Analysis species abundance data by iNEXT

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This is an simple guide for iNEXT. First install iNEXT R package from github repository (iNEXT is prepareing to submit to CRAN) by the following commends:

```r
# install.packages('devtools') # Tools to install R packages from github github repositories
devtools::install_github('iNEXT', 'JohnsonHsieh') # install iNEXT version 2.0 by devtools
```

```
## Installing github repo iNEXT/master from JohnsonHsieh
## Downloading master.zip from https://github.com/JohnsonHsieh/iNEXT/archive/master.zip
## Installing package from C:\Users\Johnson\AppData\Local\Temp\Rtmp6j5Aar/master.zip
## Installing iNEXT
## "C:/PROGRA~1/R/R-31~1.1/bin/x64/R" --vanilla CMD INSTALL  \
##   "C:\Users\Johnson\AppData\Local\Temp\Rtmp6j5Aar\devtools101c5f2177d8\iNEXT-master"  \
##   --library="C:/Users/Johnson/Documents/R/win-library/3.1"  \
##   --install-tests
```

Next, import iNEXT package and dataset

```r
library(iNEXT)
```

```
## Loading required package: ggplot2
```

```r
spec <- cbind(High =c(7,0,9,19,84,159),
              Intermediate =c(0,0,45,41,146,63),
              Low =c(15,3,3,10,126,4))
spec
```

```
##      High Intermediate Low
## [1,]    7            0  15
## [2,]    0            0   3
## [3,]    9           45   3
## [4,]   19           41  10
## [5,]   84          146 126
## [6,]  159           63   4
```
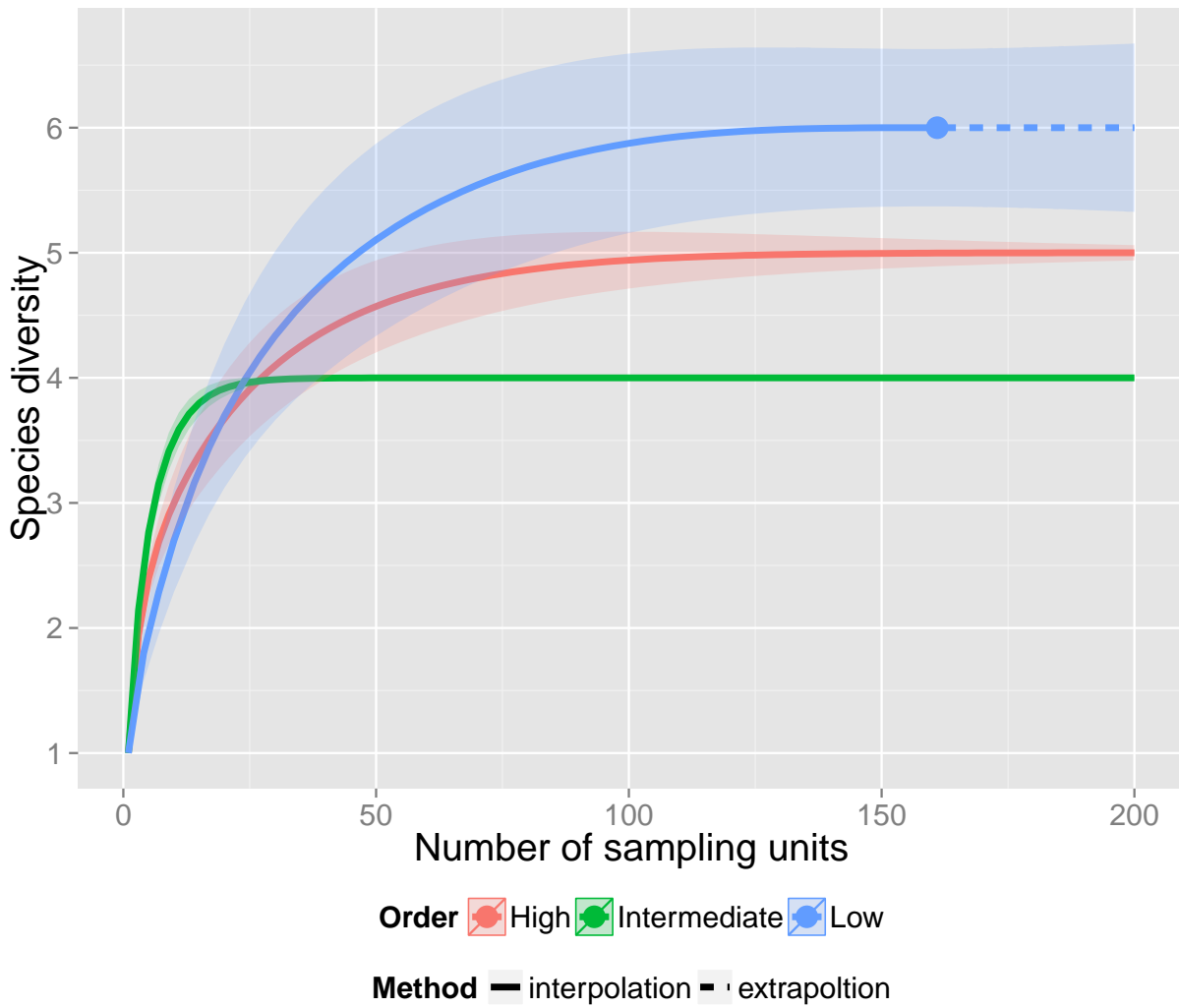
