An Introduction to the Simple Biostatistics Program (SBP)

Stanley B. Pounds

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What is SBP

- SBP is the **S**imple **B**iostatistics **P**rogram.
- SBP was develped by Dr. Stanley B. Pounds, a faculty member of the Department of Biostatistics and the Graduate School of Biomedical Sciences at St. Jude Children's Research Hospital.
- SBP is an extension of the *R* statistical computing software that simplifies introductory biostatistics for students.
- SBP defines a few simple functions that perform all the computational tasks for an introductory biostatistics course.
- SBP minimizes the technicalities of computational tasks so students can focus on concepts and interpretation.

Setting Up SBP

```
# source the SBP.setup.file
SBP.setup.file="https://raw.githubusercontent.com/stan-pounds/Simple-Biostats-Program/main/setup-SBP.R"
source(SBP.setup.file)
```

- The above commands will need to be performed during *each* R session.
- You will not be able to use the SBP functions until after the above commands are executed in R.

Reading Data with SBP

```
data.set=read.data()
```

- The above command will open a window for the user to interactively navigate through folders to the data file.
- It can read data in the *csv*, tab-delimited *txt*, *xlsx*, and *Rdata* formats.
- For *xlsx* files, it will also prompt the user to choose the sheet to be read.
- It will then read the data and open a viewer to see it.
- The data from the file will be stored under the name `data.set` in R.

Example

- Demonstrate in R studio

Get an R Package

```
get.package("penalized")
```

- R packages are R add-ons that define useful functions to perform specific tasks.
- Some R packages include example data sets.
- The above code downloads the `penalized` R package and makes it available for use in the R session.

Get an R Package data set

```
get.package("penalized")  # make the penalized package available for use
data("nki70")             # make the nki70 data set available for use
help("nki70")             # open a help page about the nki70 data set
View(nki70)               # open the nki70 data set in a data viewer
```

Data Analysis Functions

Function	Actions
`describe("x",data.set)`	Compute descriptive stats & graphs for the `data.set` column named `x` using `data.set`
`estimate("x",data.set)`	Estimate the population value for the `x` column variable using `data.set`
`compare(y~grp,data.set)`	Compare the variable `y` across the `grp` groups using `data.set`
`correlate(y~x,data.set)`	Correlate the numeric variables `y` and `x` using `data.set`
`model(y~x+grp,data.set)`	Model `y` as a function of `x` and `grp` using `data.set`

Example with `nki70` data

```r
get.package("penalized")
data("nki70")
head(nki70[,1:10])
```

```
        time event  Diam   N       ER        Grade Age      TSPYL5
125 7.748118     0 <=2cm 1-3 Positive Intermediate  50 -0.18752814
127 4.662560     1 <=2cm 1-3 Positive    Well diff  42  0.15099047
128 8.739220     0  >2cm 1-3 Positive    Well diff  50  0.11695046
129 7.567420     0 <=2cm 1-3 Positive Intermediate  43  0.10493318
130 7.296372     0 <=2cm 1-3 Negative  Poorly diff  47  0.30821656
132 6.718686     0 <=2cm 1-3 Positive Intermediate  47 -0.09643536
    Contig63649_RC      DIAPH3
125    -0.15304662 -0.29514052
127    -0.21005843  0.03355057
128    -0.25813878  0.07791767
129    -0.13687348 -0.01984126
130     0.03544526  0.15589646
132    -0.03772432 -0.05882551
```

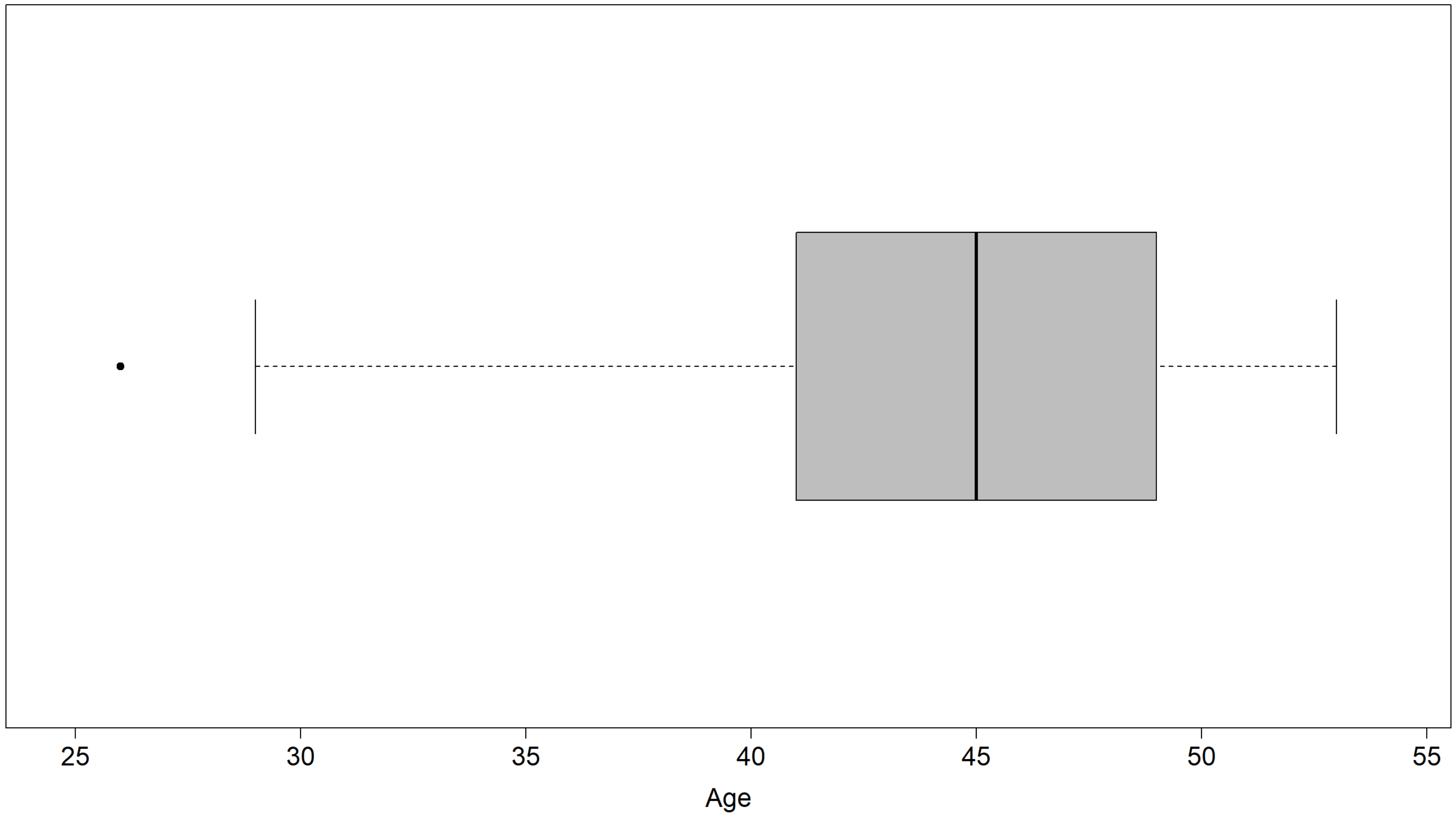
Column Names of a data set

```
colnames(nki70)
```

```
 [1] "time"           "event"          "Diam"           "N"
 [5] "ER"             "Grade"          "Age"            "TSPYL5"
 [9] "Contig63649_RC" "DIAPH3"         "NUSAP1"         "AA555029_RC"
[13] "ALDH4A1"        "QSCN6L1"        "FGF18"          "DIAPH3.1"
[17] "Contig32125_RC" "BBC3"           "DIAPH3.2"       "RP5.860F19.3"
[21] "C16orf61"       "SCUBE2"         "EXT1"           "FLT1"
[25] "GNAZ"           "OXCT1"          "MMP9"           "RUNDC1"
[29] "Contig35251_RC" "ECT2"           "GMPS"           "KNTC2"
[33] "WISP1"          "CDC42BPA"       "SERF1A"         "AYTL2"
[37] "GSTM3"          "GPR180"         "RAB6B"          "ZNF533"
[41] "RTN4RL1"        "UCHL5"          "PECI"           "MTDH"
[45] "Contig40831_RC" "TGFB3"          "MELK"           "COL4A2"
[49] "DTL"            "STK32B"         "DCK"            "FBXO31"
[53] "GPR126"         "SLC2A3"         "PECI.1"         "ORC6L"
[57] "RFC4"           "CDCA7"          "LOC643008"      "MS4A7"
[61] "MCM6"           "AP2B1"          "C9orf30"        "IGFBP5"
[65] "HRASLS"         "PITRM1"         "IGFBP5.1"       "NMU"
[69] "PALM2.AKAP2"    "LGP2"           "PRC1"           "Contig20217_RC"
[73] "CENPA"          "EGLN1"          "NM_004702"      "ESM1"
[77] "C20orf46"
```

Describe Age in nki70 data

```
age.result=describe("Age",nki70)
```



Describe Age in nki70 data

```
age.result
```

```
 **TABLES**

|               |        Age|
|:--------------|----------:|
|n.total        | 144.000000|
|n.missing      |   0.000000|
|n.available    | 144.000000|
|mean           |  44.305556|
|stdev          |   5.339230|
|median         |  45.000000|
|lower.quartile |  41.000000|
|upper.quartile |  49.000000|
|minimum        |  26.000000|
|maximum        |  53.000000|
|shapiro.pvalue |   0.000182|



 **RESULTS**

The variable Age has 144 observations (144 available; 0 missing)  with mean 44.3, standard deviation 5.3, median 45, lower quartile 41, upper
quartile 49, minimum 26, and maximum 53.
```

Describe Age in nki70 data

```
 **METHODS**

The Shapiro-Wilk (1965) test was used to evaluate the normality of the distribution of Age.


 **REFERENCES**

Shapiro, S. S.; Wilk, M. B. (1965). "An analysis of variance test for normality (complete samples)". Biometrika. 52 (3-4): 591-611.
doi:10.1093/biomet/52.3-4.591. JSTOR 2333709. MR 0205384.
```

Describe Age in `nki70` data

TABLES

	Age
n.total	144.000000
n.missing	0.000000
n.available	144.000000
mean	44.305556
stdev	5.339230
median	45.000000
lower.quartile	41.000000
upper.quartile	49.000000
minimum	26.000000
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Common Options for Data Analysis Functions

Option	Purpose
`txt=number`	produce no narrative (`txt=0`), basic narrative (`txt=1`), or detailed narrative (`txt=2`)
`fig=number`	produce no figures (`fig=0`), basic figures (`fig=1`), or more tables (`fig=2`,`fig=3`,etc)
`tbl=number`	produce no tables (`tbl=0`), basic tables (`tbl=1`), or more tables (`tbl=2`,`tbl=3`,etc)
`clr="color.name"`	use the color `color.name` in the figures
`clr=c("name1","name2")`	Use the color(s) `name1` and `name2` in the figures
`clr="palette.name"`	use the palette `palette.name` to define colors for the figures

Set fig=0 to Suppress Figures

```
describe("Age",nki70,fig=0)
```

```
 **TABLES**

|               |        Age|
|:--------------|----------:|
|n.total        | 144.000000|
|n.missing      |   0.000000|
|n.available    | 144.000000|
|mean           |  44.305556|
|stdev          |   5.339230|
|median         |  45.000000|
|lower.quartile |  41.000000|
|upper.quartile |  49.000000|
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doi:10.1093/biomet/52.3-4.591. JSTOR 2333709. MR 0205384.
```

