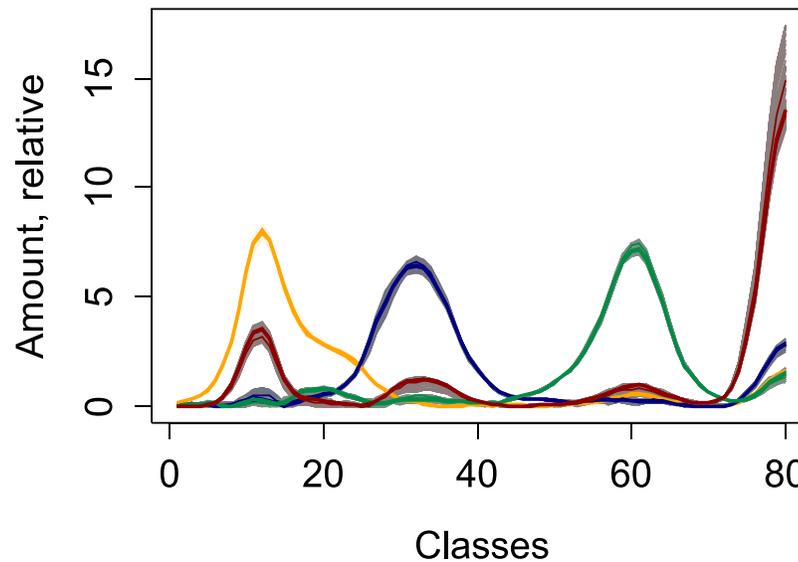
Protocol steps

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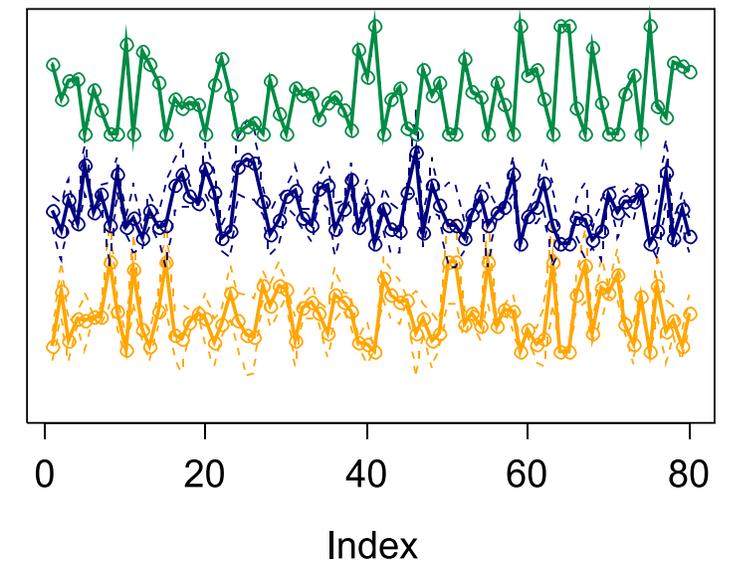
Functions: `test.robustness()`,
`Mqs.uncertainty()`

The uncertainty of the model can be analysed both, for loadings and scores.

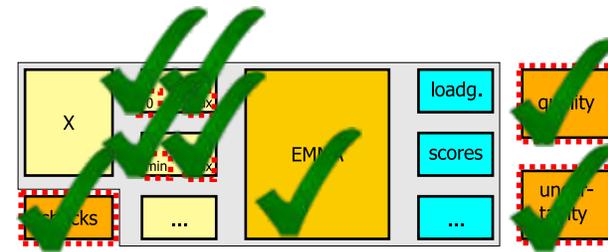
End-member loadings (V_{qsn})



End-member scores with uncertainty



Robust end-member modelling - a protocol suggestion



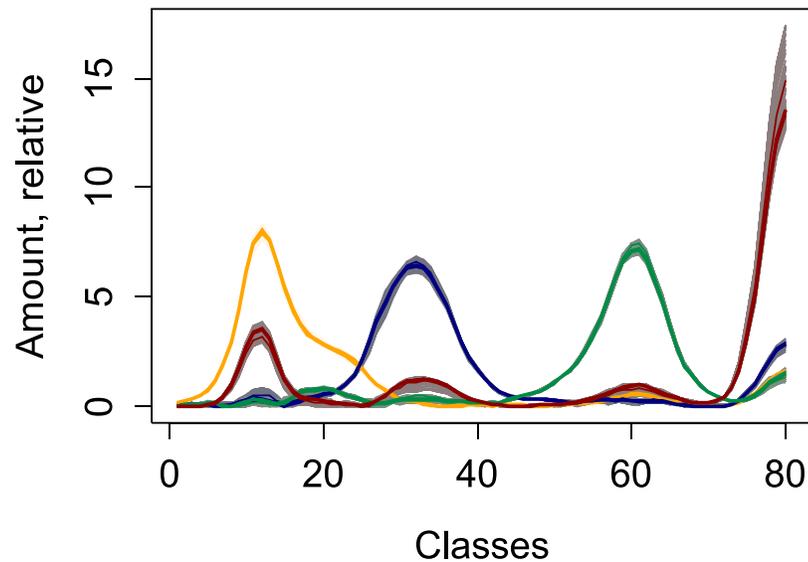
Protocol steps

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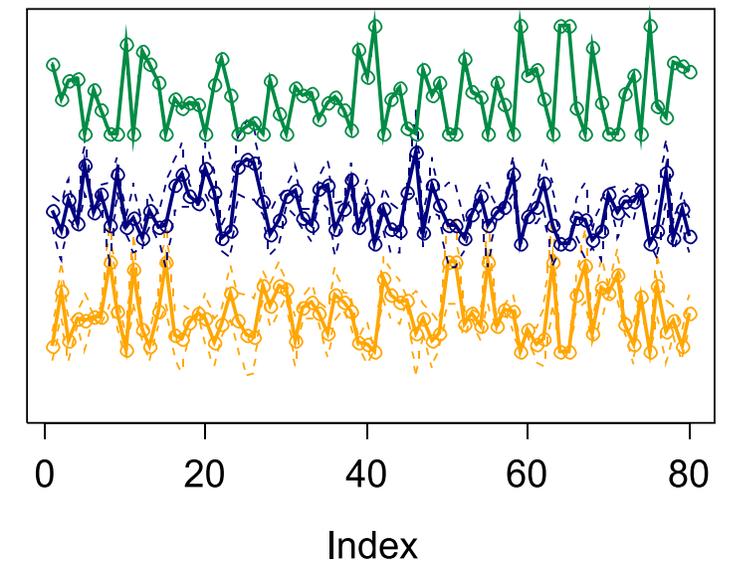
Functions: `test.robustness()`,
`Mqs.uncertainty()`

The uncertainty of the model can be analysed both, for loadings and scores.

