

# nordpred

## Fit power5 and poisson Age-Period-Cohort models for prediction of cancer incidence

### Description

'nordpred' uses the power5 and poisson Age-Period-Cohort (APC) models to calculate prediction of cancer incidence and mortality

### Usage

```
nordpred(cases,pyr,startestage,startuseage,noperiods=NULL,recent=NULL,
         cuttrend=c(0,.25,.5,.75,.75),linkfunc="power5")
```

### Arguments

<code>cases</code>	A <code>data.frame</code> with number of cases
<code>pyr</code>	A <code>data.frame</code> with observed and forecasted person years.
<code>startestage</code>	Youngest age group to be included in the regression model. Predictions for age groups below this limit it based on average rates from the last 10 years.
<code>startuseage</code>	Youngest age group which uses regression model as basis for predicted rates
<code>noperiods</code>	A list of candidate number of periods in prediction base (e.g 4:6).If the goodness of fit test is rejected based on the widest base (e.g.6 periods), the first period is exclude etc. Use a fixed number to force a specific prediction base. If e.g. <code>noperiods=5</code> , predictions is based on the last 5 five-year periods, irrespective of the result a goodness of fit evaluation
<code>recent</code>	Project average trend or use the slope for the last 10 years? (If <code>recent=F</code> , average trend for the whole observation period is used, if <code>recent=T</code> , the slope from the last 10 years is used. If <code>NULL</code> (default) the choice is based on a significance test for departure from linear trend
<code>cuttrend</code>	Cut trend in predictions? Default is 0, 25 %, 50 %, 75 %, 75 % cut in drift (a vector of proportions of drift to cut in each projection period)
<code>linkfunc</code>	Link function to use in the model. Default is special version used in the Nordpred project ("power5"), where the link is $g(x)=x^{0.2}$ , while the alternative is the poisson function ("poisson"), where the link is $g(x)=\log(x)$

### Details

For details of the choice of prediction base, significance test for using recent slope, and for the power5 model, see Møller B., Fekjær H. et al. (2002), see references

## Value

an object of class "nordpred".

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
# Reading package:
source("nordpred.S")
# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)
```

```

# Fit model & predict new incidence:
res <-
nordpred(indata, inpop, startestage=5, startuseage=6, cuttrend=c(0, .25, .5, .
75, .75))
res2 <-
nordpred(indata, inpop, startestage=5, startuseage=6, cuttrend=c(0, .25, .5, .
75, .75), linkfunc="poisson")

# Print / get results:
print(res)
nordpred.getpred(res)
summary(res, printpred=F)

# Get results with standardisation:
wstand <- c(0.12, 0.1, 0.09, 0.09, 0.08, 0.08, 0.06, 0.06, 0.06,
0.06, 0.05,
          0.04, 0.04, 0.03, 0.02, 0.01, 0.005, 0.005)
round(nordpred.getpred(res, incidence=T, standpop=NULL), 2)
round(nordpred.getpred(res, incidence=T, standpop=wstand), 2)

# Plot results:
plot(res, standpop=wstand)

# Plot results with power5 and poisson links:
plot(res2, standpop=wstand)
plot(res, new=F, lty=c(1,2), standpop=wstand)

# Different cut trend scenarios, using average drift (recent=F):
plot(nordpred.prediction(est, startuseage=6, cuttrend=c(0,0,0,0,0), recent
=F), standpop=wstand, new=T)
plot(nordpred.prediction(est, startuseage=6, cuttrend=c(1,1,1,1,1), recent
=F), standpop=wstand, new=F, lty=c(1,2))
plot(nordpred.prediction(est, startuseage=6, cuttrend=c(0, .25, .5, .75, .75)
, recent=F), standpop=wstand, new=F, lty=c(1,4))

```

---

# nordpred.estimate

## Estimate power5 and poisson Age-Period-Cohort models

### Description

'nordpred.estimate' estimates parameters in the power5 or poisson Age-Period-Cohort (APC) model

### Usage