Set `tbl=0` to Suppress Tables

```
describe("Age",nki70,tbl=0,fig=0)
```

```
 **RESULTS**

The variable Age has 144 observations (144 available; 0 missing)  with mean 44.3, standard deviation 5.3, median 45, lower quartile 41, upper
quartile 49, minimum 26, and maximum 53.


 **METHODS**

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doi:10.1093/biomet/52.3-4.591. JSTOR 2333709. MR 0205384.
```

Set `txt=0` to Suppress Text

```
describe("Age",nki70,txt=0,fig=0)
```

```
 **TABLES**

|               |        Age|
|:--------------|----------:|
|n.total        | 144.000000|
|n.missing      |   0.000000|
|n.available    | 144.000000|
|mean           |  44.305556|
|stdev          |   5.339230|
|median         |  45.000000|
|lower.quartile |  41.000000|
|upper.quartile |  49.000000|
|minimum        |  26.000000|
|maximum        |  53.000000|
|shapiro.pvalue |   0.000182|



 **METHODS**

The Shapiro-Wilk (1965) test was used to evaluate the normality of the distribution of Age.


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doi:10.1093/biomet/52.3-4.591. JSTOR 2333709. MR 0205384.
```
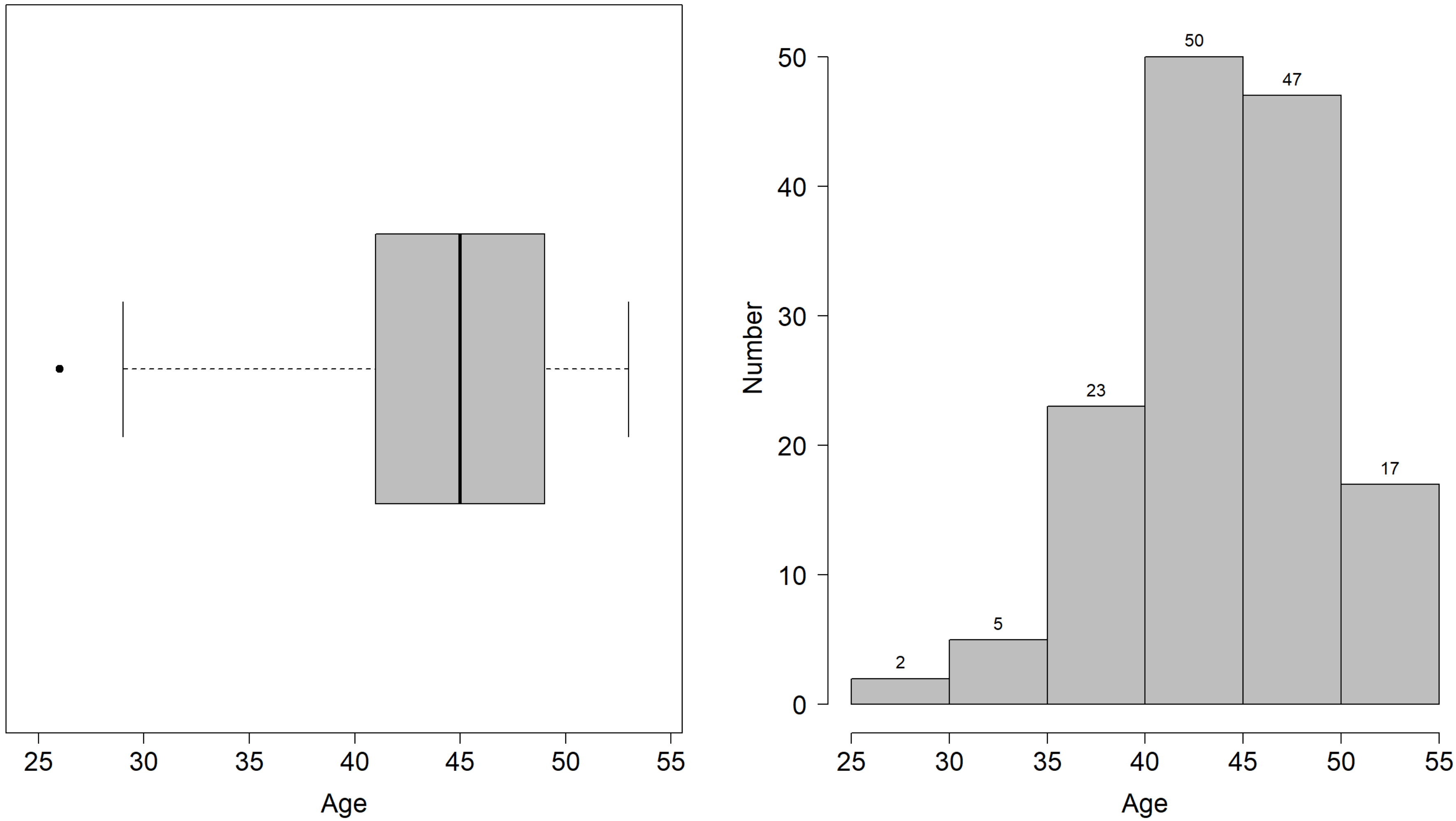
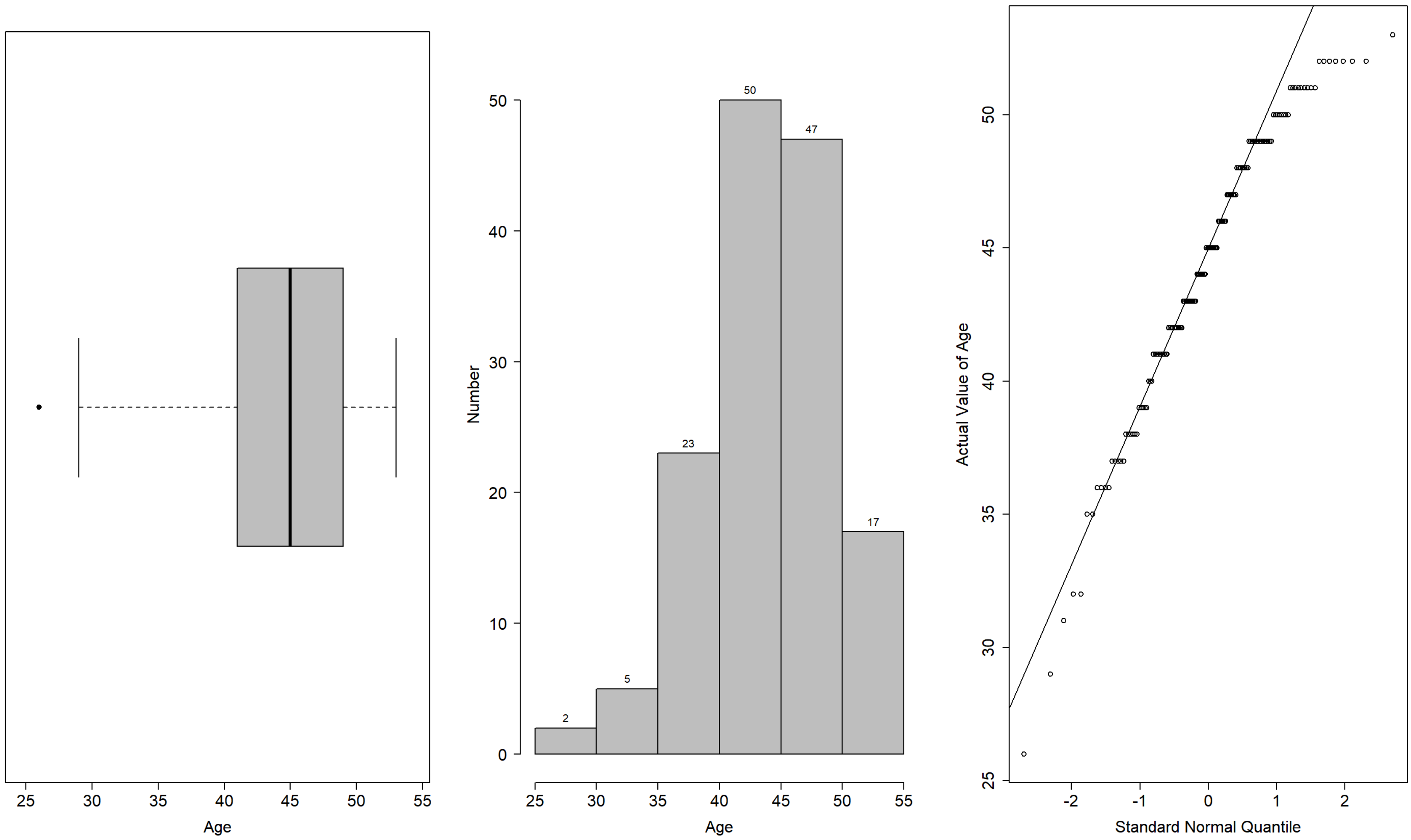

Set fig=2 to Get More Figures

```
describe("Age",nki70,fig=2)
```



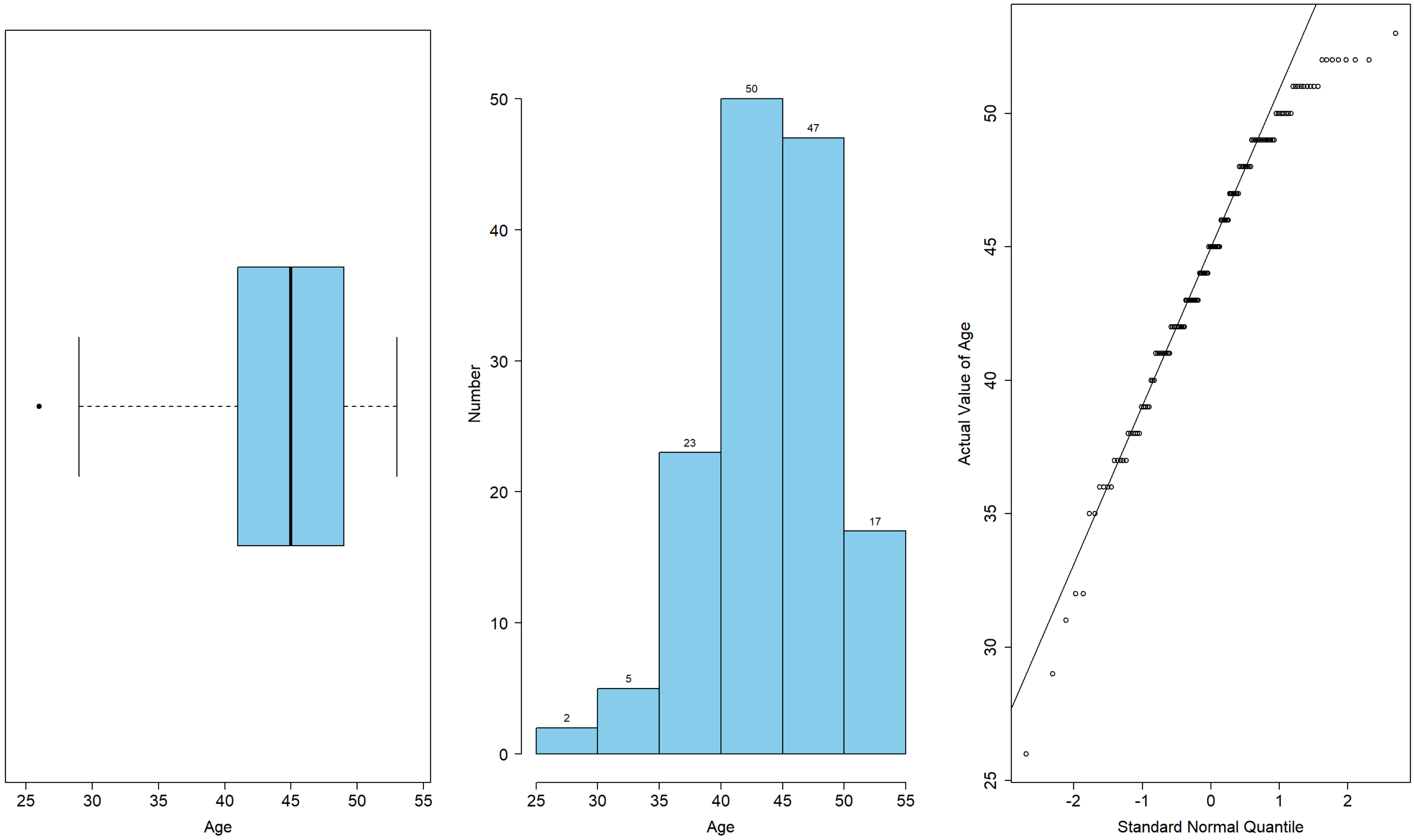
Set fig=3 to Get Even More Figures

```
describe("Age",nki70,fig=3)
```