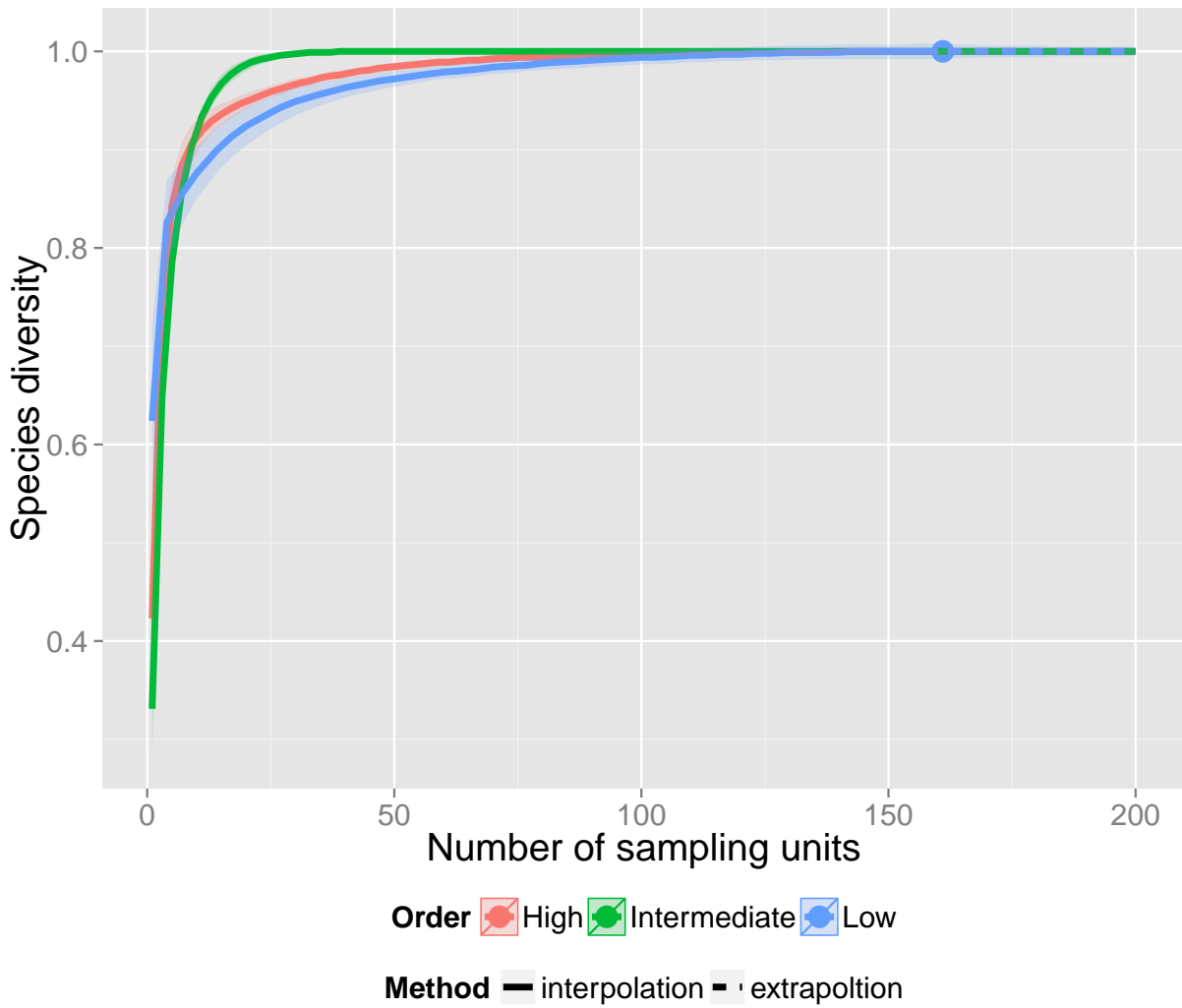Third, calculus species accumulation for each sites Compute species accumulations

```r
out <- iNEXT(x=spec, datatype="abundance", endpoint=200, knots=100, nboot=100)
```
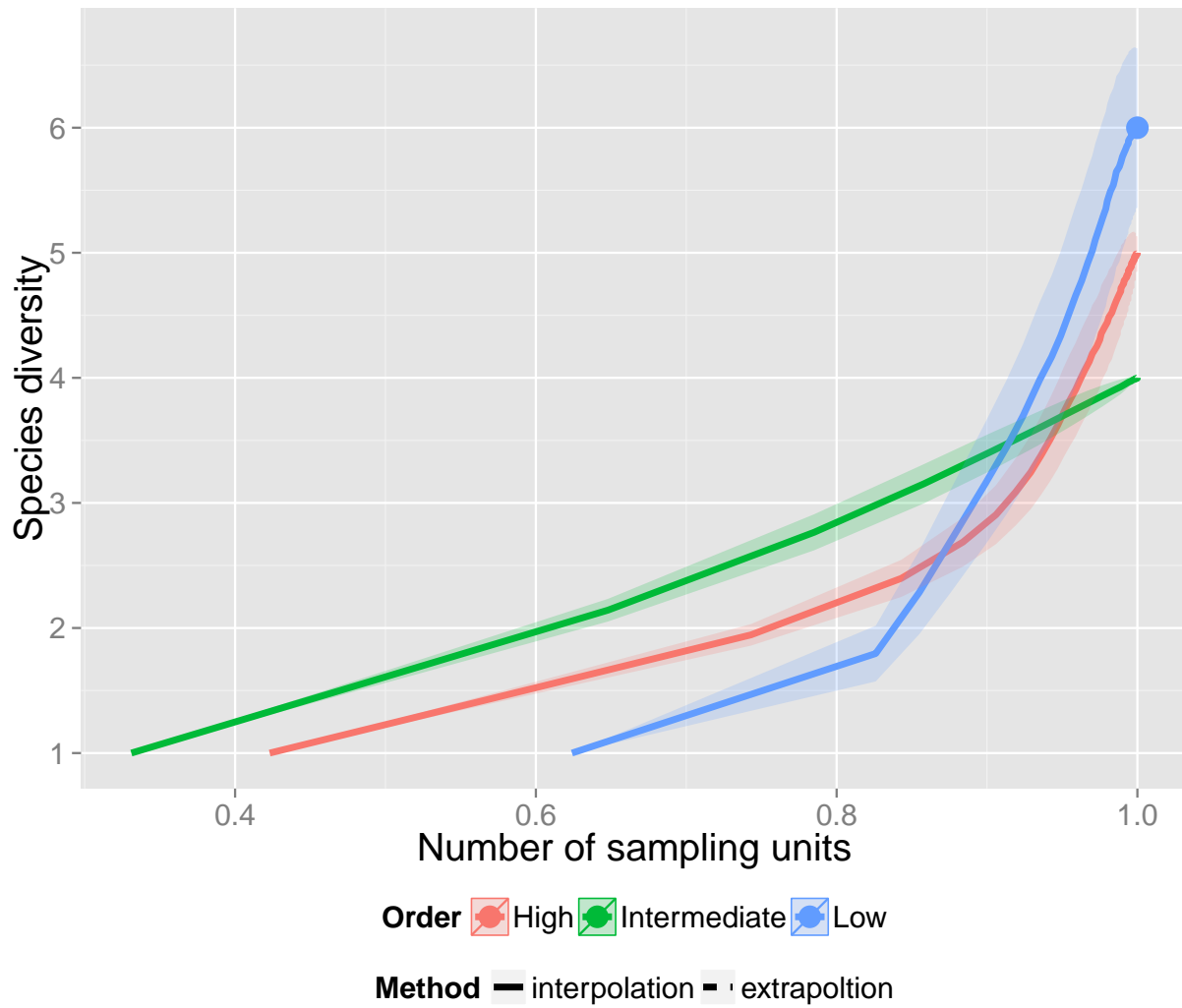
Data visualization
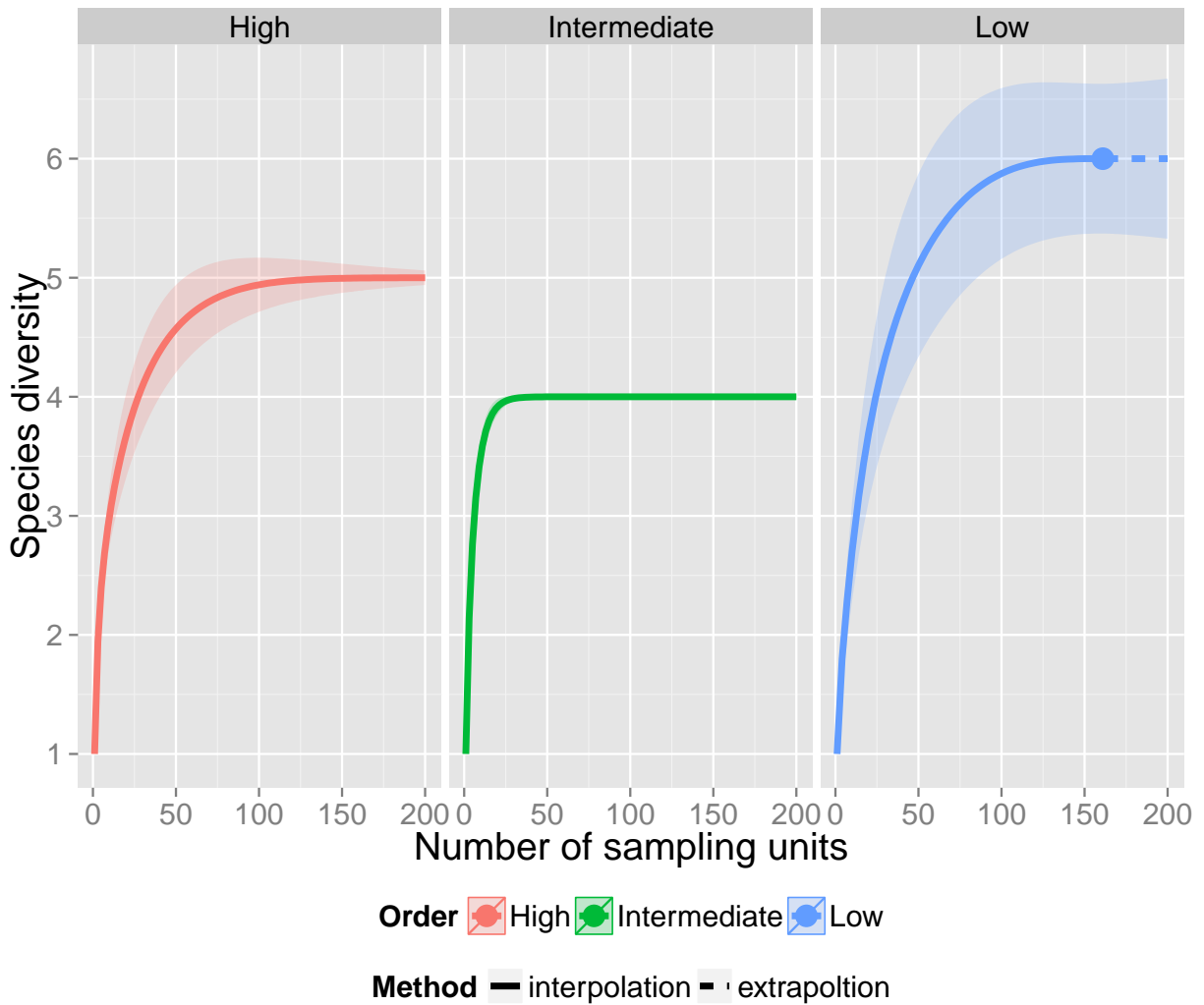
```r
ggiNEXT(out, type=1, color.var = "site")
```

```
ggiNEXT(out, type=2, color.var = "site")
```

Species diversity vs Number of sampling units

Order: High (red), Intermediate (green), Low (blue)