```
nordpred.estimate(cases,pyr,noperiod,startestage,linkfunc="power5")
```

## Arguments

`cases` A `data.frame` with number of cases  
`pyr` A `data.frame` with observed and forecasted person years.  
`startestage` Youngest age group to include in the regression model  
`noperiod` The number of periods to be used in prediction base.  
`linkfunc` Link function to use in the model. Default is special version used in the Nordpred project ("power5"), where the link is  $g(x)=x^{0.2}$ , while the alternative is the poisson function ("poisson"), where the link is  $g(x)=\log(x)$

## Details

For details of the power5 model, see Møller B., Fekjær H. et al. (2002), see references

## Value

An object of class "nordpred.estimate".

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction

of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## See Also

nordpred, plot.nordpred, summary.nordpred, print.nordpred, getpred, nordpred.prediction, print.nordpred.estimate, nordpred.estimate.object

## Examples

```
# Reading package:
source("nordpred.S")
# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1, inpop2)

# Fit model using powerlink (default):
est <-
nordpred.estimate(cases=indata, pyr=inpop, noperiod=4, startestage=5)

# Fit model using poisson link:

est2 <- nordpred.estimate(indata, inpop, 4, 5, linkfunc="poisson")

# Print results:
print(est)
print(est$glm)

# Use estimat object to make predictions:

res <-
nordpred.prediction(est, startuseage=6, cuttrend=c(0, .25, .5, .75, .75), rece
nt=T)
```

---

## nordpred.estimate.object

**Nordpred.estimate-object with fit of power5 and poisson Age-Period-Cohort models for prediction of cancer incidence**

## Description

'nordpred' uses the power5 and poisson Age-Period-Cohort (APC) models to calculate prediction of cancer incidence and mortality

This class of objects is returned by the `nordpred.estimate` class of functions to represent a fit of power5 and poisson Age-Period-Cohort models for prediction of cancer incidence

Objects of this class have methods for the functions `print`, `summary` and `plot`.

## COMPONENTS

The following components must be included in a legitimate `nordpred` object.

<code>glm</code>	Fitted glm-object
<code>cases</code>	A <code>data.frame</code> with number of cases
<code>pyr</code>	A <code>data.frame</code> with observed and forecasted person years
<code>noperiod</code>	Number of periods used in estimate
<code>gofpvalue</code>	P-value for goodness of fit
<code>startstage</code>	Youngest age group which have been included in the regression model. Predictions for age groups below this limit it based on average rates from the last 10 years.
<code>suggestionrecent</code>	Indicator recommendation build on <code>pvaluerecent</code> for projecting of average trend or use the slope for the last 10 years? If <code>recent=F</code> , recommendation is to use average trend for the whole observation period, and if <code>recent=T</code> recommendation is to use the slope from the last 10 years
<code>pvaluerecent</code>	P-value for use of recent trend based on a significance test for departure from linear trend
<code>linkfunc</code>	Link function used in the model. Default is special version used in the Nordpred project ("power5"), where the link is $g(x)=x^{0.2}$ , while the alternative is the poisson function ("poisson"), where the link is $g(x)=\log(x)$

The object will also contain the following, for documentation see the `lm` object: `formula`, `terms`, `assign` and `call`.

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## See Also

`plot.nordpred`, `summary.nordpred`, `print.nordpred`, `nordpred.estimate`, `getpred`, `nordpred.prediction`, `print.nordpred.estimate`, `nordpred.object`

---

# nordpred.getpred

## Gets the observed and predicted incidence rates on matrix form

### Description

'nordpred.getpred' uses a nordpred object to extract the observed and predicted incidence rates

### Usage