Set `clr="skyblue"` to Get Sky Blue Figures

```
describe("Age",nki70,fig=3,clr="skyblue")
```

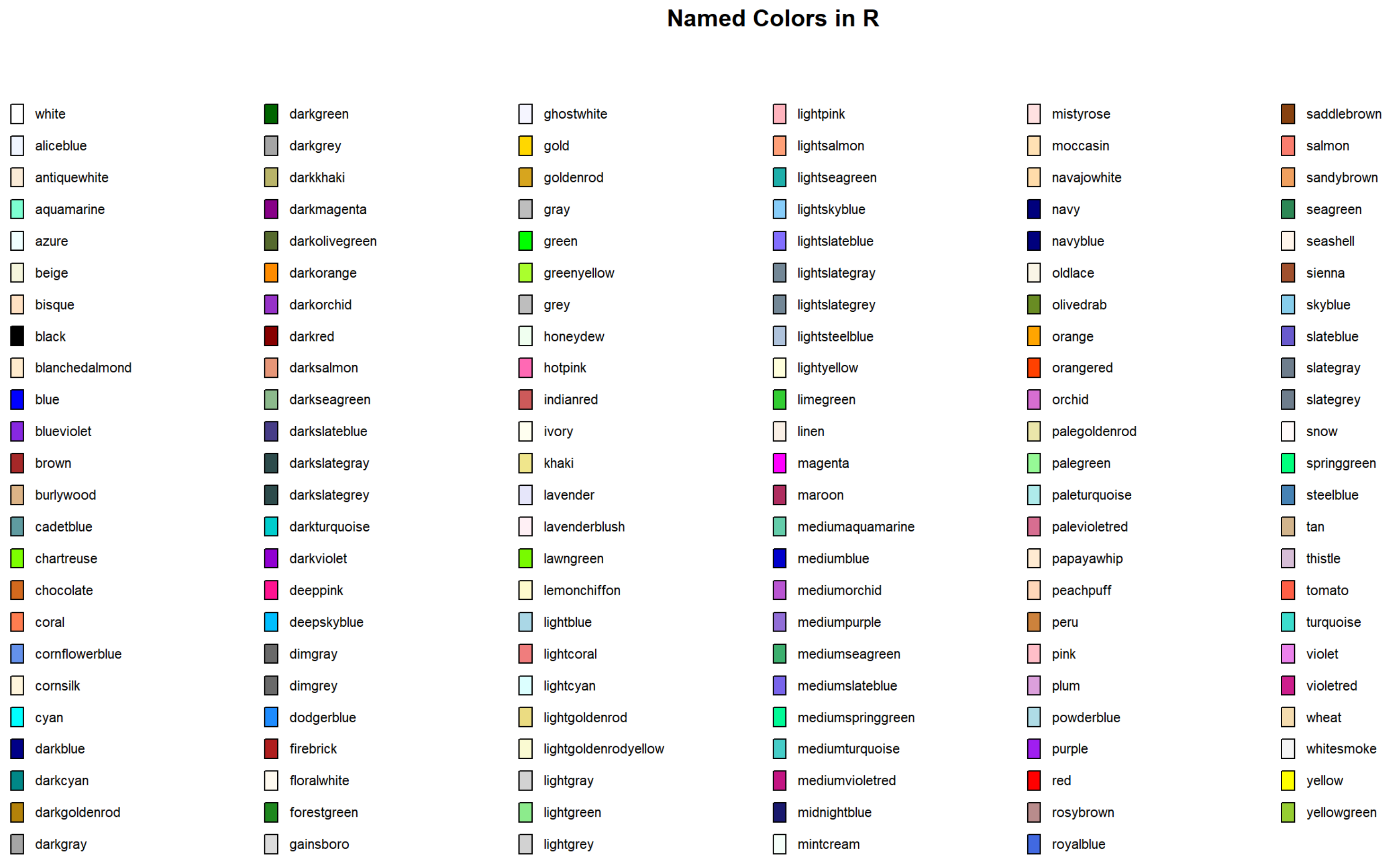


Colors in SBP

- Use the `clr` option to specify colors for figures.
- One may specify the name of one color, names of multiple colors, or the name of a color palette.
- Use the function `show.colors()` to see the colors and their names.
- Use `show.palettes(n)` to see palettes of `n` colors.

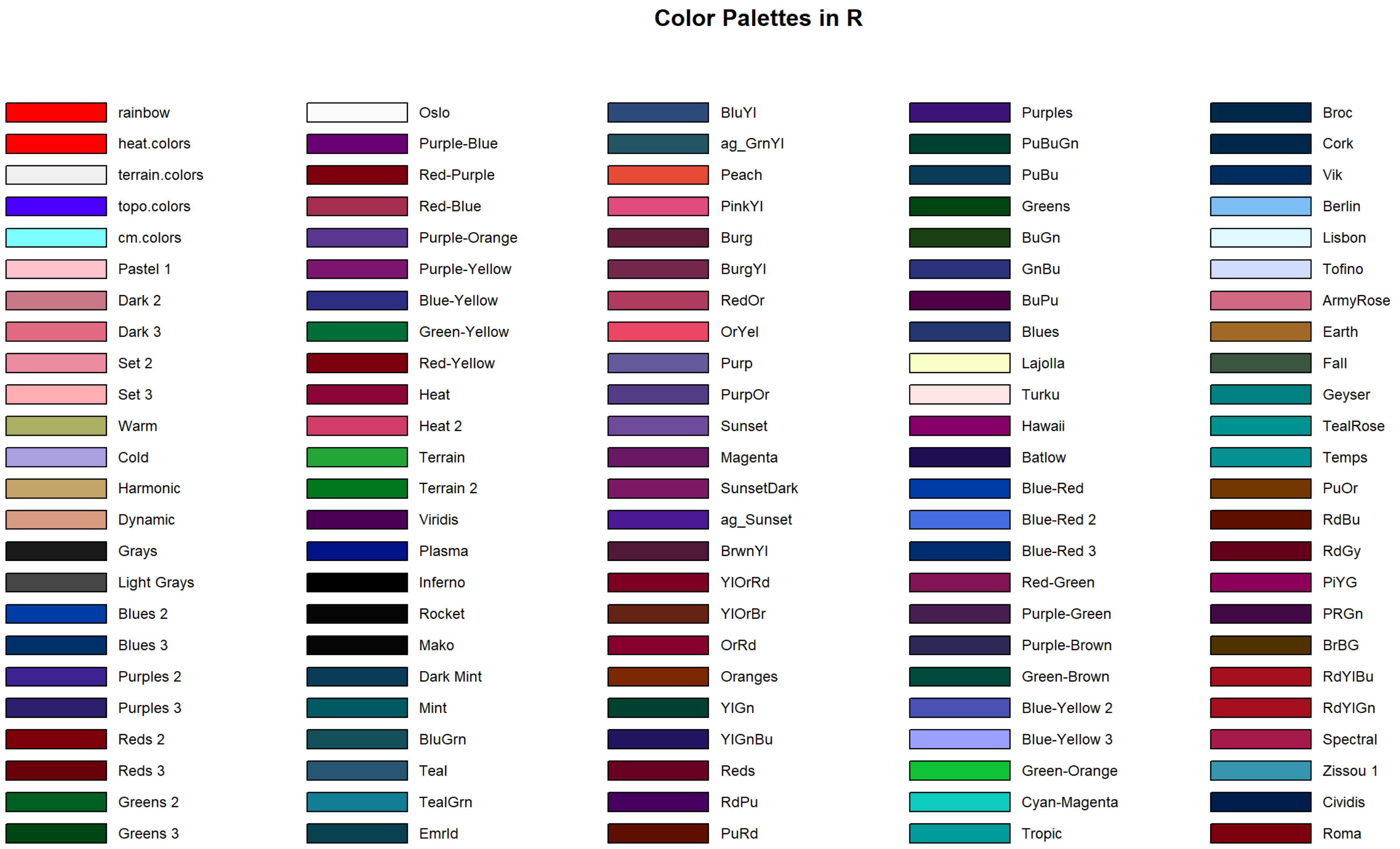
Colors in SBP

```
show.colors()
```



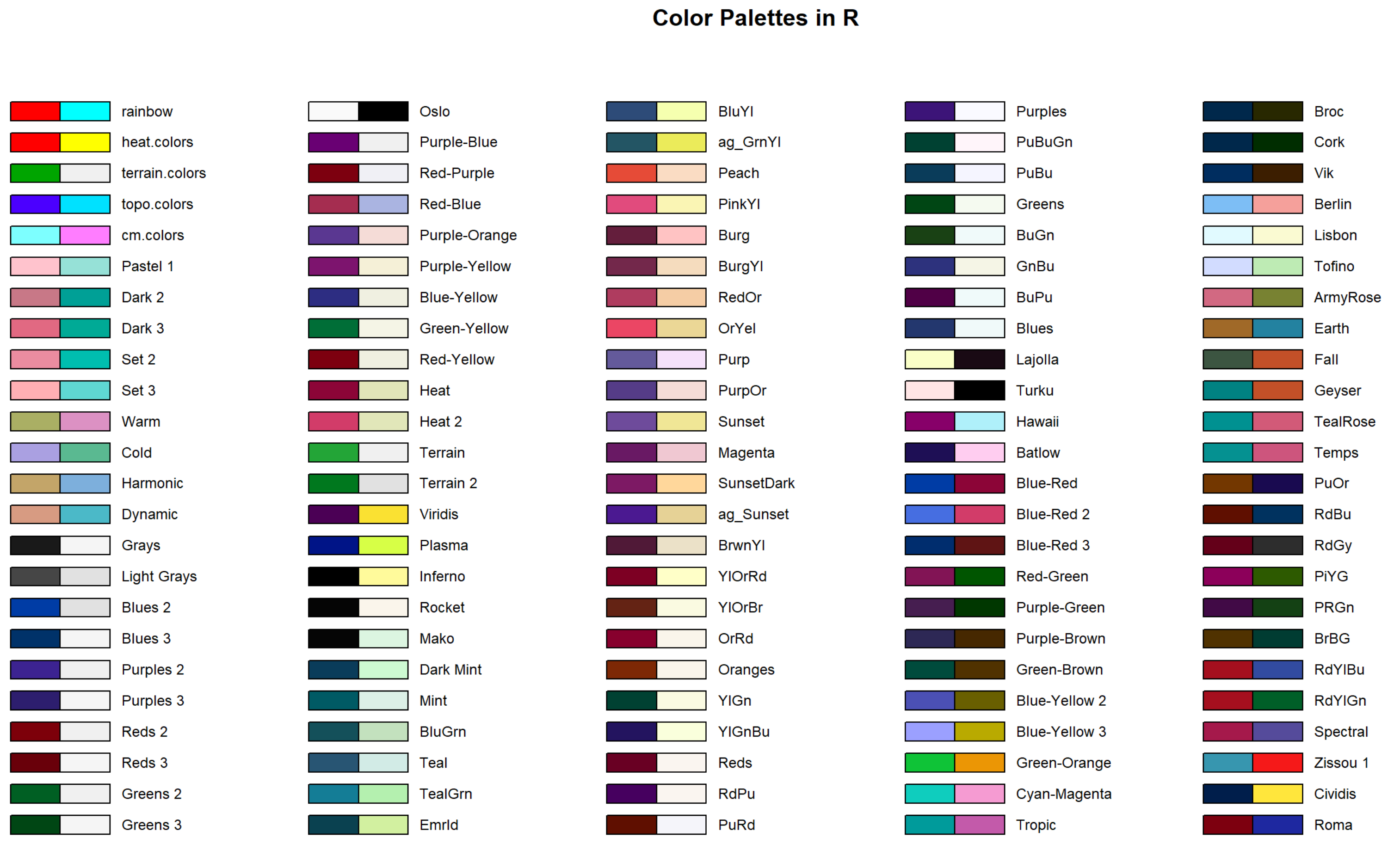
One-Color Palettes in SBP

```
show.palettes(1)
```