End-member loadings (V_{qsn})



End-member scores with uncertainty



Validation and testing of the algorithm

Pick four process end-members

Measure their individual grain-size distributions

Mix them with given fractions

Measure the mixed samples (n = 100)

Perform EMMA on mixed samples

Evaluate model outputs

loadings (i.e. end-member shape)

scores (i.e. end-member contribution to each sample)

performance with only three end-members

protocol efficiency

...

The R-package
●●●●●●●●●●●●●●●●

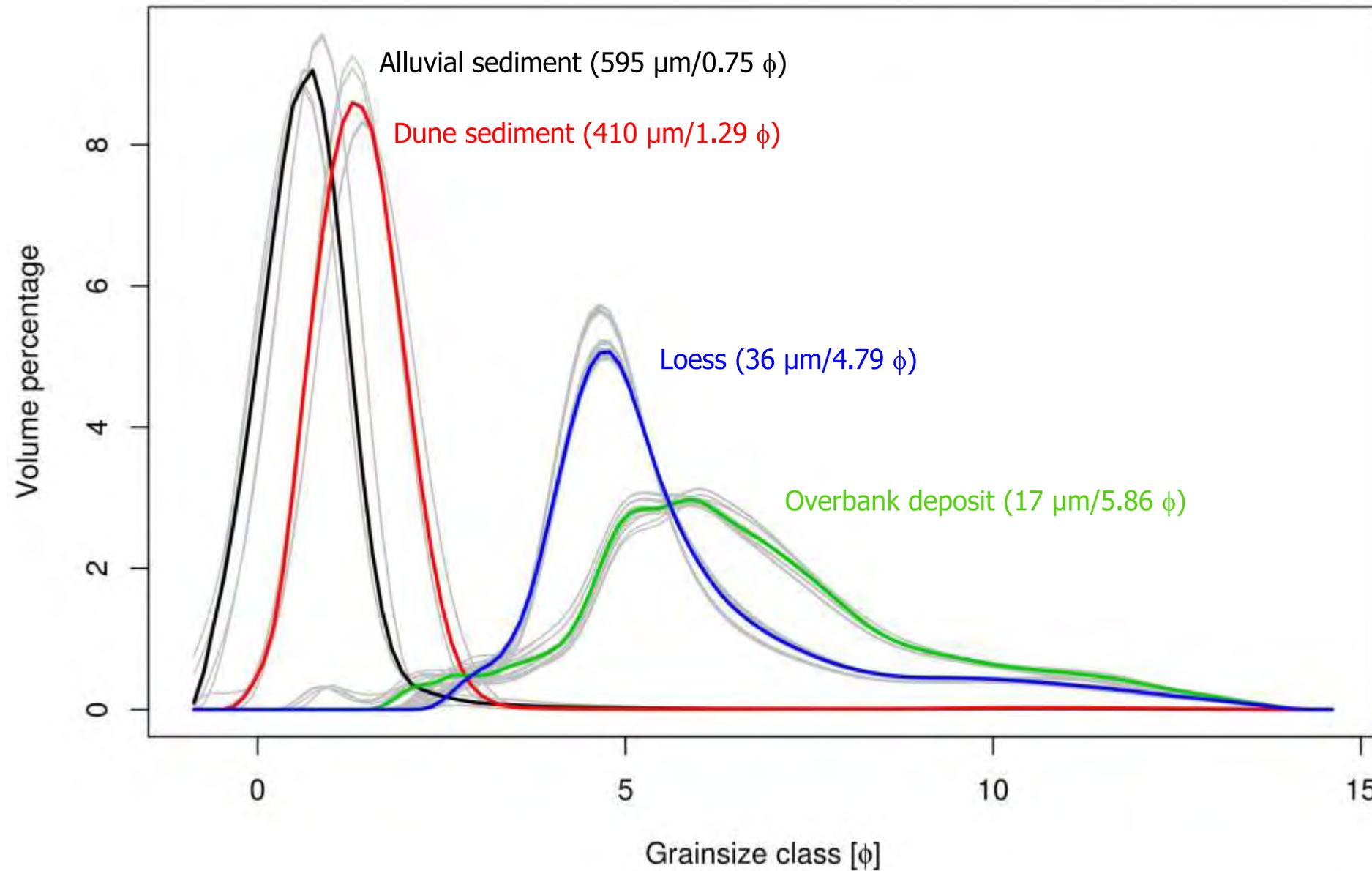
A universal modelling protocol
●●●●●●●●

Validation