```
nordpred.getpred(nordpred.object, incidence=T, standpop=NULL, excludeobs=F, byage, agegroups="all")
```

## Arguments

<code>nordpred.object</code>	An object based on the 'nordpred()' or 'nordpred.prediction()' function
<code>incidence</code>	Indicates whether to give incidence or number of cases
<code>standpop</code>	A vector of weights for age standardisation. Default is no standardisation (crude rates), but using a standardisation (for the suitable no of age groups) is recommended
<code>excludeobs</code>	Exclude number for observed periods and only give numbers for predicted periods
<code>byage</code>	Report numbers by age groups. If false, crude or age standardised rates are given
<code>agegroups</code>	Which agegroups to include. E.g. <code>c(5:18)</code> includes age groups five to eighteen

## Value

an object of class "nordpred".

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction

of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
# Reading package:
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model & predict new incidence:
res <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75))
res2 <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75),linkfunc="poisson")

# Print / get results:
print(res)
nordpred.getpred(res)
summary(res,printpred=F)

# Get results with standardisation:
wstand <- c(0.12, 0.1, 0.09, 0.09, 0.08, 0.08, 0.06, 0.06, 0.06,
0.06,0.05,
          0.04, 0.04, 0.03, 0.02, 0.01, 0.005, 0.005)
round(nordpred.getpred(res,incidence=T,standpop=NULL),2)
round(nordpred.getpred(res,incidence=T,standpop=wstand),2)
```

---

## nordpred.object

**Nordpred-object with fit of power5 and poisson Age-Period-Cohort models and related predictions for use on of cancer incidence data**

### Description

'nordpred' uses the power5 and poisson Age-Period-Cohort (APC) models to calculate prediction of cancer incidence and mortality

This class of objects is returned by the `nordpred` class of functions to represent a fit of power5 and poisson Age-Period-Cohort models for prediction of cancer incidence

Objects of this class have methods for the functions `print`, `summary` and `plot`.

## COMPONENTS

The following components must be included in a legitimate `nordpred` object.

`predictions`

A `data.frame` with forecasted number of cases

`pyr`

A `data.frame` with observed and forecasted person years

`nopred`

Number of periods predicted

`noperiod`

Number of periods used in estimate

`gofpvalue`

P-value for goodness of fit

`recent`

Indicator for project of average trend or use the slope for the last 10 years? If `recent=F`, average trend for the whole observation period have been used, and if `recent=T` the slope from the last 10 years have been used

`pvaluerecent`

P-value for use of recent trend based on a significance test for departure from linear trend

`cuttrend`

Degree of trend cut in predictions

`startuseage`

Youngest age group which uses regression model as basis for predicted rates

`startstage`

Youngest age group which have been included in the regression model. Predictions for age groups below this limit it based on average rates from the last 10 years.

`glm`

Fitted `glm`-object

The object will also contain the following, for documentation see the `lm` object: `formula`, `terms`, `assign` and `call`.

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## See Also

`plot.nordpred`, `summary.nordpred`, `print.nordpred`, `nordpred.estimate`, `getpred`, `nordpred.prediction`, `print.nordpred.estimate`, `nordpred.estimate.object`

---

# nordpred.prediction

## Calculates predictions based on a nordpred.estimate object

### Description

'nordpred.prediction' uses a nordpred.estimate object to calculate prediction of cancer incidence and mortality

### Usage

```
nordpred.prediction(nordpred.estimate.object, startuseage, recent, cuttrend=c(0, .25, .5, .75, .75))
```

## Arguments

<code>nordpred.estimate.object</code>	A glm-object based on the 'nordpred.estimate()' function
<code>startuseage</code>	Youngest age group which uses regression model as basis for predicted rates
<code>recent</code>	Project average trend or use the slope for the last 10 years? (If recent=F, average trend for the whole observation period is used, if recent=T, the slope from the last 10 years is used)
<code>cuttrend</code>	Cut trend in predictions? (a vector of proportions of drift to be cut in each projection period)

## Details

For details of the significance test for using recent slope, see Møller B., Fekjær H. et al. (2003) 22:2751-2766, see references

## Value

an object of class "nordpred.prediction".