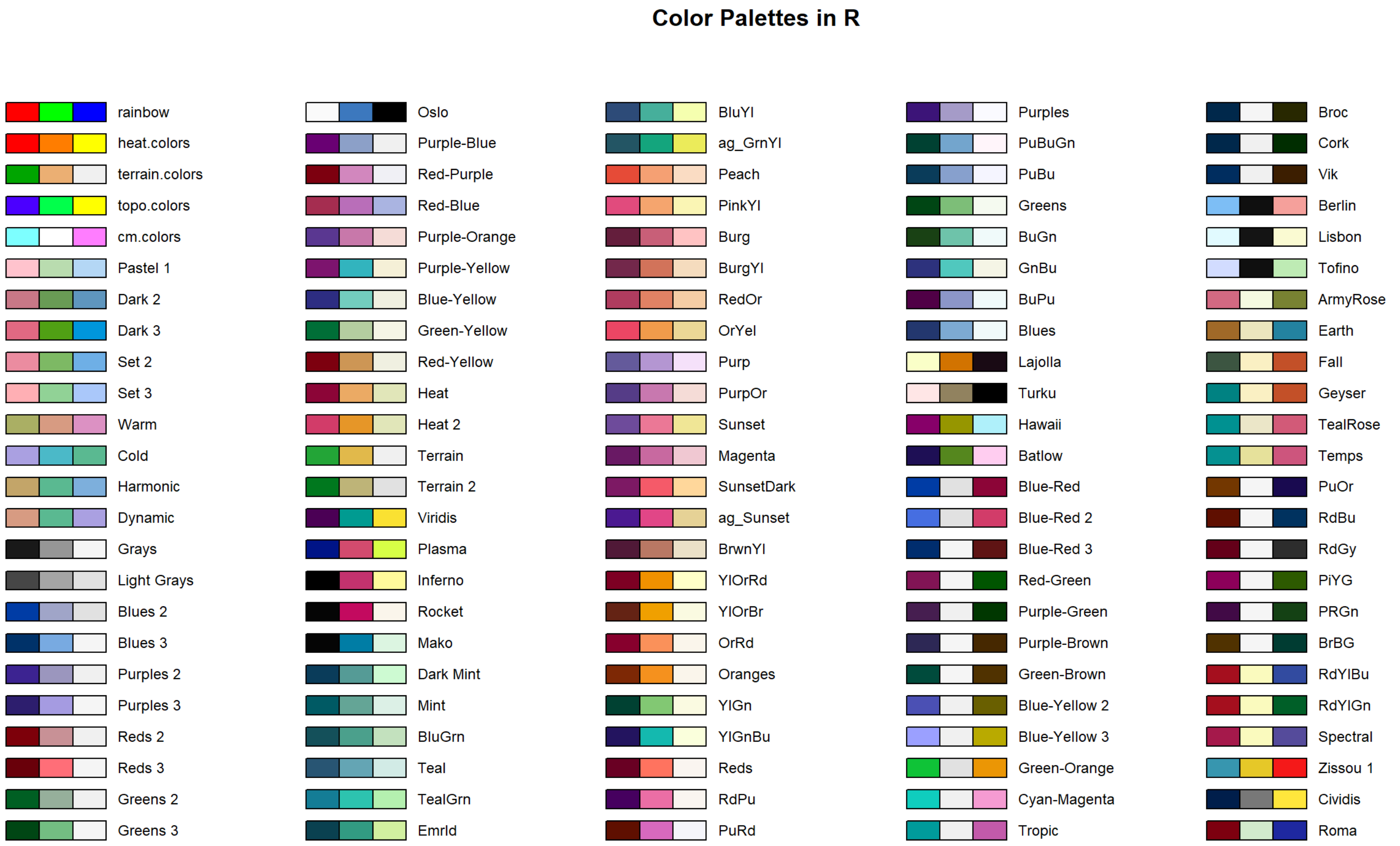
Two-Color Palettes in SBP

```
show.palettes(2)
```



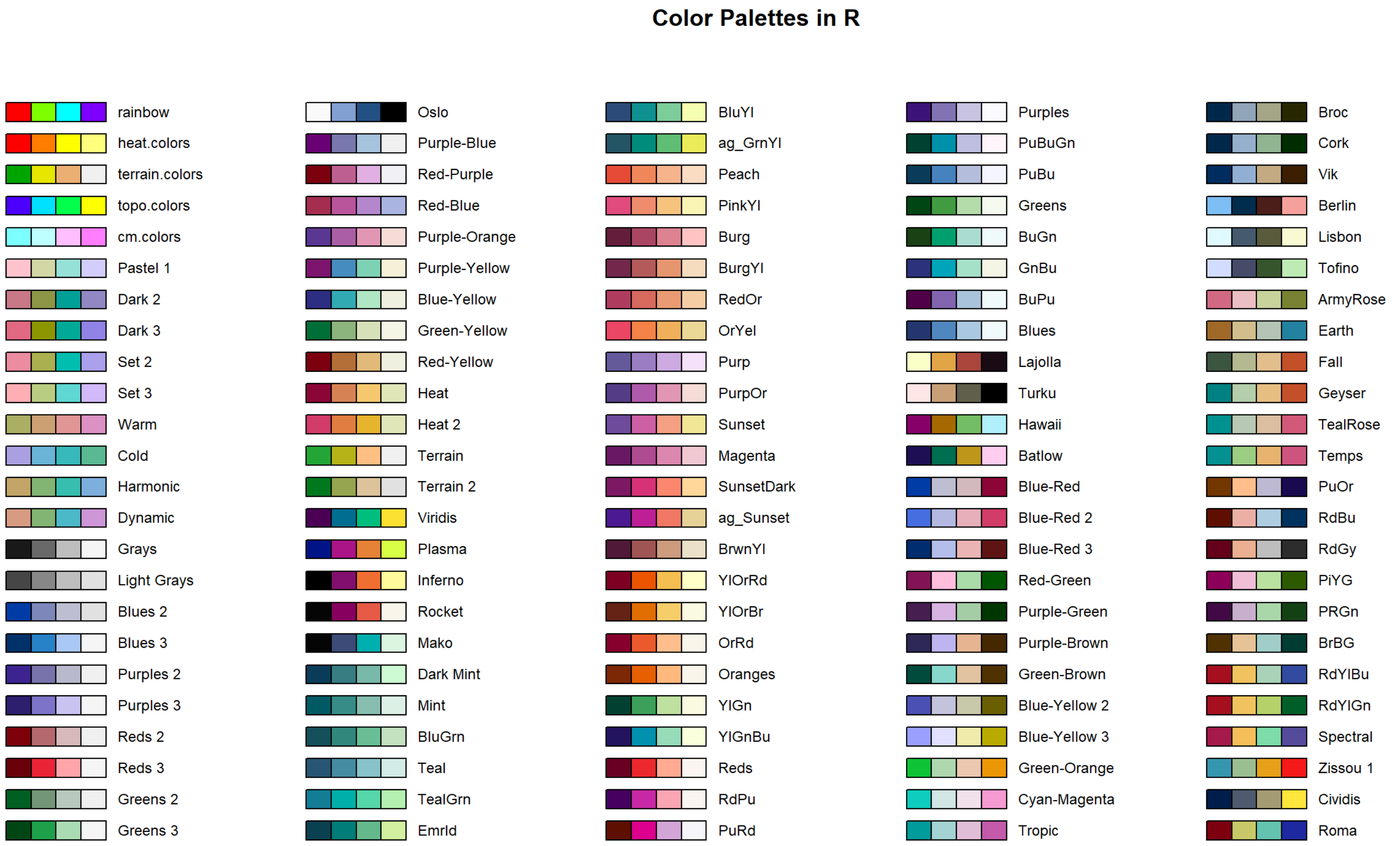
Three-Color Palettes in SBP

```r
show.palettes(3)
```



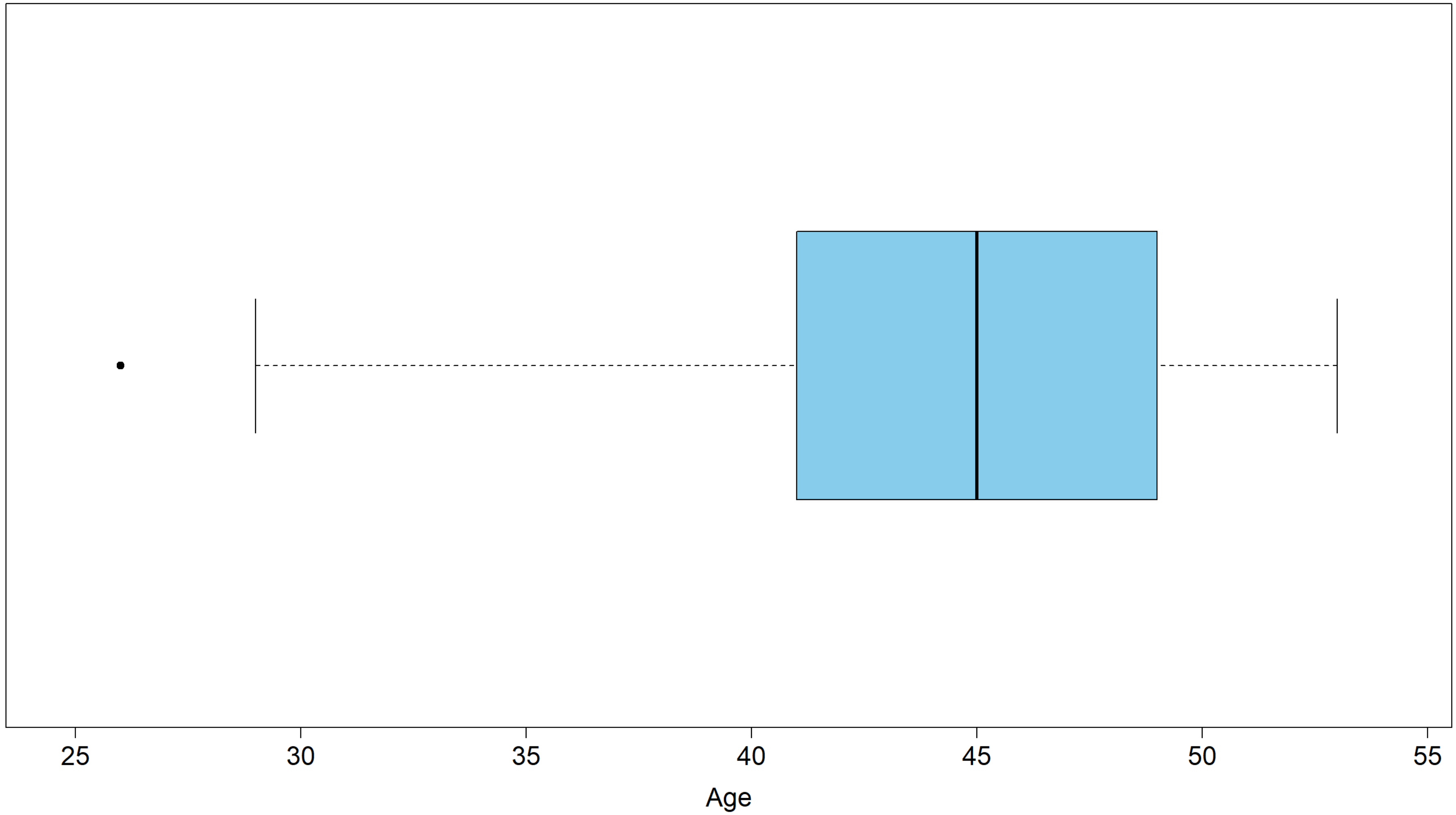
Four-Color Palettes in SBP

```r
show.palettes(4)
```