Method: interpolation (solid), extrapoltion (dashed)

```
ggiNEXT(out, type=3, color.var = "site")
```

```
ggiNEXT(out, type=1, facet.var = "site", color.var = "site")
```

Further, you can compute species diversity accumulations (e.g. Shannon entropy and Simpson index), see more introduction in Chao et al. (2014) Compute species accumulations

```
out <- iNEXT(x=spec, q=c(0,1,2), datatype="abundance", endpoint=200, knots=100, nboot=100)
```
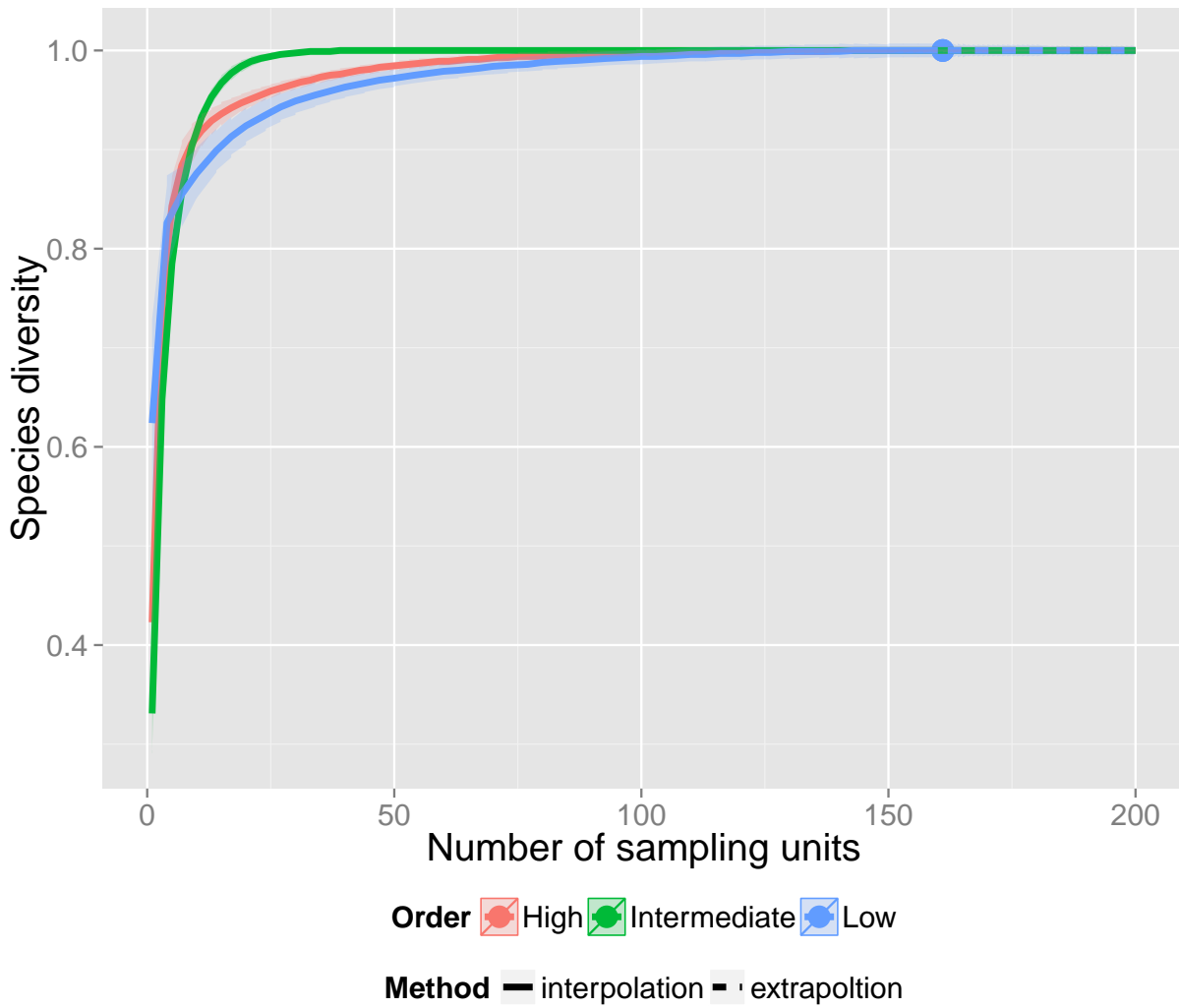