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
# Reading package:
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model using powerlink (default):
est <-
nordpred.estimate(cases=indata,pyr=inpop,noperiod=4,startestage=5)

# Fit model using poisson link:

est2 <- nordpred.estimate(indata,inpop,4,5,linkfunc="poisson")

# Use estimat object to make predictions:

res <-
nordpred.prediction(est,startuseage=6,cuttrend=c(0,.25,.5,.75,.75),rece
nt=T)
res2 <-
nordpred.prediction(est2,startuseage=6,cuttrend=c(0,.25,.5,.75,.75),rec
ent=T)

# Get results:
print.nordpred(res)
nordpred.getpred(res)
summary(res,printpred=F)
```

---

# plot.nordpred

**plots the predicted rates from a nordpred object**

## Description

'plot.nordpred' uses nordpred object to plot observed and predicted rates

## Usage

```
plot.nordpred  
(nordpred.object, incidence=T, standpop=NULL, agegroups="all", startplot=1,  
xlab="", ylab="", main="", labels=NULL, ylim=NULL, lty=c(1,3), col=c(1,1), new  
=T, ...)
```

## Arguments

nordpred.object	An object based on the 'nordpred()' or 'nordpred.prediction()' function
incidence	Indicates whether to plot incidence or number of cases
standpop	A vector of weights for age standardisation. Default is no standardisation (crude rates), but using a standardisation (for the suitable no of age groups) is recommended
agegroups	Which agegroups to include
noperiods	Number of five year periods to make predictions for. Upper limit is five periods
recent	Project average trend or use the slope for the last 10 years? (If recent=F, average trend for the whole observation period is used, if recent=T (default) the slope from the last 10 years is used based on a significance test for departure from linear trend)
cuttrend	Cut trend in predictions? Default is 0, 25 %, 50 %, 75 %, 75 % cut in drift (a vector of proportions of drift to be cut in each projection period)
linkfunc	Link function to use in the model. Default is special version used in the Nordpred project ("power5"), where the link is $g(x)=x^{0.2}$ , while the alternative is the poisson function ("poisson"), where the link is $g(x)=\log(x)$

## Details

This function is a method for the generic function `plot` for class `nordpred`. It can be invoked by calling `plot` for an object `x` of the appropriate class, or directly by calling `plot.nordpred` regardless of the class of the object. For more available options, see `plot`

For details of the significance test for using recent slope, and for the power5 model, see Møller B., Fekjær H. et al. (2003) 22:2751-2766, see references

## Value

an object of class "nordpred".

## Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model & predict new incidence:
res <-
nordpred(indata, inpop, startestage=5, startuseage=6, cuttrend=c(0, .25, .5, .
75, .75))
res2 <-
nordpred(indata, inpop, startestage=5, startuseage=6, cuttrend=c(0, .25, .5, .
75, .75), linkfunc="poisson")
```

```

# Get results with stanardiziotion:
wstand <- c(0.12, 0.1, 0.09, 0.09, 0.08, 0.08, 0.06, 0.06, 0.06,
0.06,0.05,
          0.04, 0.04, 0.03, 0.02, 0.01, 0.005, 0.005)
round(nordpred.getpred(res,incidence=T,standpop=NULL),2)
round(nordpred.getpred(res,incidence=T,standpop=wstand),2)

# Plot results:
plot(res,standpop=wstand)

# Plot results with power5 and poisson links:
plot(res2,standpop=wstand)
plot(res,new=F,lty=c(1,2),standpop=wstand)

# Different cut trend scenarios, using average drift (recent=F):
plot(nordpred.prediction(est,startuseage=6,cuttrend=c(0,0,0,0,0),recent
=F),standpop=wstand,new=T)
plot(nordpred.prediction(est,startuseage=6,cuttrend=c(1,1,1,1,1),recent
=F),standpop=wstand,new=F,lty=c(1,2))
plot(nordpred.prediction(est,startuseage=6,cuttrend=c(0,.25,.5,.75,.75)
,recent=F),standpop=wstand,new=F,lty=c(1,4))

```

---

# print.nordpred

## Prints a nordpred object

### Description

'print.nordpred' prints the observed and predicted number of cases in a nordpred object

### Usage

```
print.nordpred(nordpred.object,digits=1)
```

### Arguments

`nordpred.object` An object based on the 'nordpred()' or 'nordpred.prediction()' function  
`digits` Specifies the number of digits in the tabulation

### Value

an object of class "nordpred".

### Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

## Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

## References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
# Reading package:
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model & predict new incidence:
res <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75))
res2 <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75),linkfunc="poisson")

# Print / get results:
```

```
print(res)
nordpred.getpred(res)
summary(res, printpred=F)
```

---

# print.nordpred.estimate

## Prints a nordpred estimate object

### Description

'print.nordpred.estimate' prints the estimation information from a nordpred.estimate object

### Usage

```
print.nordpred.estimate(nordpred.estimate.object)
```

### Arguments

nordpred.estimate.object An object produced by the 'nordpred.estimate()' function

### Value

an object of class "nordpred".

### Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

### Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

### References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer incidence in the Nordic countries: Empirical comparison of different approaches" *Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## See Also

`plot.nordpred`, `summary.nordpred`, `print.nordpred`, `nordpred.estimate`, `getpred`, `nordpred.prediction`, `print.nordpred`, `nordpred.estimate.object`

## Examples

```
# Reading package:
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model using powerlink (default):
est <-
nordpred.estimate(cases=indata,pyr=inpop,noperiod=4,startestage=5)

# Fit model using poisson link:

est2 <- nordpred.estimate(indata,inpop,4,5,linkfunc="poisson")

# Print results:
print(est)
print(est$glm)

# Use estimat object to make predictions:

res <-
nordpred.prediction(est,startuseage=6,cuttrend=c(0,.25,.5,.75,.75),rece
nt=T)
```

---

# summary.nordpred

## Makes a summary of a nordpred object

### Description

'summary.nordpred' uses a nordpred object to summarize the information

### Usage

```
summary.nordpred(nordpred.object, printpred=T, printcall=F, digits=1)
```

### Arguments

nordpred.object	An object based on the 'nordpred()' or 'nordpred.prediction()' function
printpred	Indicates whether to print the observed and predicted number of cases
printcall	Indicates whether to print the function call
digits	Specifies the number of digits in the tabulation

### Value

an object of class "nordpred".

### Note

Remark for S-PLUS users: Powerlink is made via a special modification in S-PLUS. This works fine for the point estimates, but the variance estimates found via the glm-objects are wrong. For variance estimates, we would rather recommend using R.

### Author(s)

Harald Fekjær and Bjørn Møller (Cancer Registry of Norway)

### References

A website for nordpred is available at: <http://www.kreftregisteret.no/software/nordpred/>

Examples is distributed with the package.

Background for the methods can be found in: Møller B., Fekjær H., Hakulinen T., Sigvaldason H, Storm H. H., Talbäck M. and Haldorsen T "Prediction of cancer

incidence in the Nordic countries: Empirical comparison of different approaches"  
*Statistics in Medicine* 2003; 22:2751-2766

An application of the function, using all the default settings, can be found in: Møller B, Fekjær H, Hakulinen T, Tryggvadóttir L, Storm HH, Talbäck M, Haldorsen T. Prediction of cancer incidence in the Nordic countries up to the year 2020. *Eur J Cancer Prev Suppl* 2002; 11: S1-S96

## Examples

```
# Reading package:
source("nordpred.S")

# Reading data (Colon cancer for Norwegian males)
indata <- read.table("data//colon-men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop1 <- read.table("data//men-Norway.txt",header
=T,sep=" ",row.names=1)
inpop2 <- read.table("data//men-Norway-pred.txt",header
=T,sep=" ",row.names=1)

# Include possible population predictions
inpop <- cbind(inpop1,inpop2)

# Fit model & predict new incidence:
res <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75))
res2 <-
nordpred(indata,inpop,startestage=5,startuseage=6,cuttrend=c(0,.25,.5,.
75,.75),linkfunc="poisson")

# Print / get results:
print(res)
nordpred.getpred(res)
summary(res,printpred=F)
```

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