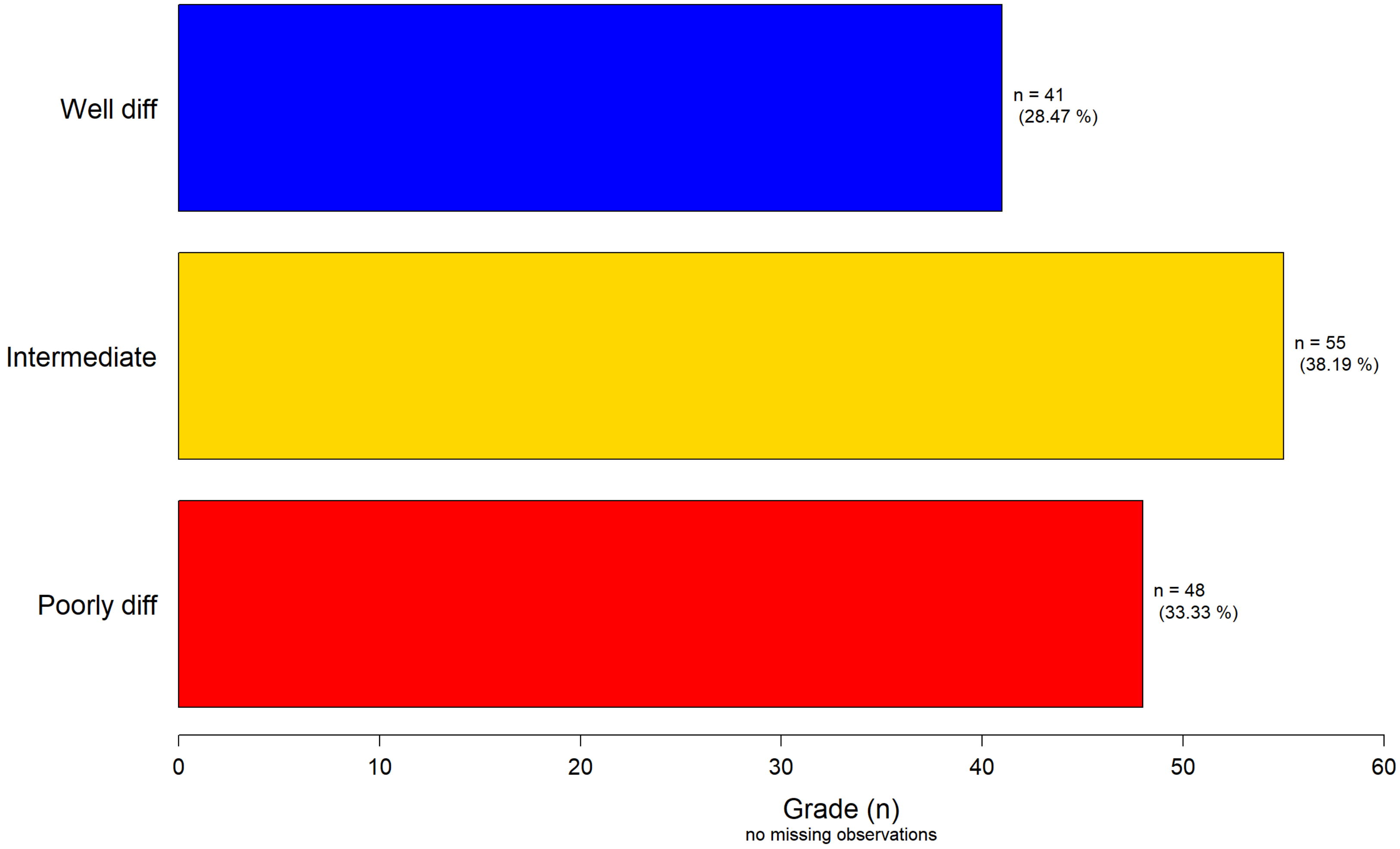
Produce Sky Blue Figures

```
describe("Age",nki70,clr="skyblue")
```



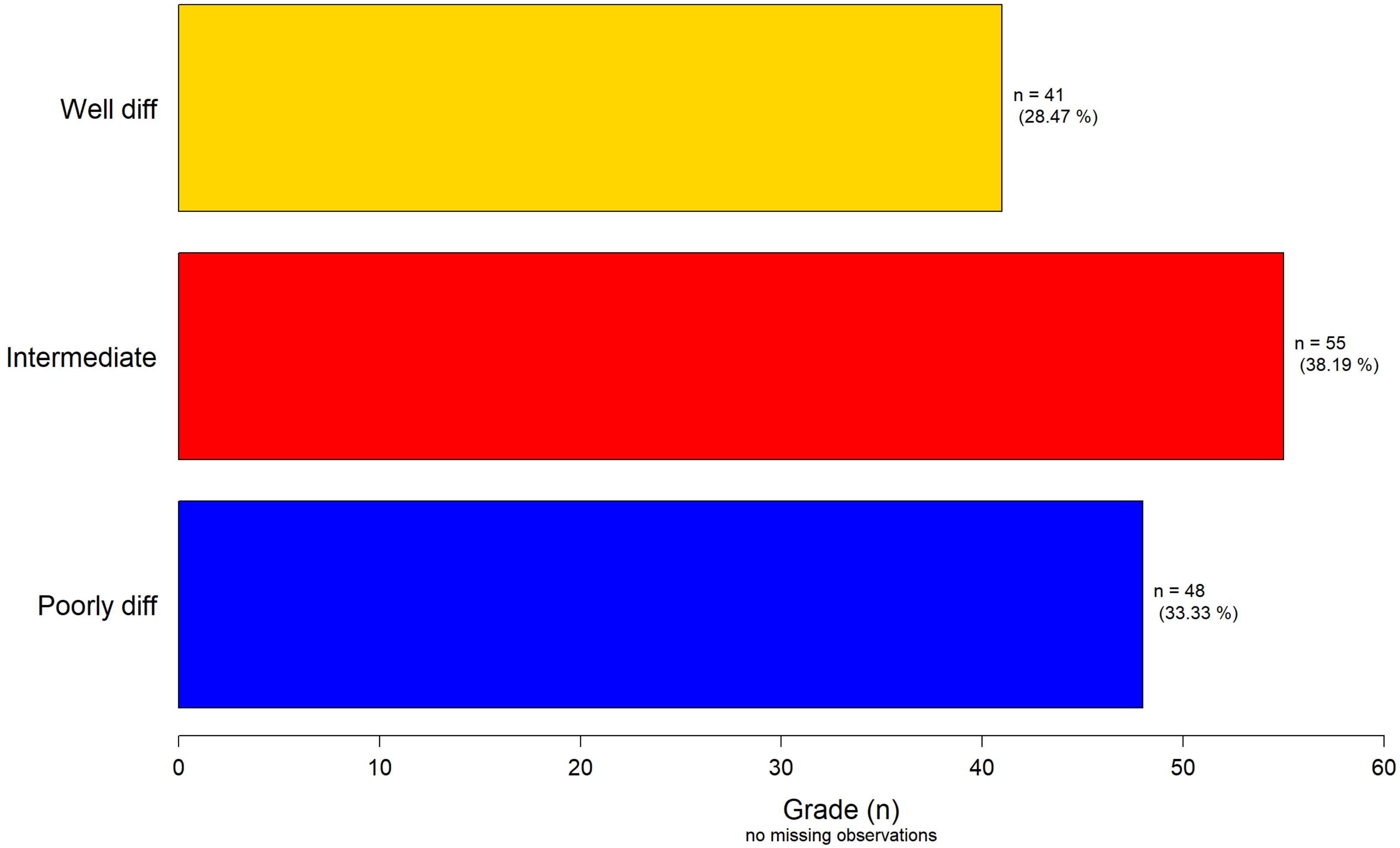
Specify Multiple Color Names

```
describe("Grade",nki70,clr=c("red","gold","blue"))
```



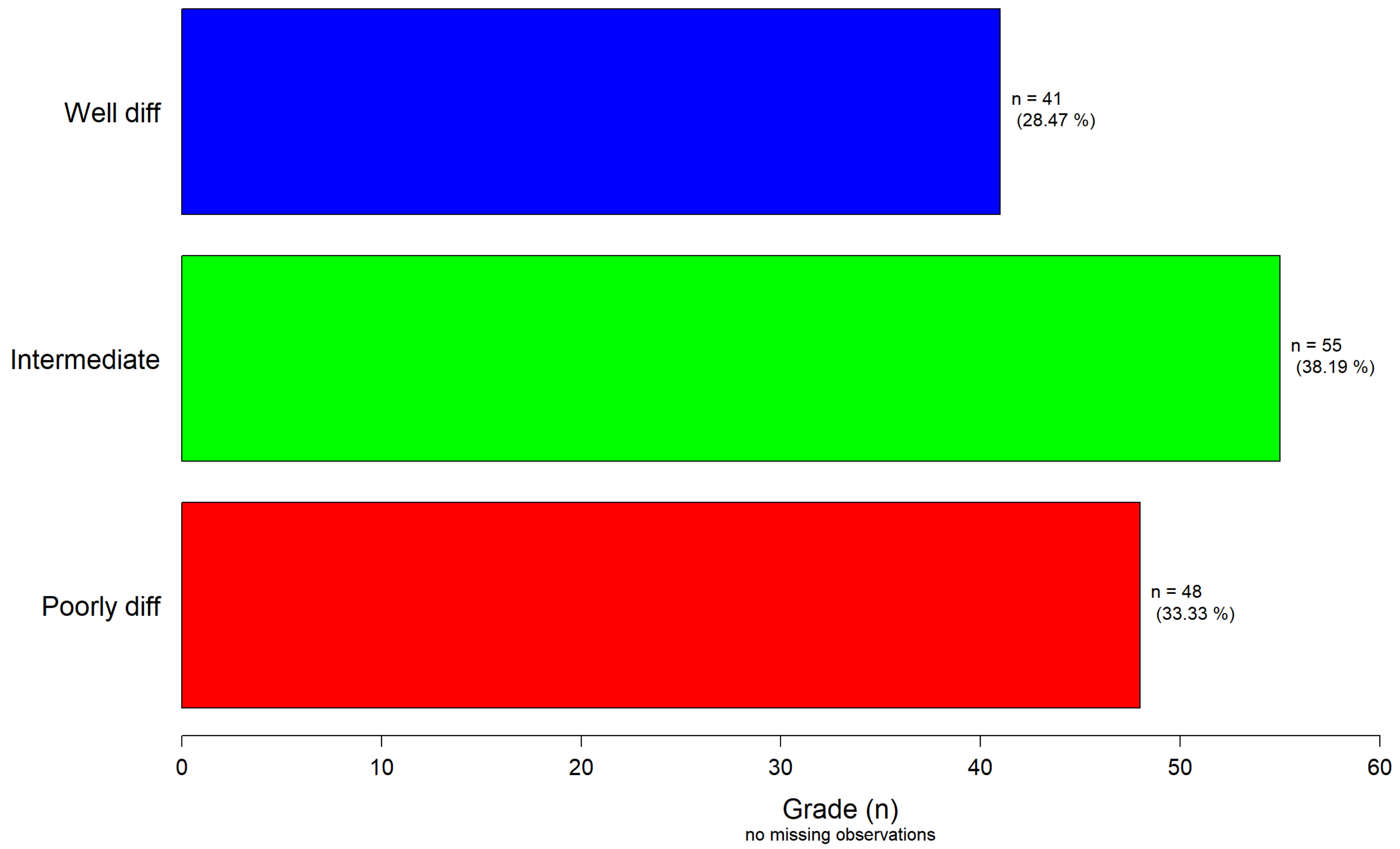
Specify Multiple Color Names

```
describe("Grade",nki70,clr=c("blue","red","gold"))
```



