

### Getting Started in Each New R Session

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

#### Read and name data

```
data.name = read.data()  
# Choose file in pop-up window
```

#### Preview data

```
View(data.name)  
colnames(data.name)
```

#### General Syntax

```
result = function(info1, info2, ...)  
# user chooses result name
```

#### Color Name Legend

```
show.colors()  
show.palettes(number)
```

#### Descriptive Stats & Graphs

```
describe("column.name", data.name)
```

#### Copy Figure to Word

In the *Plots* tab, Click *Export > Copy to Clipboard > Copy Plot*.

#### Estimate One Population Parameter

```
estimate("column.name", data.name)
```

#### Copy Tabular Result to Word

```
word.table(result.name)
```

#### Compare a Variable across Groups

```
compare(variable.name~group.name, data.name)
```

#### Correlate Two Numeric Variables

```
correlate(y.name~x.name, data.name)
```

#### Fit a Predictive Model

```
model(y.name~x1.name+x2.name, data.name)
```

#### Common Options

*Narrative*: txt = 0 (none), 1 (some), 2 ... (more)

*Tables*: tbl = 0 (none), 1 (some), 2 ... (more)

*Figures*: fig = 0 (none), 1 (some), 2 ... (more)

*Colors*: clr = c("color1.name", "color2.name")

*Colors*: clr = "palette.name"

*Output Labels*: y.name, x.name, or grp.name = "name"

#### Specific Options

*estimate*: null = number

*correlate*: line = NA (no line), 0 (flat line), 1 (fitted line)