How can I generate a Venn diagram in R?

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A Venn diagram is a graphical representation of the relationships between two or more sets of data. In order to generate a Venn diagram in R, there are a few simple steps to follow. First, you will need to install and load the "VennDiagram" package in R. Then, you can use the "draw.pairwise.venn" function to input your data and customize the diagram according to your preferences. This function allows you to specify the sizes and labels of the sets, as well as the colors and fonts used in the diagram. By following these steps, you can easily create a professional-looking Venn diagram in R to visually display the relationships between your data sets.

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**Venn diagrams are a very commonly used graphing technique that
illustrates levels of overlap between groups in data. They can be
created in R using code written as part of the Bioconductor
Project. We are following the directions supplied here for installing a package
for linear models for microarray data (`limma`).**

For more information on how to install packages from Bioconductor you can look at this page: https://bioconductor.org/install

Note that you need to install the latest version of R for this package to work properly!

To install the package `limma` we need to install package `BiocManager.`

```
install.packages("BiocManager")
BiocManager::install("limma")
```

Finally, we need to load this package.

```
library(limma)
```

We can now use the commands in this package for generating Venn diagrams. The data needed for a Venn diagram consists of a set of binary variables indicating membership. We will be using the hsb2 dataset consisting of data from 200 students including scores from writing, reading, and math tests. We will create indicators for "high" values in each of these variables and generate Venn diagrams that tell us about the degree of overlap in high math, writing, and reading scores.

```
hsb2 <- read.csv("https://stats.idre.ucla.edu/wp-content/uploads/2016/02/hsb2-3.csv")
```

```
attach(hsb2)
hw <- (write >= 60)
hm <- (math >= 60)
hr <- (read >= 60)
c3 <- cbind(hw, hm, hr)
```

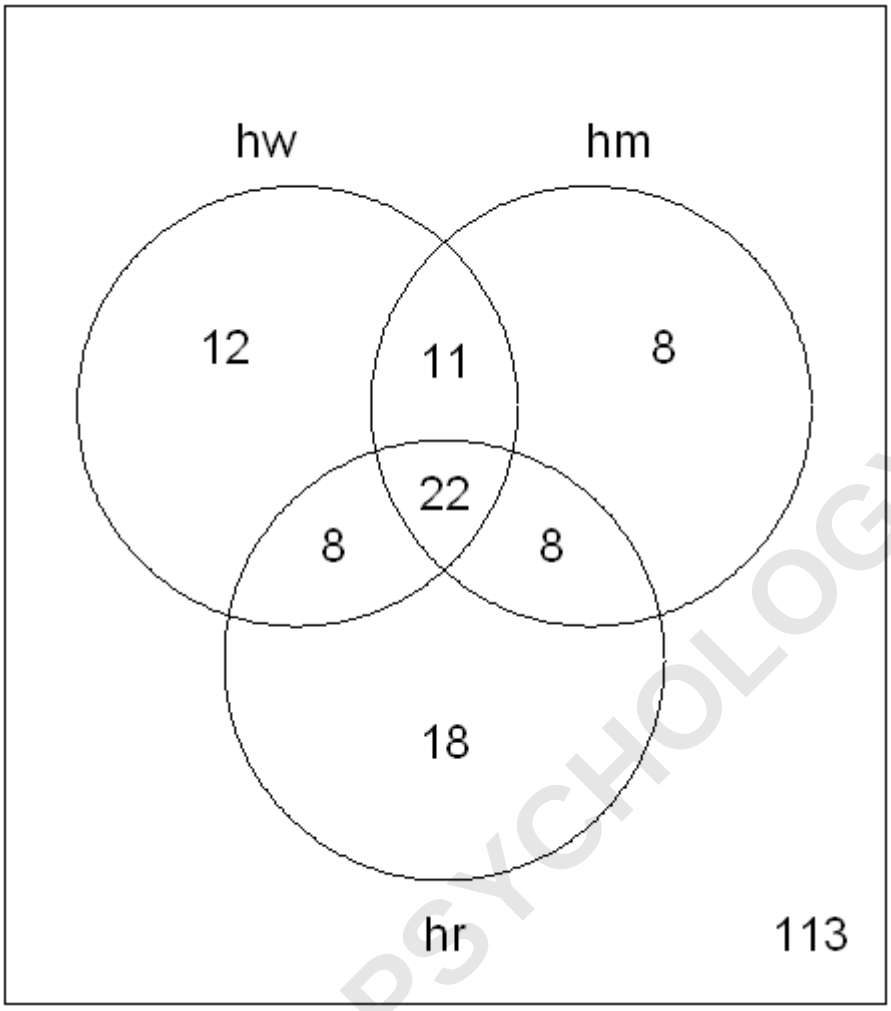
Next, we can use the `vennCounts` command to impose the structure needed to generate the Venn diagram.

```
a <- vennCounts(c3)
```

a
hw hm hr Counts
0 0 0 113
0 0 1 18
0 1 0 8
0 1 1 8
1 0 0 12
1 0 1 8
1 1 0 11
1 1 1 22
attr(,"class")
"VennCounts"