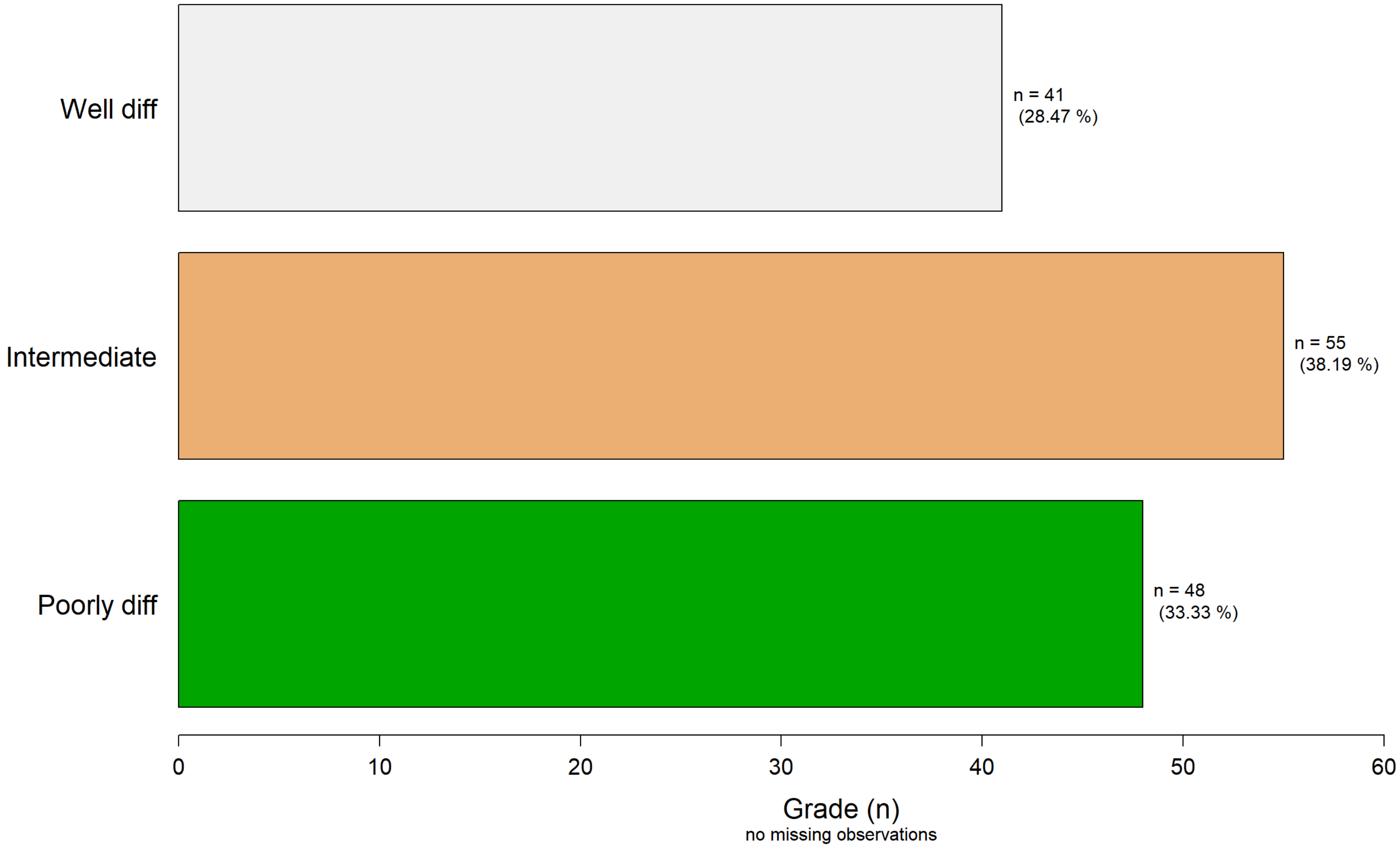
Specify the Rainbow Color Palette

```
describe("Grade",nki70,clr="rainbow")
```



Specify the Terrain Color Palette

```
describe("Grade",nki70,clr="terrain.colors")
```



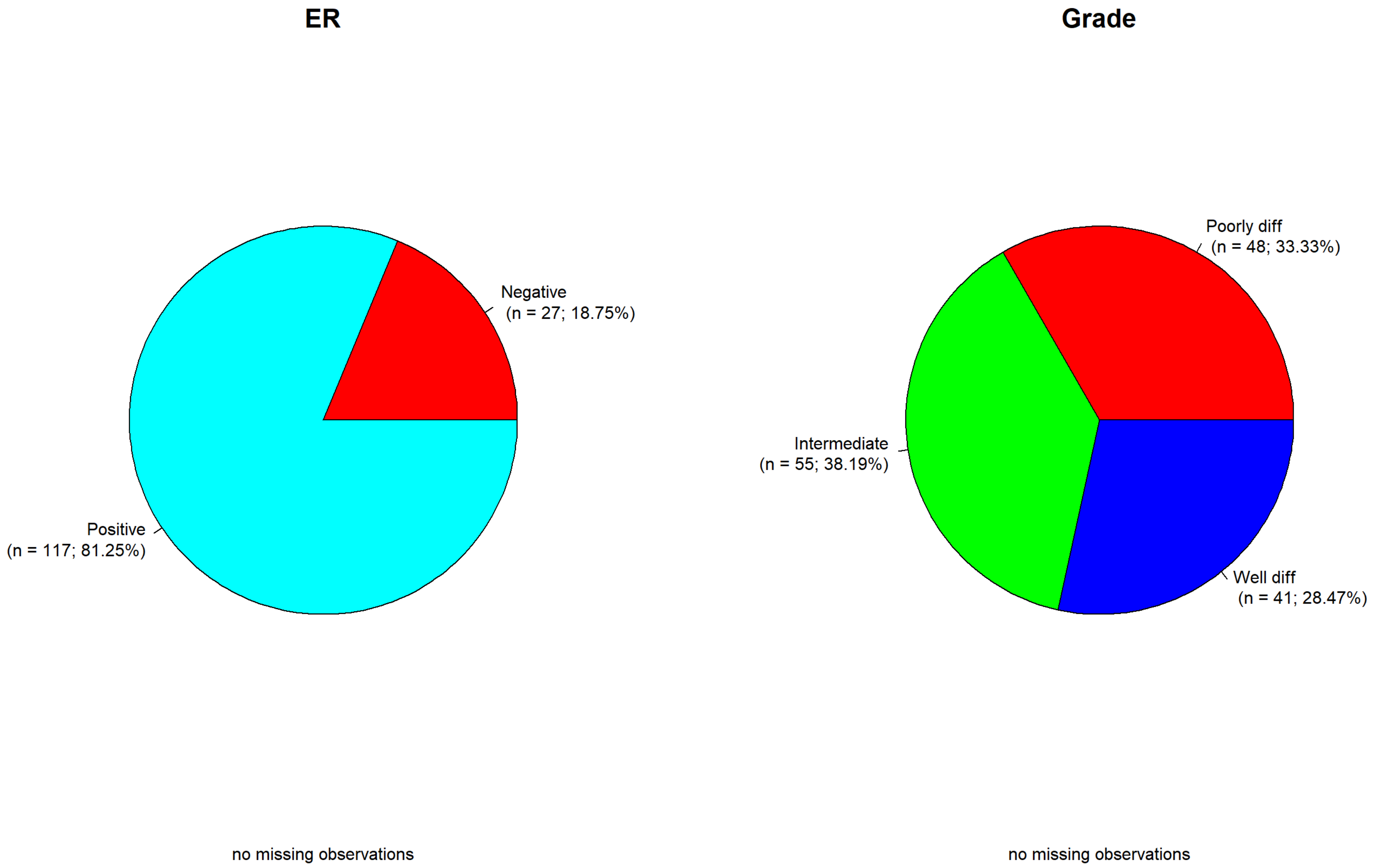
Specific Options for Data Analysis Functions

Graphics Functions

Function	Purpose
`pie.plot("y",data.set)`	Produce a pie chart of the categorical data column y of `data.set`
`bar.plot("y",data.set)`	Produce a bar plot or histogram of the y column of `data.set`
`box.plot("y",data.set)`	Produce a box plot of the numeric data column y of `data.set`
`box.plot(y~grp,data.set)`	Produce side-by-side boxplots of the numeric y by the group `grp` of `data.set`
`nqq.plot("y",data.set)`	Produce a normal quantile-quantile plot of the numeric y column of `data.set`
`mosaic.plot(y~x,data.set)`	Produce a mosaic plot for the categorical data columns y and x of `data.set`
`scatter.plot(y~x,data.set)`	Produce a scatter plot of y versus x for `data.set`
`event.plot("evnt",data.set)`	Plot the survival or cumulative incidence of the `evnt` column of `data.set`
`event.plot(evnt~grp,data.set)`	Plot the survival or cumulative incidence of the `evnt` by `grp` groups