●●○○○○

Future perspectives
○○○○○○

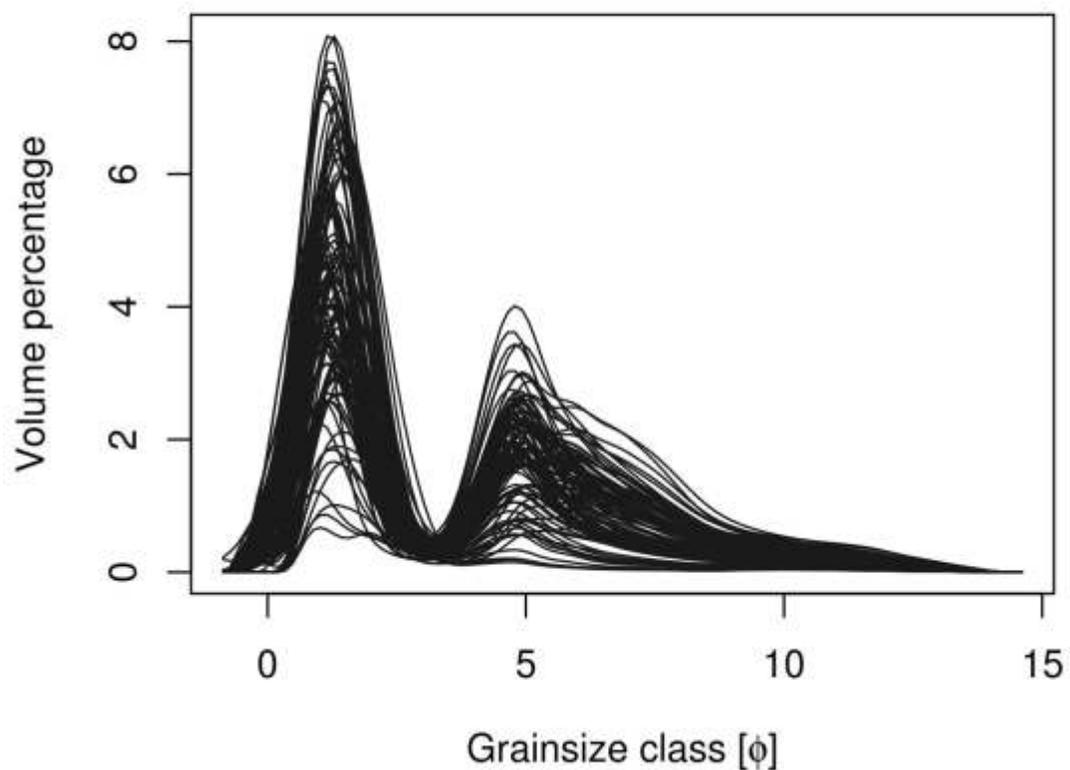


Grain-size distribution of four natural process end-members

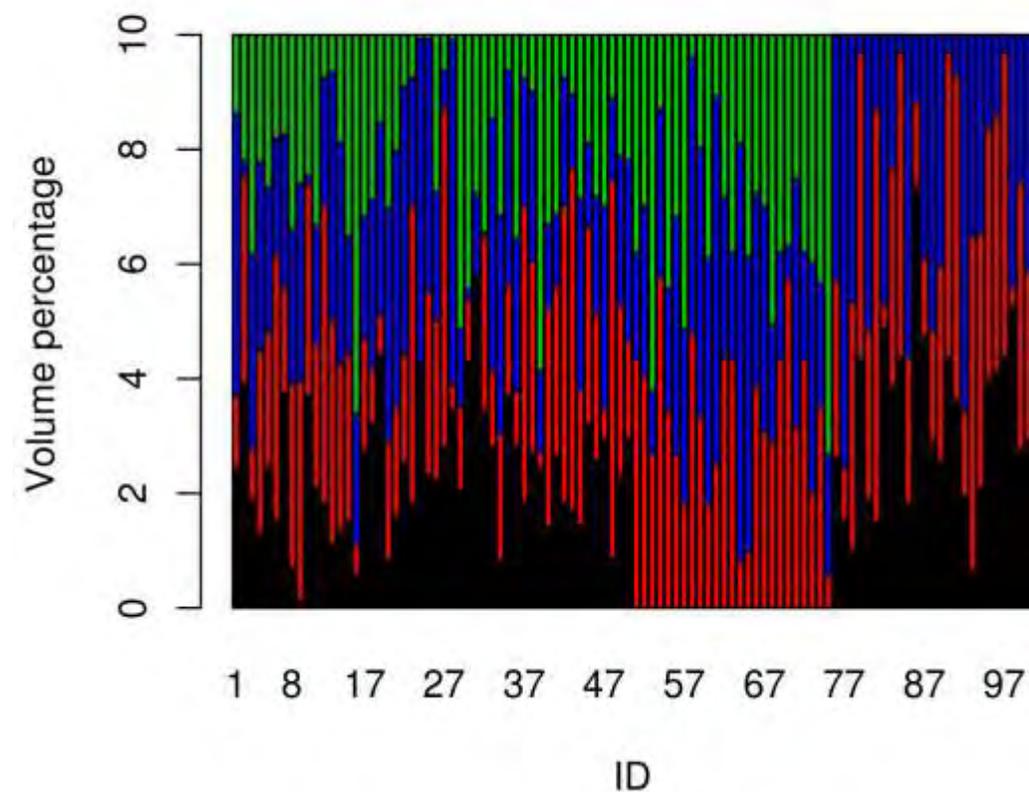


Grain-size distribution and mixing proportions of mixed samples

Mixed samples

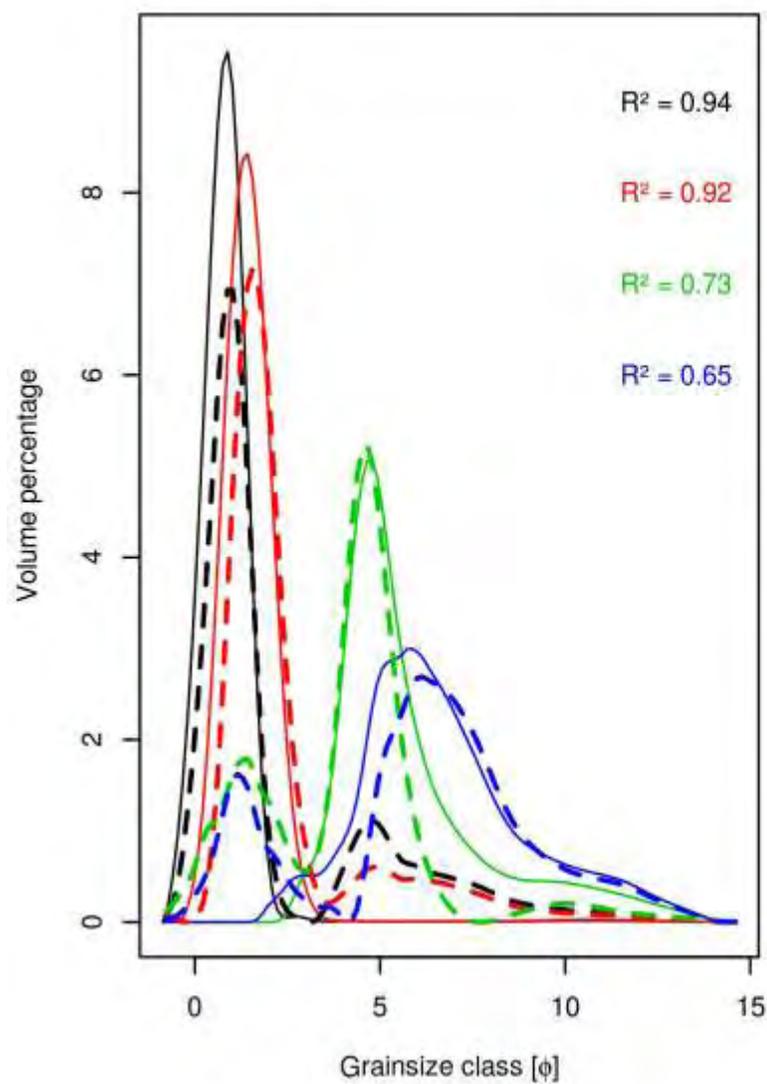


