1 Using SASnatch

1.1 Installation

SASnatch is available on github and can be installed using the `devtools` in R:

```
require("devtools")
install_github("SASnatch", "imouzon", arg = "-l U://Documents/R/win-library/3.0")
```

1.2 Setting up a .rnw file

SASnatch requires knitr to run

```
require("knitr")
require("SASnatch")
```

and the following set in any chunk before the first SASnatch chunk:

```
path_to_SAS.EXE <<- "\"C:/Program Files/SASHome/SASFoundation/9.3/sas.exe\""
knit_hooks$set(SASnatch = SASnatch_hook)
```

where `path_to_SAS.EXE` is the full path to the version of SAS installed on your machine. The hook `SASnatch = SASnatch_hook` allows for SASnatch to work as a hook option. At this point you are ready to use SASnatch.

2 A brief example

Consider the following dataset:

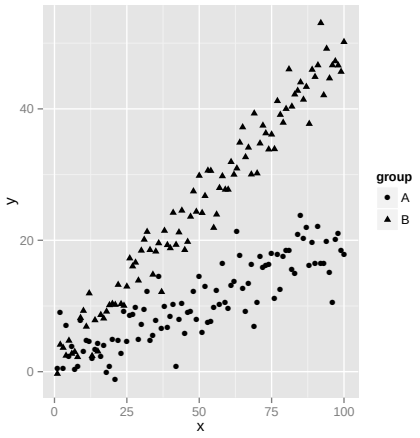
```
d.1 <- data.frame(x = 1:100, y = 0.3 + 0.2 * (1:100) + rnorm(100, 0, 3), group = rep("A",
    100))
d.2 <- data.frame(x = 1:100, y = 0.1 + 0.5 * (1:100) + rnorm(100, 0, 3), group = rep("B",
    100))
d <- rbind(d.1, d.2)
```

We can plot these datasets simply enough: – plotchunk: R plot (results in document)

```
require(ggplot2)

## Loading required package:  ggplot2

qplot(x, y, data = d, shape = group)
```



Which can be run in SAS using the following:

```
makeSAScache()
```

```
## Error:  could not find function "expand.path"
```

we can now insert the LaTeX results:

```
printSASnatch(SASgroupreg.snatch, type = "TeX")
```

```
## Error:  object 'SASgroupreg.snatch' not found
```

and since we requested regd_out be returned to R we can now plot the residuals against the predicted:

```
regd_out = SASgroupreg.snatch@out@SAS2R$regd_out
```

```
## Error:  object 'SASgroupreg.snatch' not found
```

```
head(regd_out)
```

```
## Error:  object 'regd_out' not found
```

```
qplot(yhat, resid, data = regd_out)
```

```
## Error:  object 'regd_out' not found
```