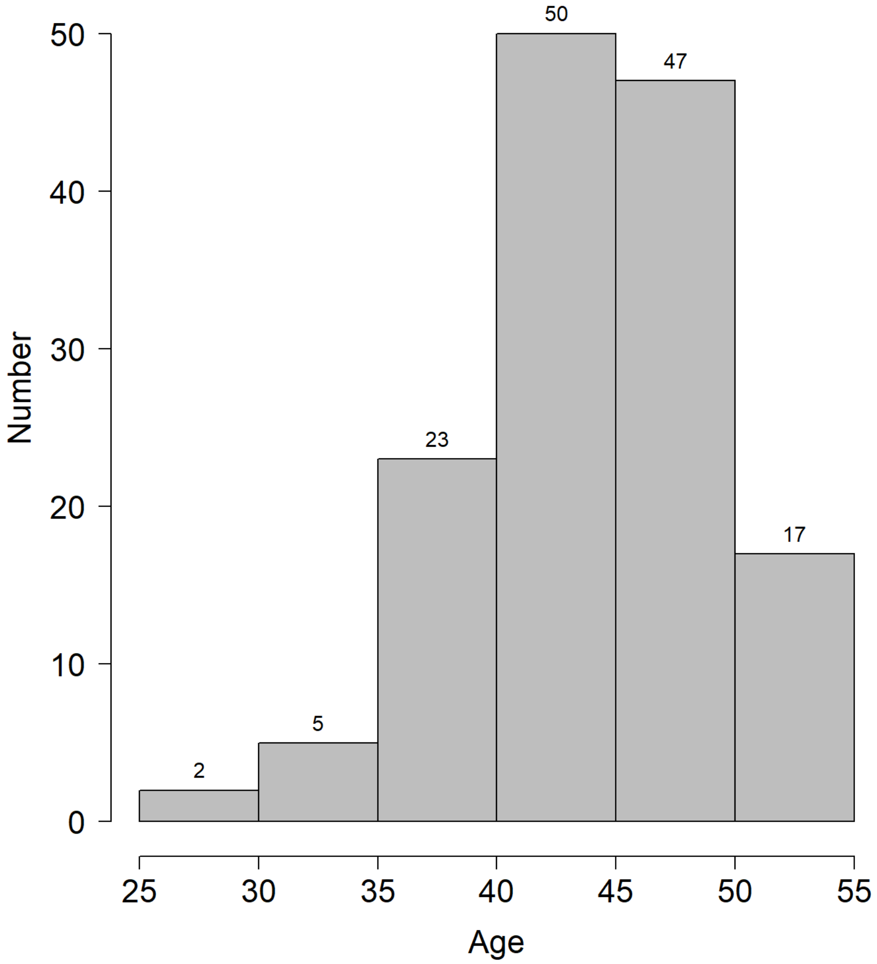
Pie Plot Examples

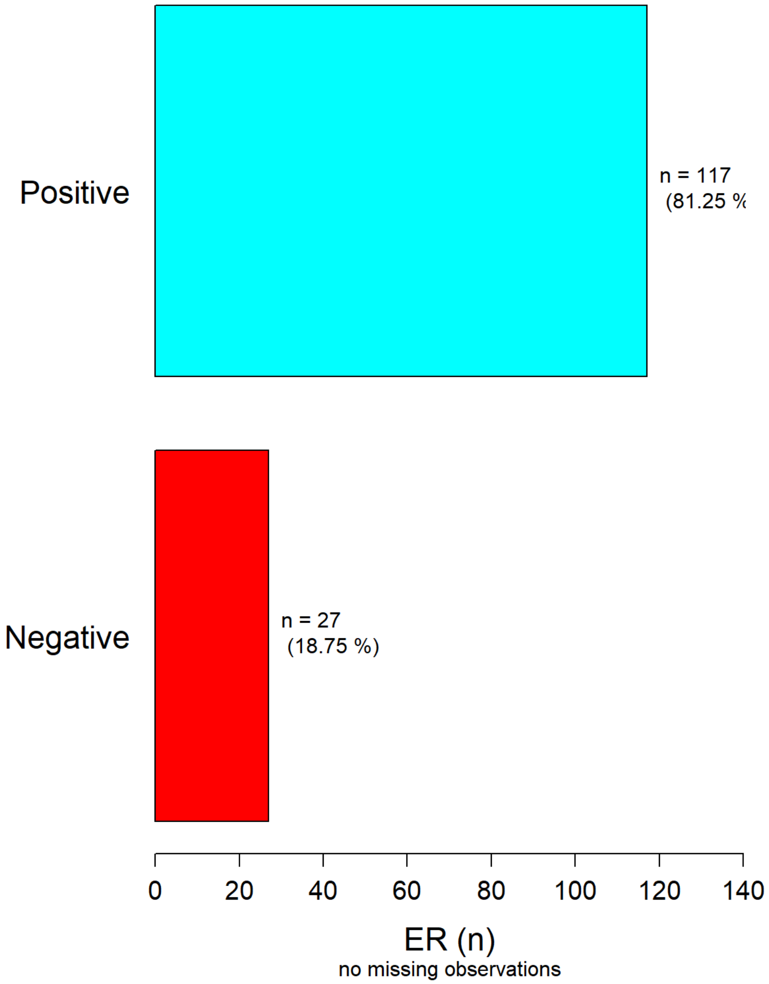
```
pie.plot("ER",nki70)     # pie chart for ER status
pie.plot("Grade",nki70)  # pie chart of Tumor Grade
```



Bar Plot Examples

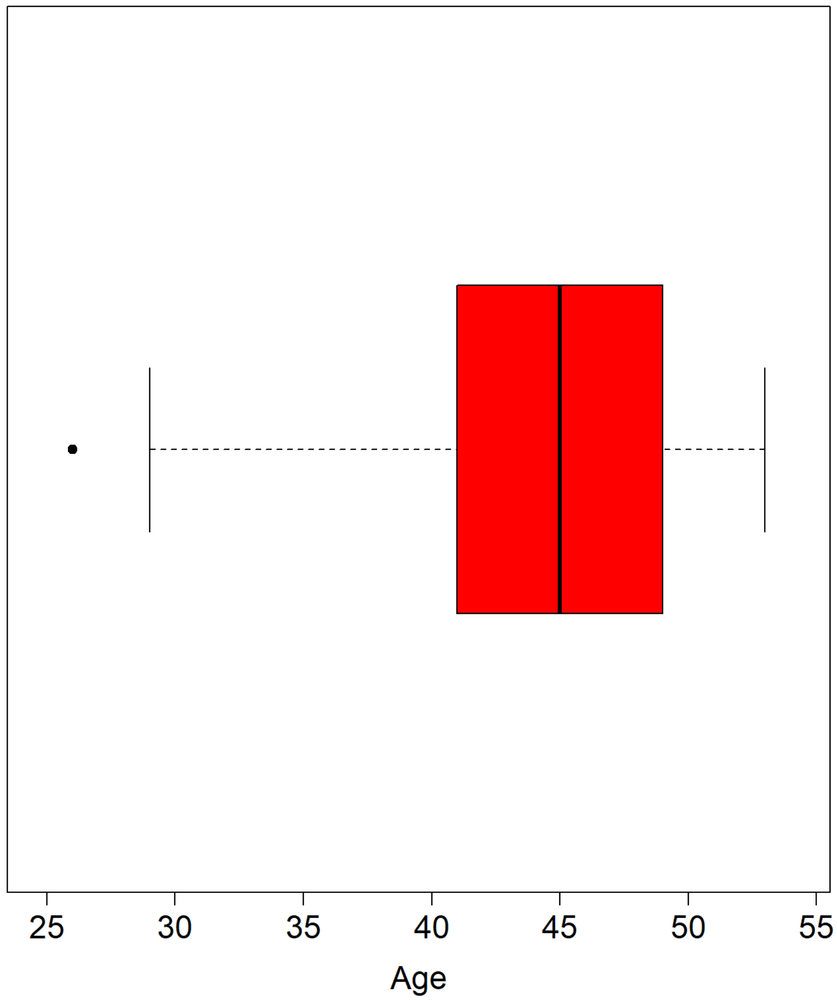
```
bar.plot("Age",nki70) # histogram for a numeric variable
bar.plot("ER",nki70)  # bar plot for a categorical variable
```

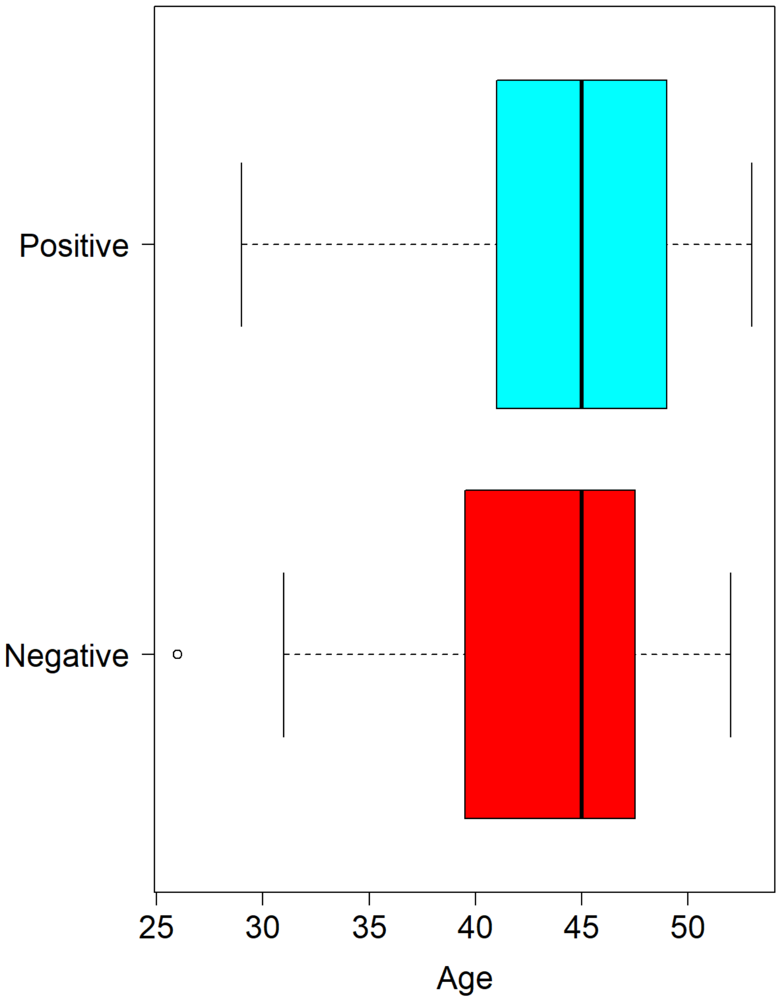




Box Plot Examples

```
box.plot("Age",nki70)   # box plot of Age for all data
box.plot(Age~ER,nki70)  # side-by-side boxplots of Age by ER status
```