Mixing proportions

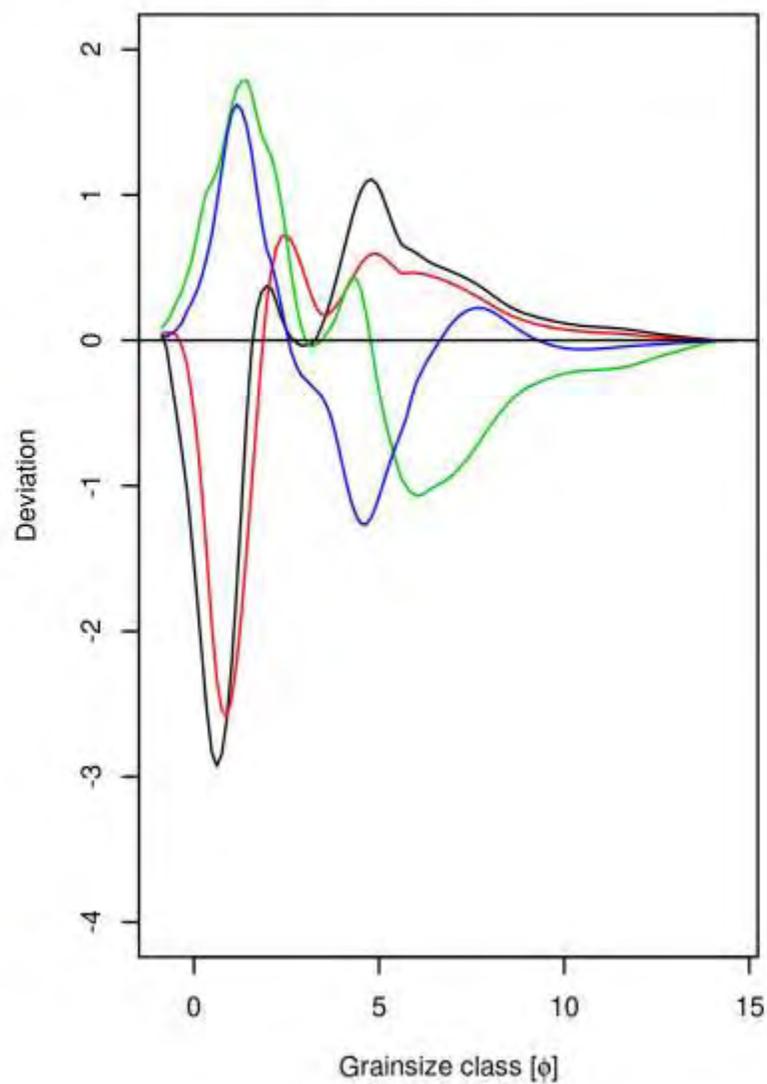


Visual validation of the model - loadings

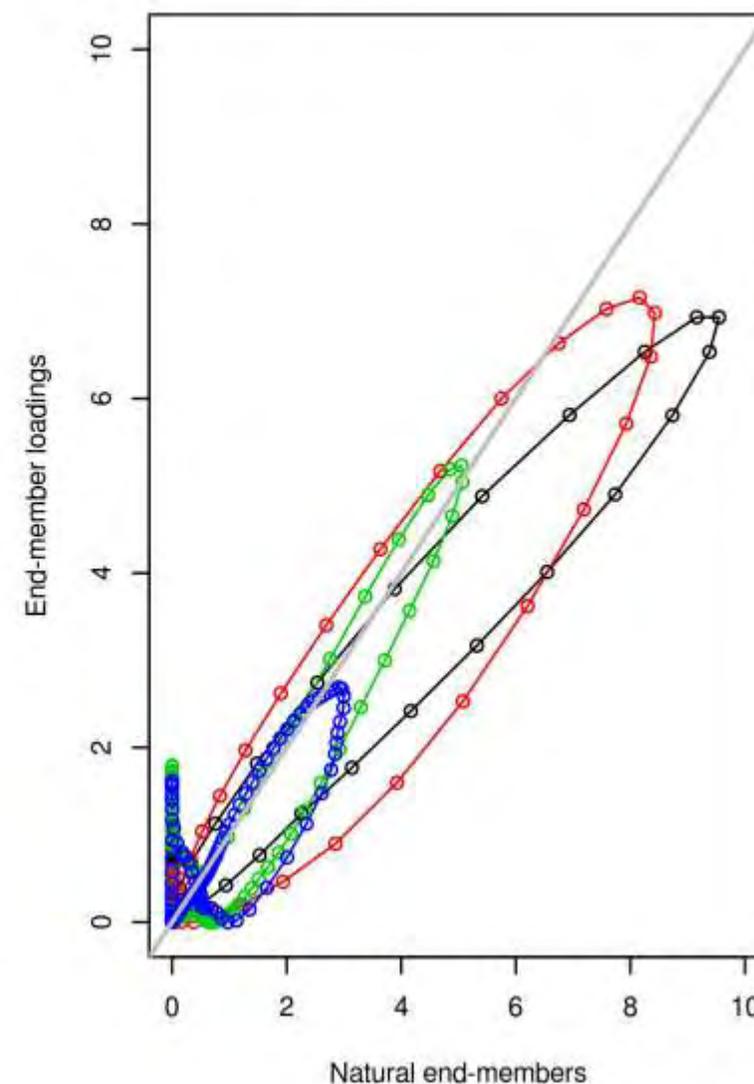
Natural and modelled end-members



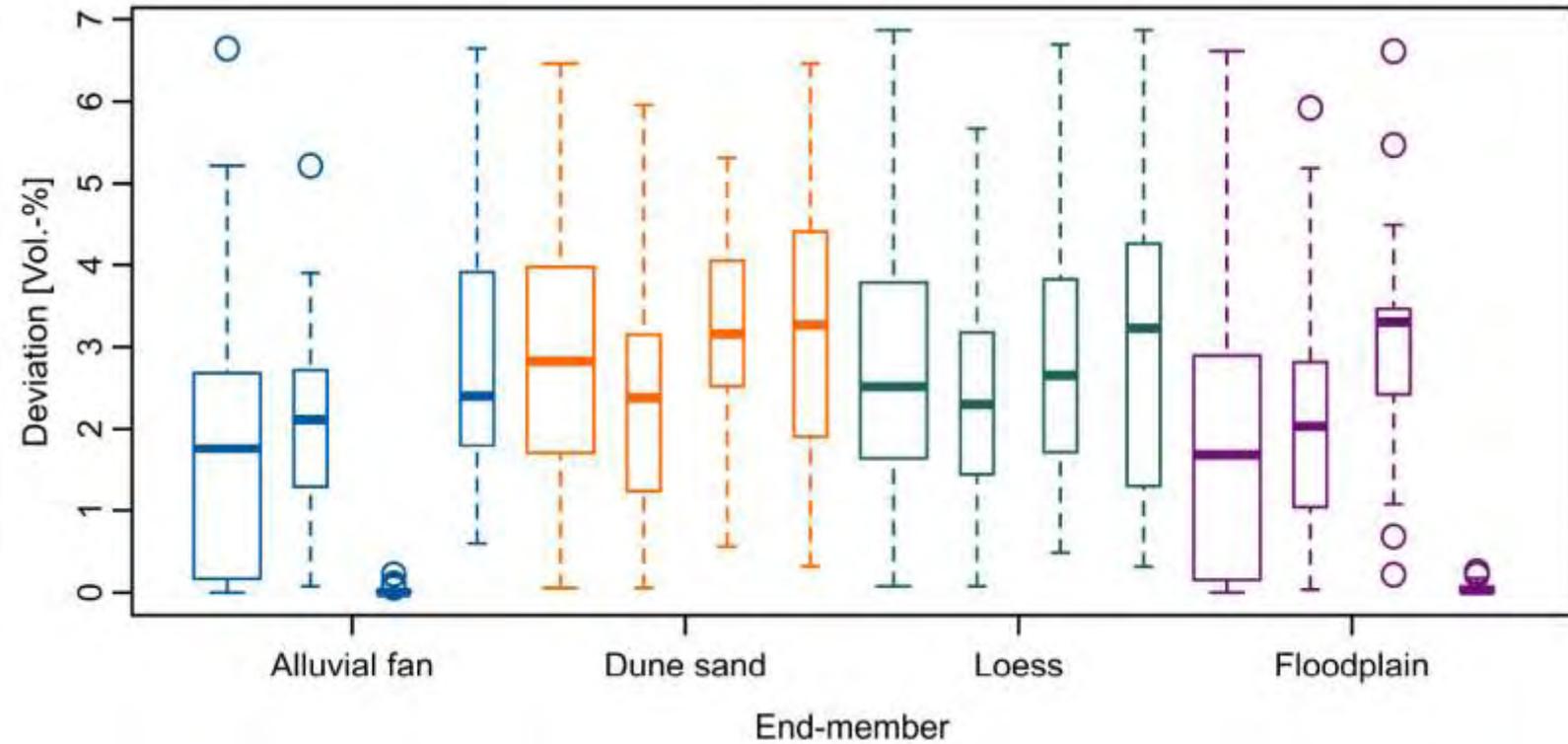
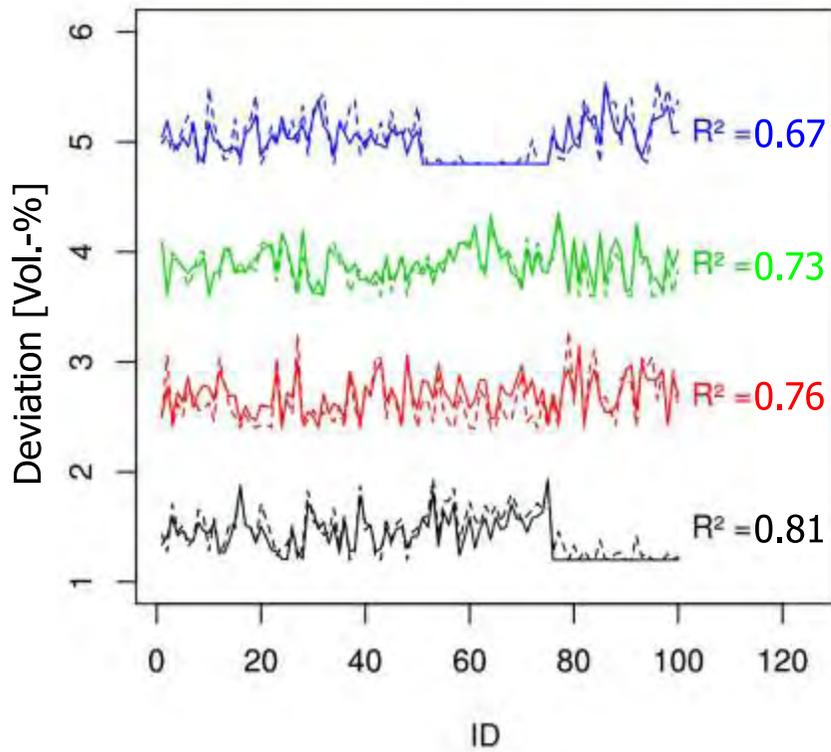
Model deviation