We can now generate our Venn diagram with the `vennDiagram` command:

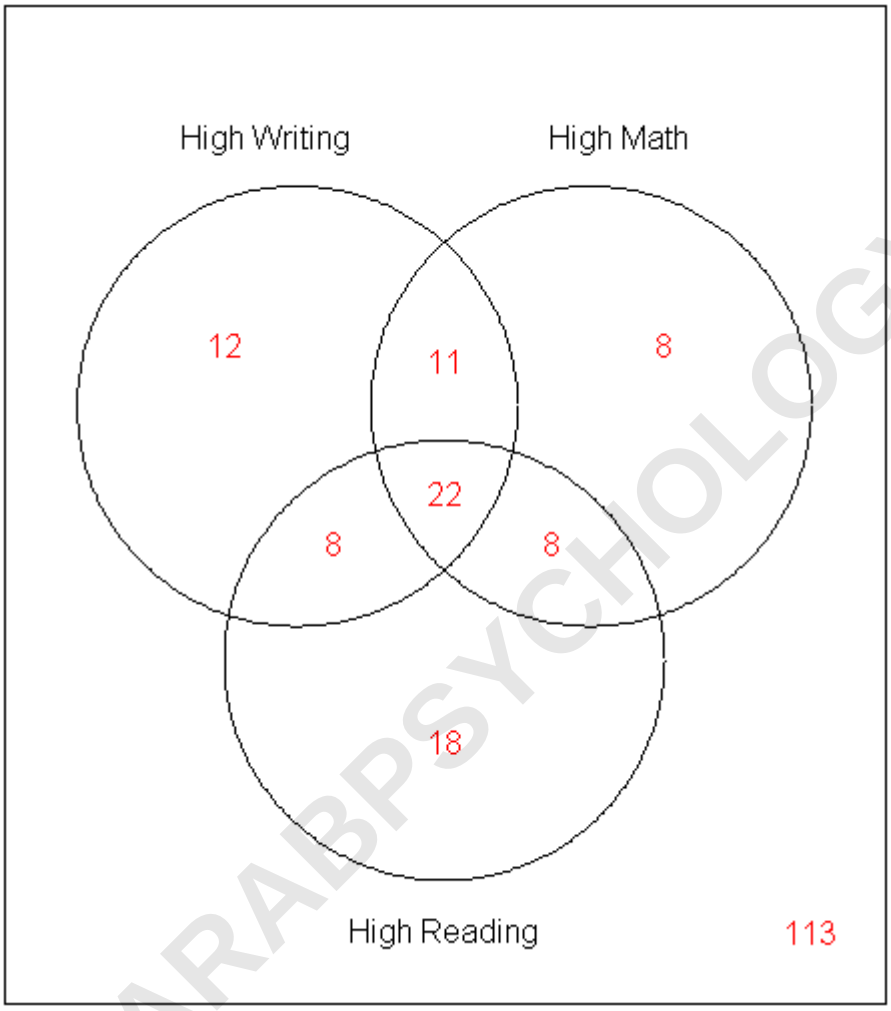
```
vennDiagram(a)
```



While some of the options for the `vennDiagram` command are specific to tests run on microarray data, we can change some of
the formatting. Below, we add names to the groups, we change the
relative size of the labels and counts, and we opt for the counts to

appear in red.

```
vennDiagram(a, include = "both",
names = c("High Writing", "High Math", "High Reading"),
cex = 1, counts.col = "red")
```



We could opt to present just two groups in this way, but it is not possible to add a fourth. Note that the size of the areas of overlap do not coincide with the relative counts. It is

also worth noting that the areas in these Venn diagrams may suggest overlap where there, in fact, is none. The example below illustrates this.

```
g <- cbind(
g1 = c(rep(0, 6), rep(1, 3)),
g2 = c(rep(1, 6), rep(0, 3)))
d <- vennCounts(g)
vennDiagram(d)
```