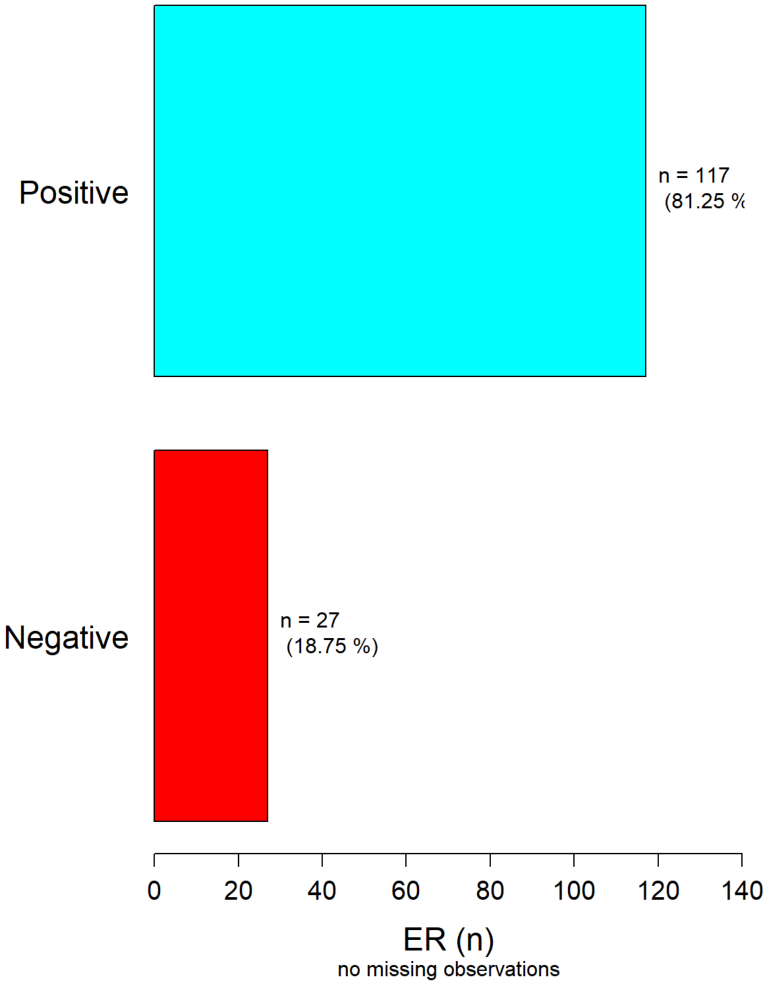


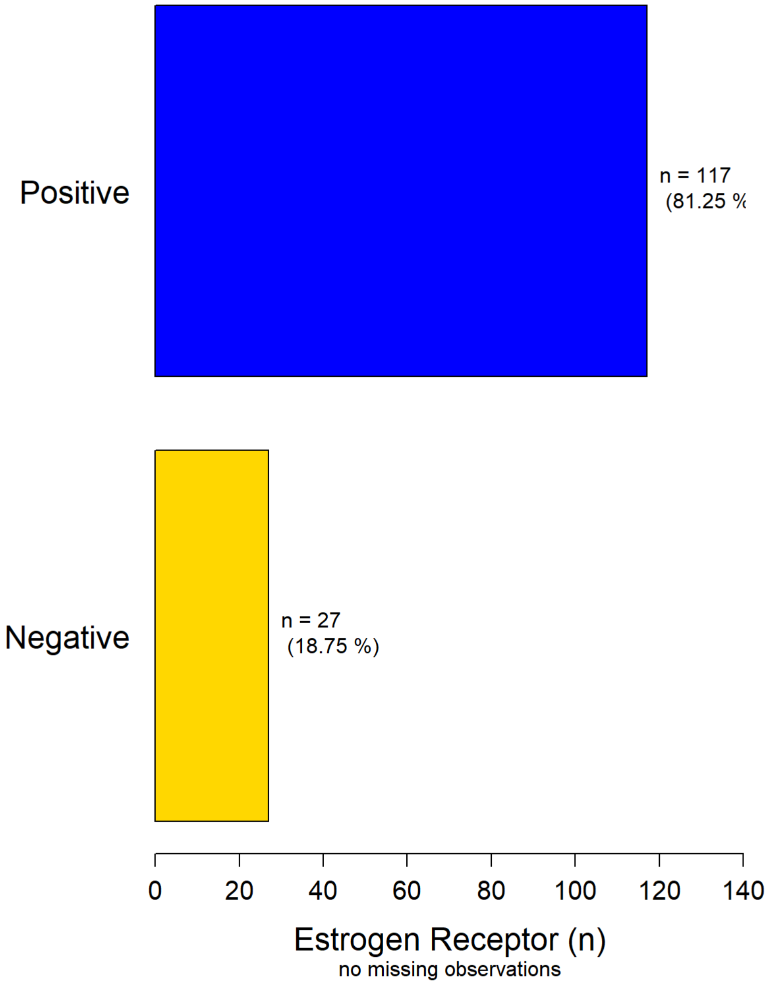
Common Options for Graphics Functions

Option	Action
`clr=color.name`	Specify colors or palette for figure
`y.name="name"`	Use `"name"` to label the y variable in the figure

Example

```
bar.plot("ER",nki70)
bar.plot("ER",nki70,y.name="Estrogen Receptor",clr=c("gold","blue"))
```



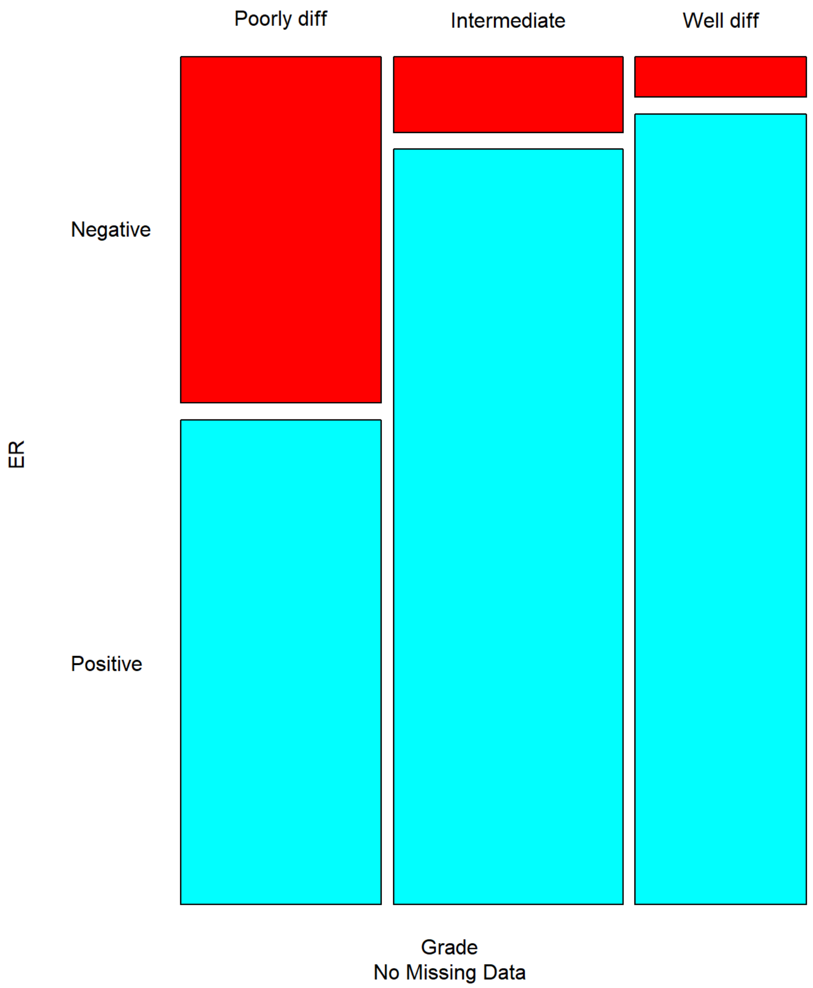


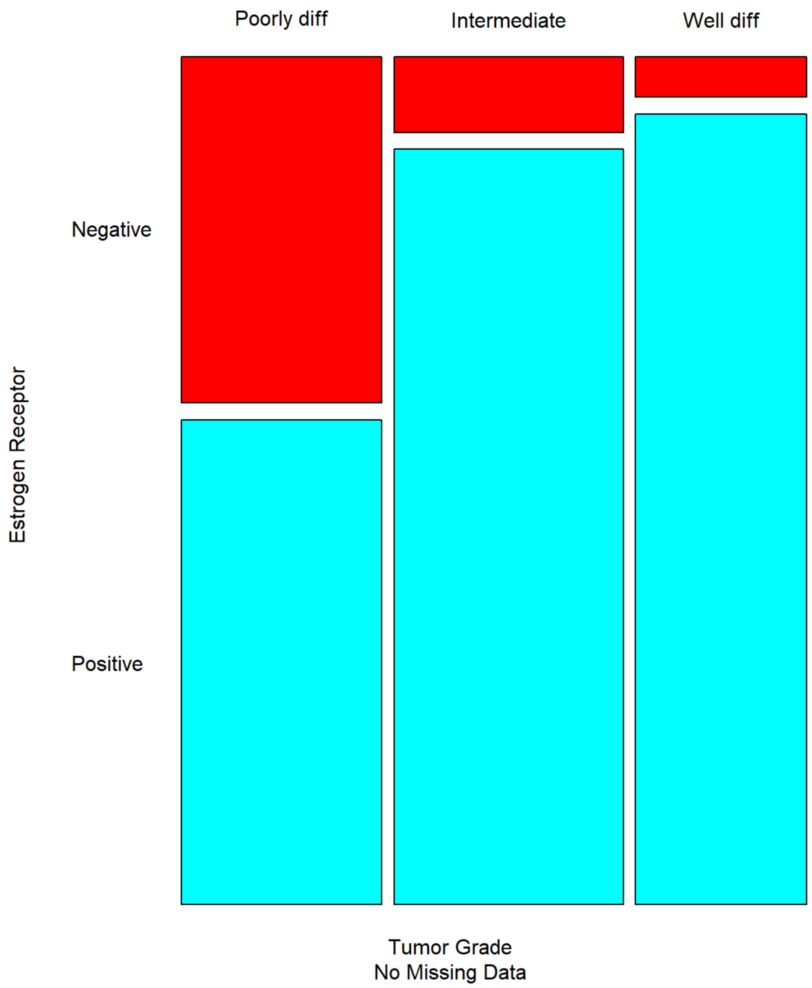
Specific Options for Graphics Functions

Function(s)	Option	Action
`mosiac.plot`	`grp.name="name"`	Use `"name"` to label the group variable in the figure
`scatter.plot`	`x.name="name"`	Use `"name"` to label the x-axis in the figure
`bar.plot`, `pie.plot`	`all=FALSE` or `all=TRUE`	Indicates whether to use **all** data by including missing data as a distinct category
`scatter.plot`	`line=0,1,`, or `NA`	Add a flat line (`line=0`), a fitted line (`line=1`) or no line (`line=NA`)

Example

```
mosaic.plot(ER~Grade,nki70)
mosaic.plot(ER~Grade,nki70,y.name="Estrogen Receptor",grp.name="Tumor Grade")
```





Including Tables in Word

```
age.result=describe("Age",nki70,fig=0)
word.table(age.result)
```

```
Age
n.total,144
n.missing,0
n.available,144
mean,44.3055555555556
stdev,5.3392304227652
median,45
lower.quartile,41
upper.quartile,49
minimum,26
maximum,53
shapiro.pvalue,0.000181978293787236



**INSTRUCTIONS**
1. Copy the output into Word.
2. Highlight the output in Word.
3. Go to Insert>Table>Convert Text to Table.
```

Including Figures in Word

- In R Studio, click on the *Plots* panel.
- Use the left and right arrows to navigate to the figure of interest.
- Click the *Export* button.
- Choose *Copy to Clipboard*.
- Click "Copy Plot"
- Paste the plot into Word.

Summary

- The Simple Biostatistics Program (SBP) provides a simple *R* interface to produce tables, figures, and narratives for the statistical procedures covered in an introductory biostatistics class.
- Use the function `` `read.data `` to read data into R.
- Use the function `get.package` to make an R package available for use in an R session.
- Data Analysis Functions: `describe`, `estimate`, `compare`, `correlate`, `model`.
- Graphics Functions: `bar.plot`, `pie.plot`, `box.plot`, `nqq.plot`, `mosaic.plot`, `scatter.plot`, `event.plot`
- Use `word.table` to generate tabular output to copy and paste into Word. Then, use *Insert>Table>Convert Text to Table* to represent the output as a table in Word.
- Use the *Export* button in R studio to copy a figure to the clipboard. Then paste the figure into Word.

Practice Exercise (Not Homework)

- Describe the `Diam`, `FGF18`, `GSTM3` columns of the `nki70` data. Tinker with the `txt`, `fig`, `tbl`, and `clr` options.
- Use the graphics functions to create the figures without generating the narrative and tabular output.
- Copy your narrative, tabular, and graphical results into Word.