Data versus model

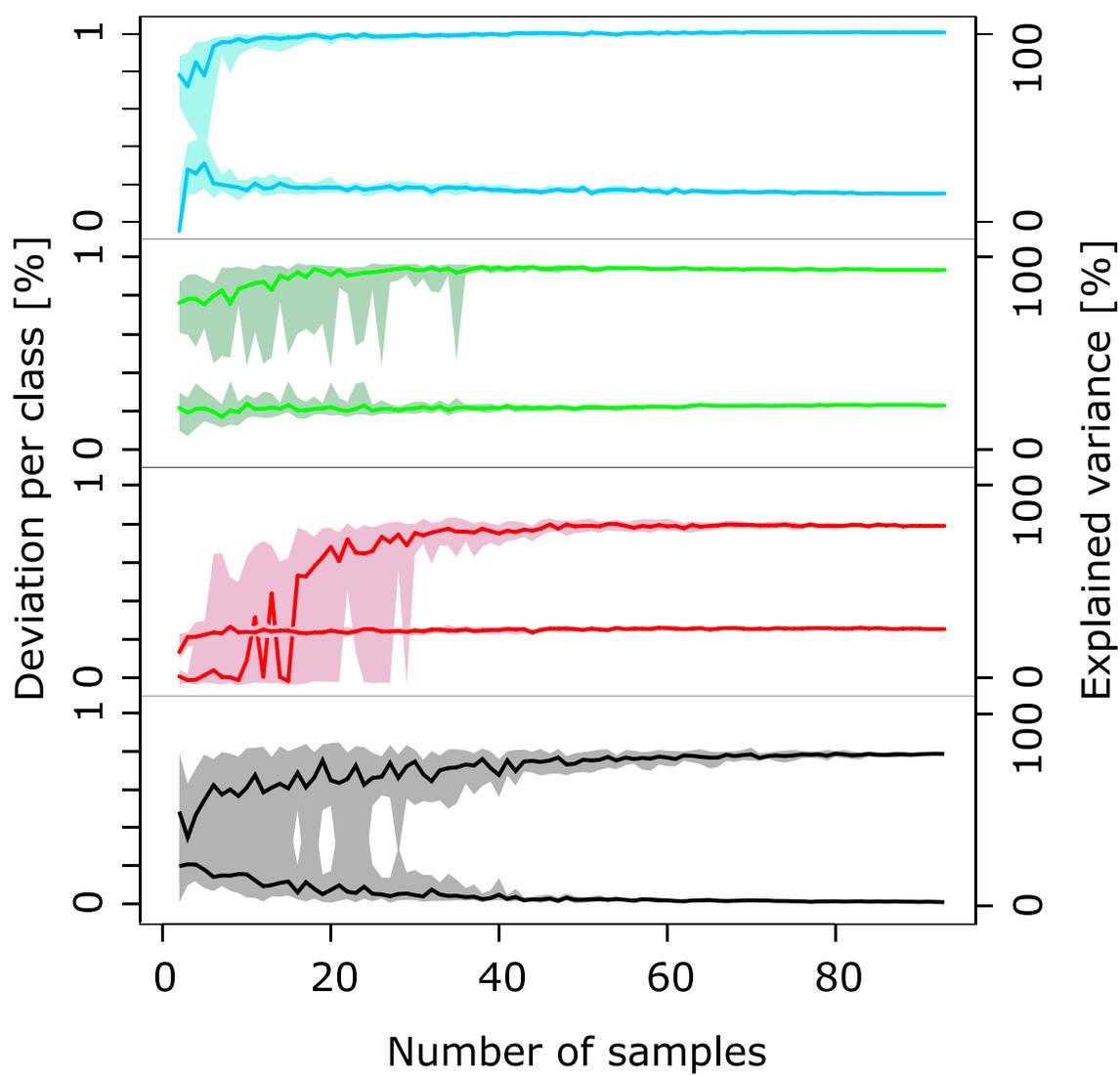


Visual validation of the model - scores

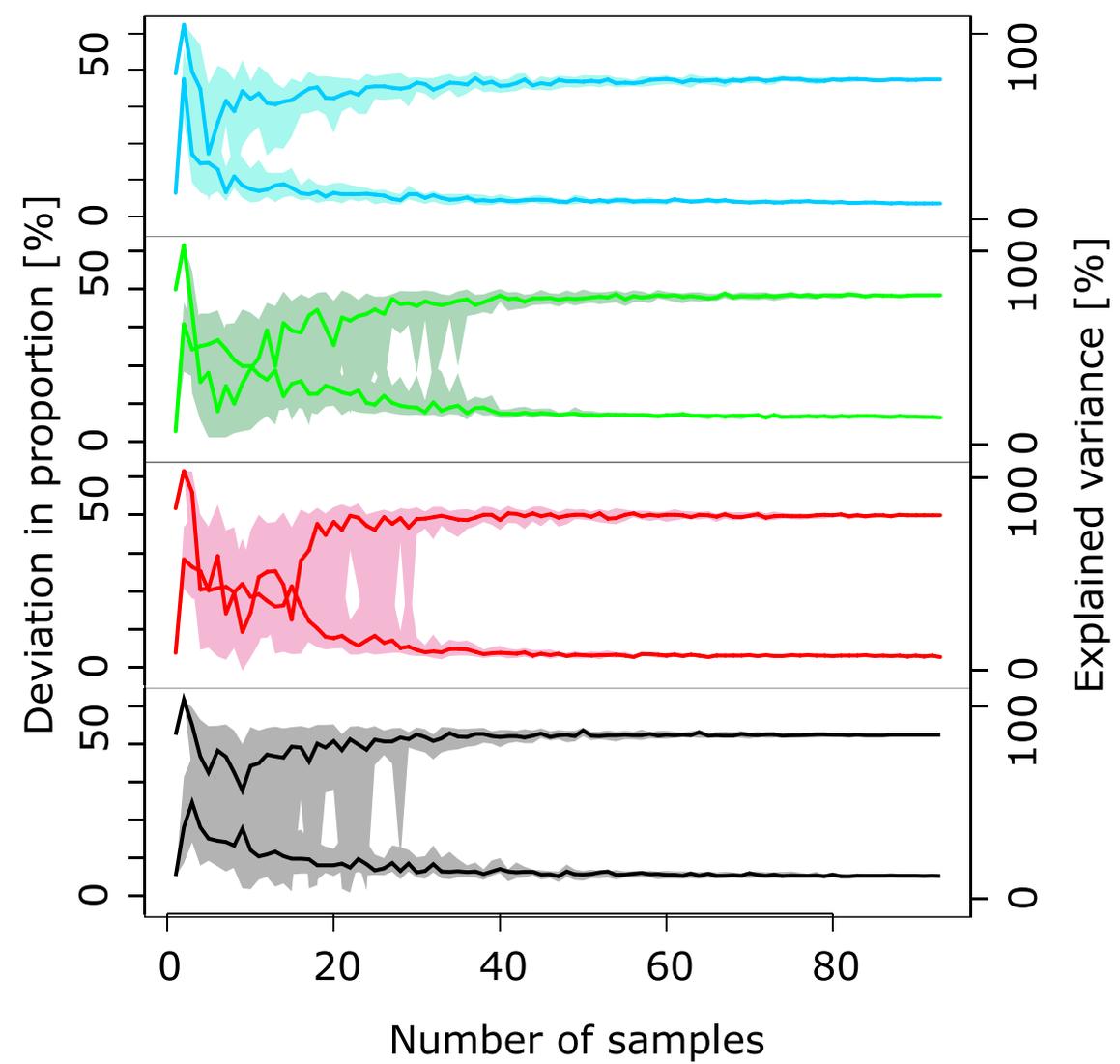