Data visualization

```
ggiNEXT(out, type=1, facet.var = "site", color.var = "order")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```
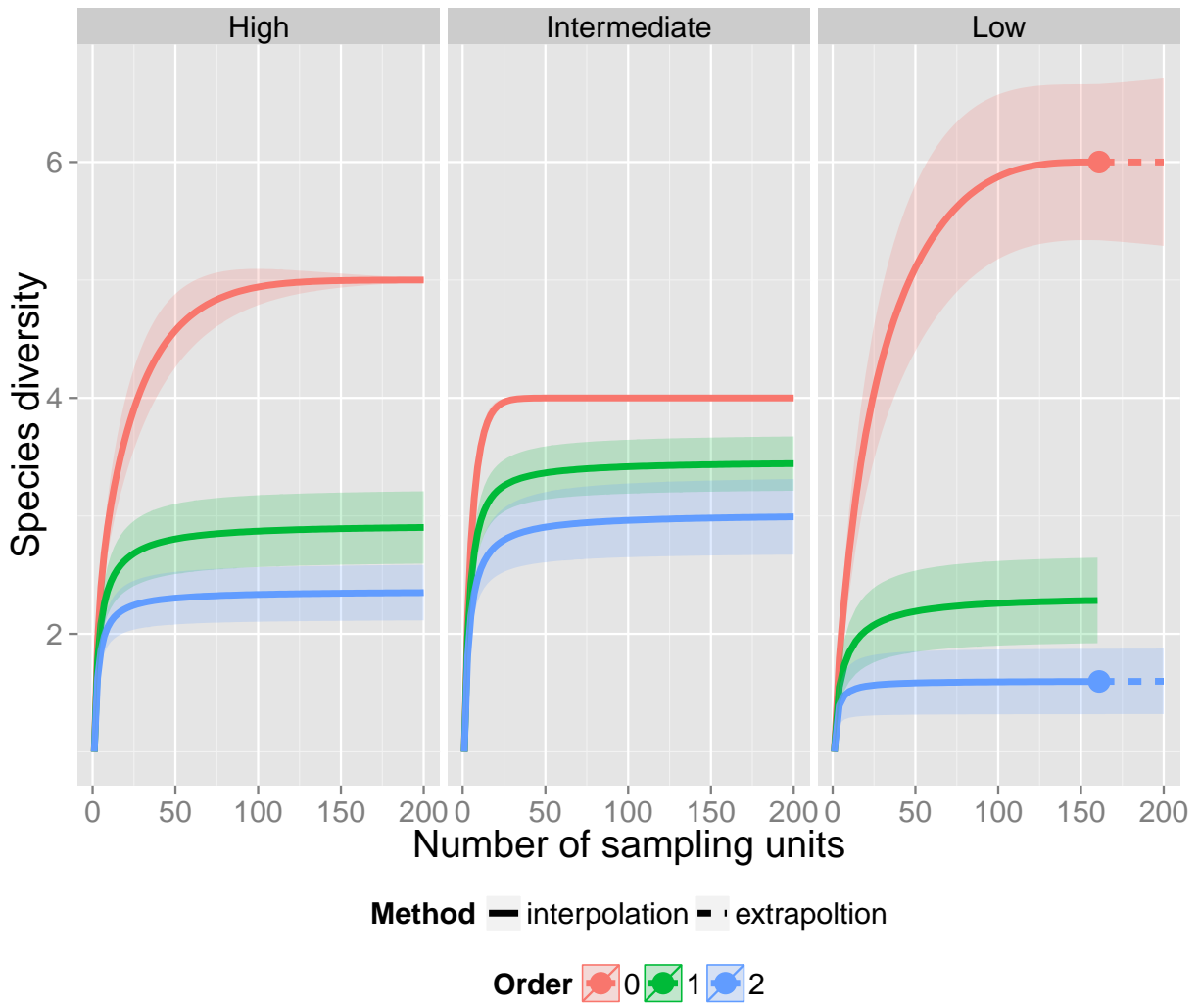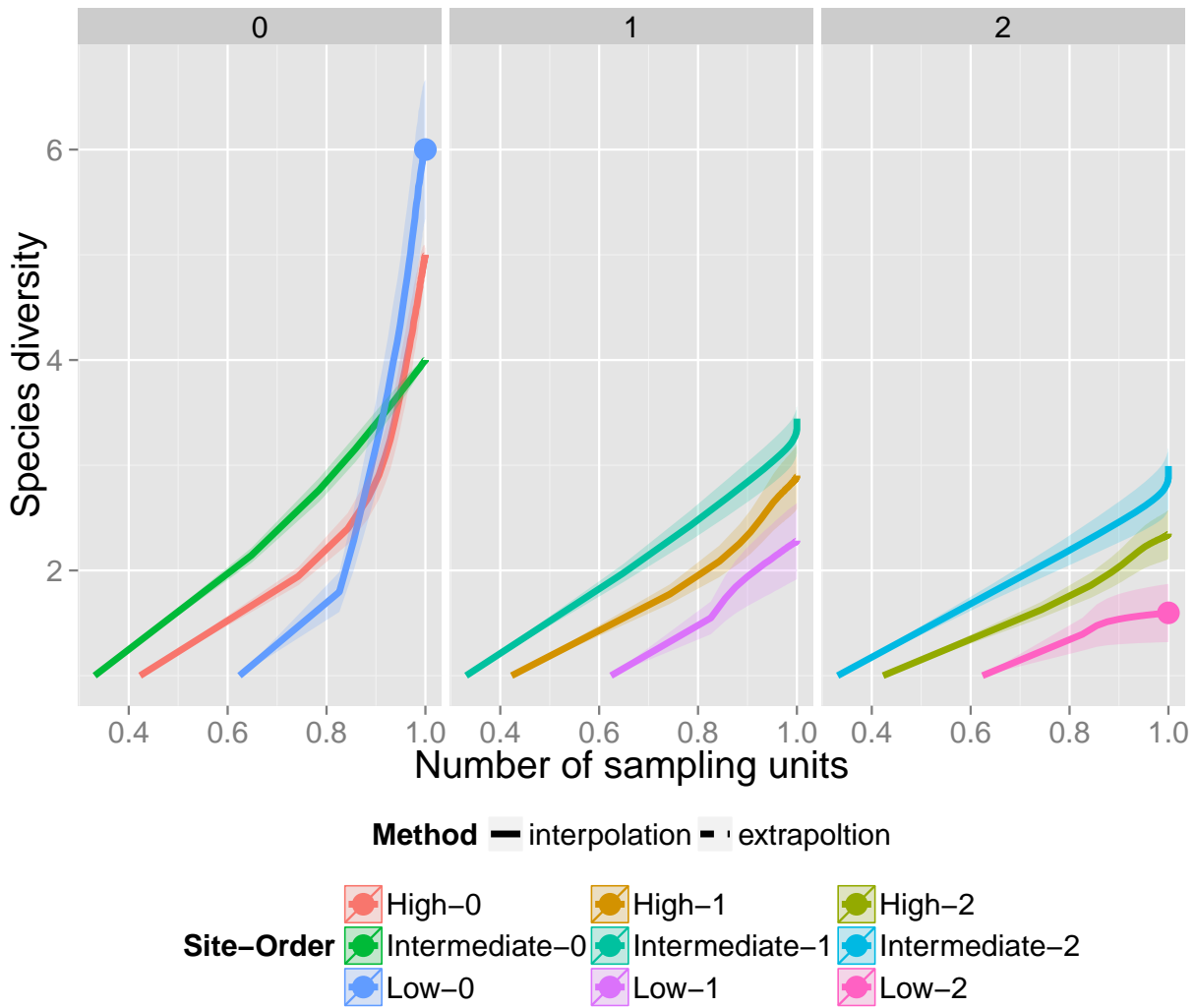
```
ggiNEXT(out, type=2, color.var = "site")
```

```
ggiNEXT(out, type=3, facet.var = "order", color.var = "both")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```

How to cite this package

Use the following command

```
citation("iNEXT")
```

To cite iNEXT in publications use:

T. C. Hsieh, K. H. Ma and Anne Chao. 2014. iNEXT: iNterpolation
and EXTrapolation for species diversity. R package version 2.0,
URL: http://chao.stat.nthu.edu.tw/blog/software-download

Anne Chao, Nicholas J. Gotelli, T. C. Hsieh, Elizabeth L.
Sander, K. H. Ma, Robert K. Colwell, and Aaron M. Ellison 2014.
Rarefaction and extrapolation with Hill numbers: a framework for
sampling and estimation in species diversity studies. Ecological
Monographs 84:45-67.