Visual validation of the model - number of samples

Loadings

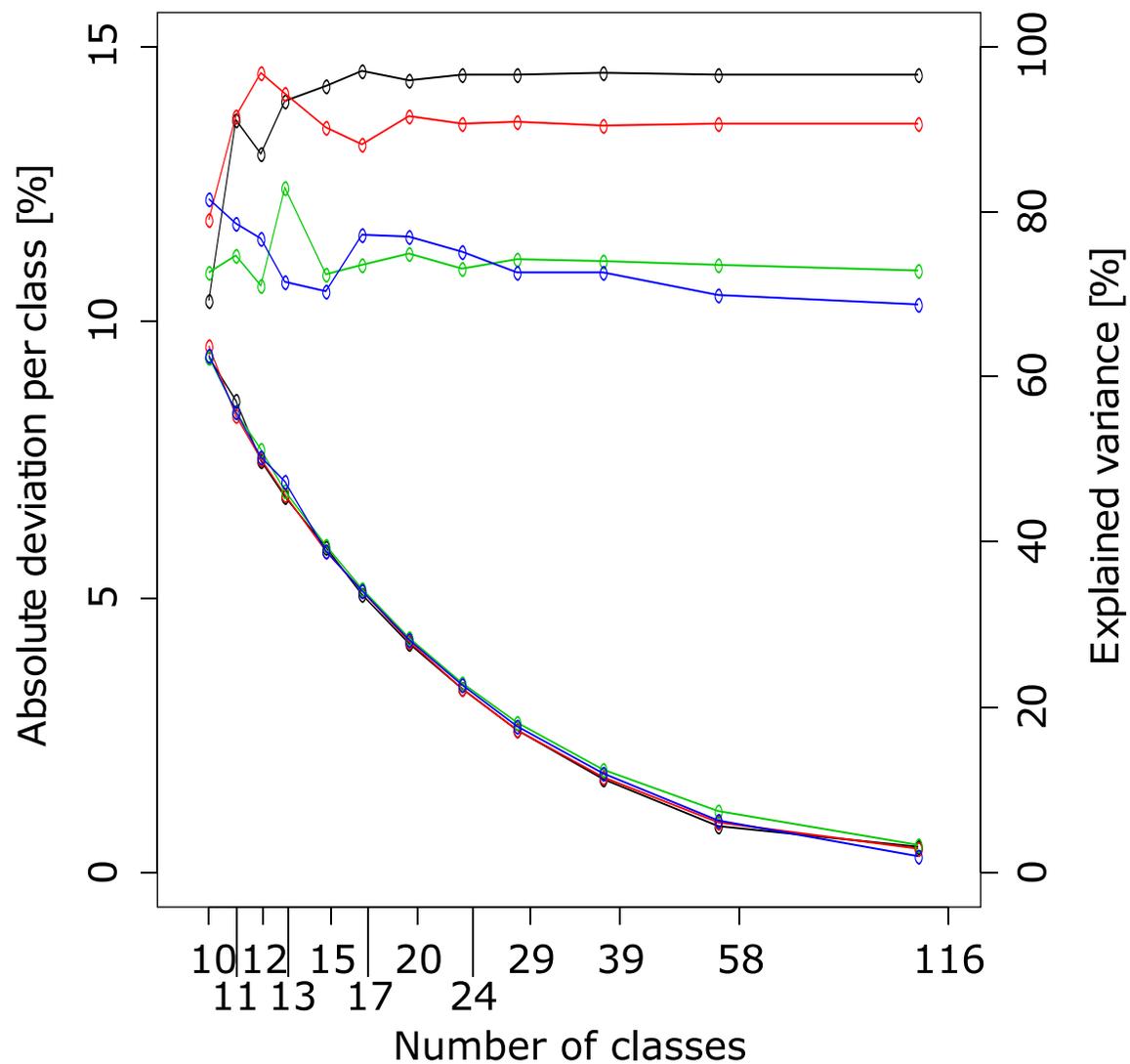


Scores

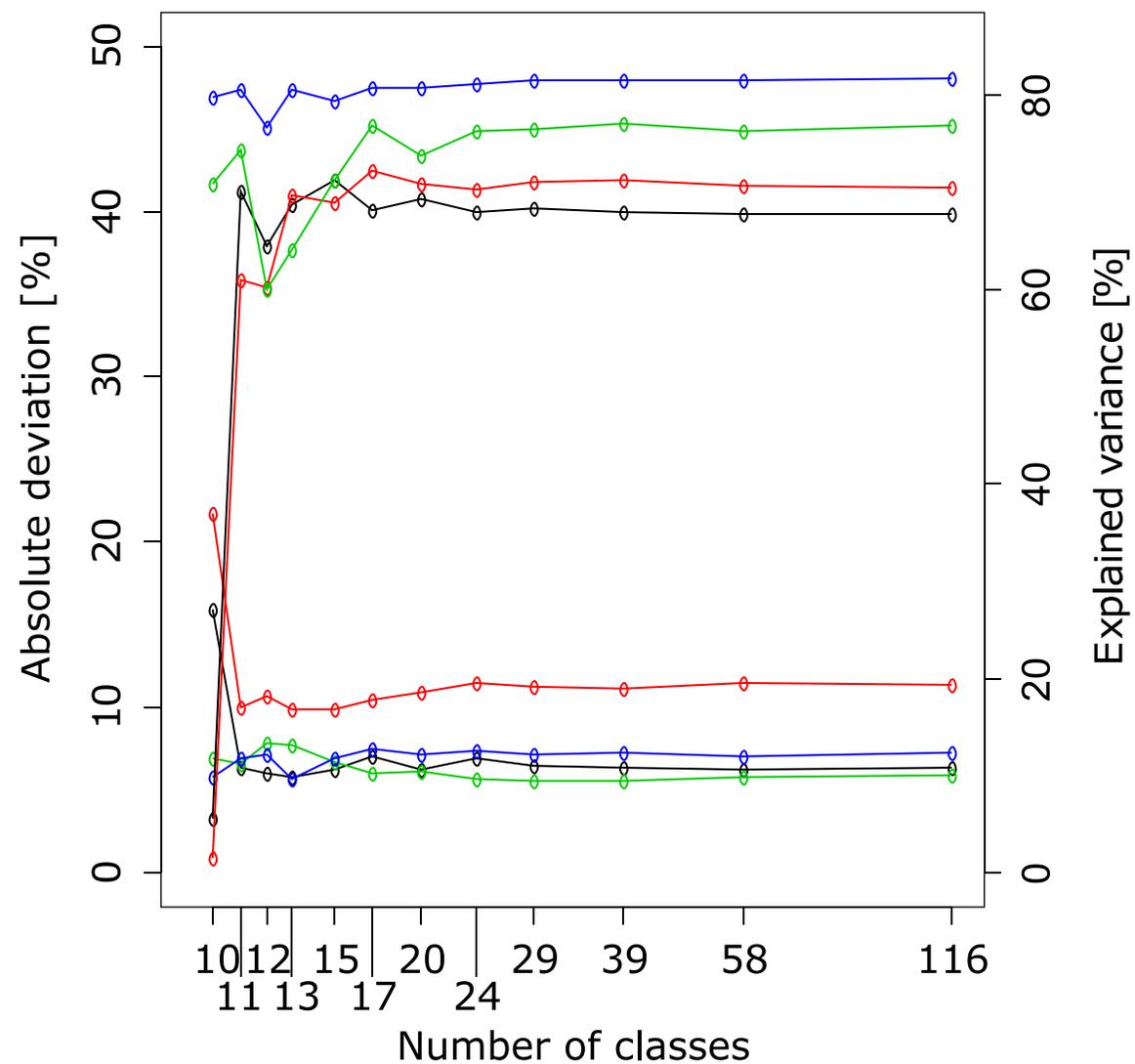


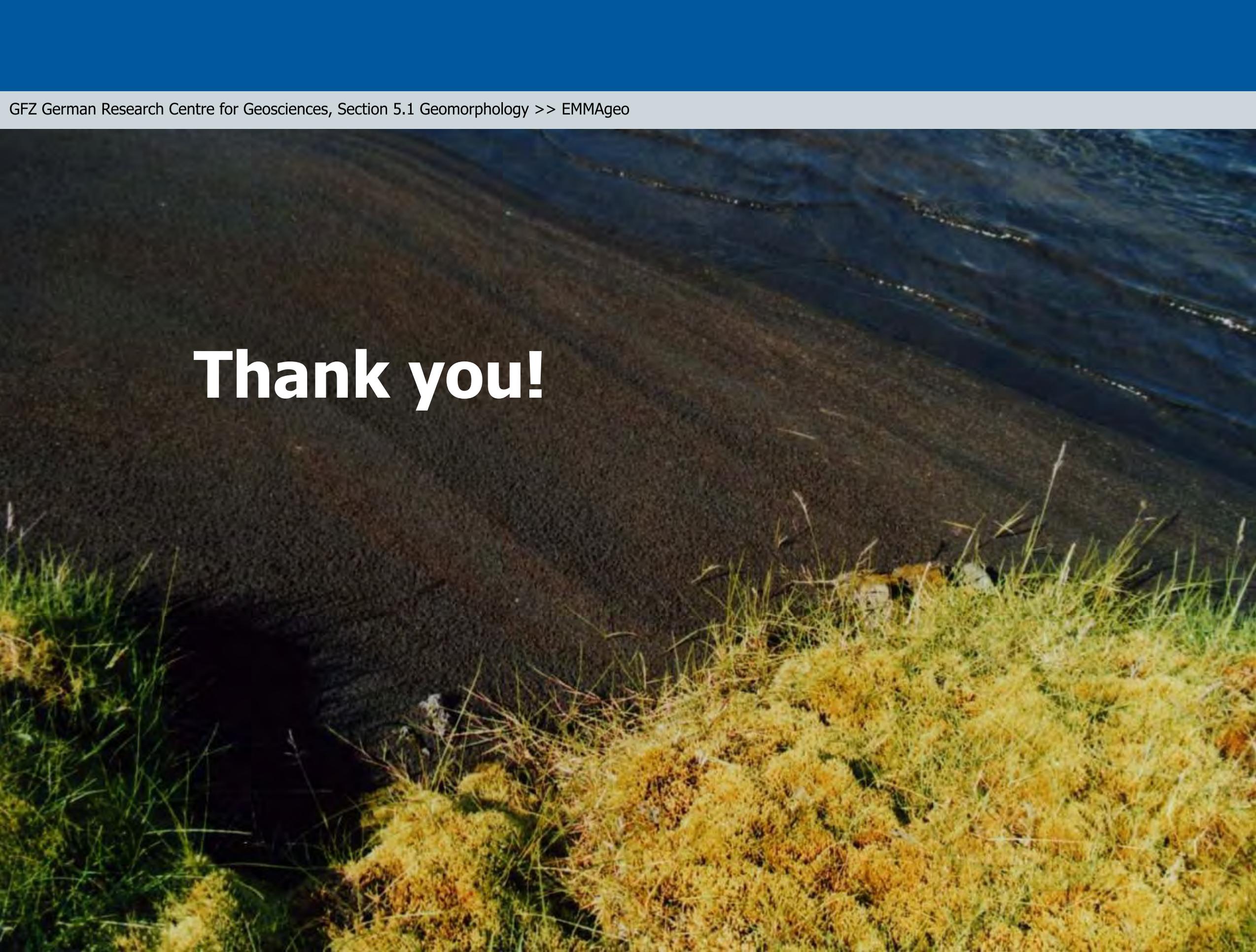
Visual validation of the model - number of classes

Loadings



Scores





Thank you!