0.1 `resid` - Extracting Model Residuals

- `residuals` is a generic function which extracts model residuals from objects returned by modeling functions.
- The abbreviated form `resid` is an alias for residuals. It is intended to encourage users to access object components through an accessor function rather than by directly referencing an object slot.
- All object classes which are returned by model fitting functions should provide a residuals method. (Note that the method is for `residuals` and not `resid`.)
- Methods can make use of `naresid` methods to compensate for the omission of missing values. The default, nls and smooth.spline methods do.

```
residuals(fit)

resid(fit)
```

```
residuals(fit1)
```

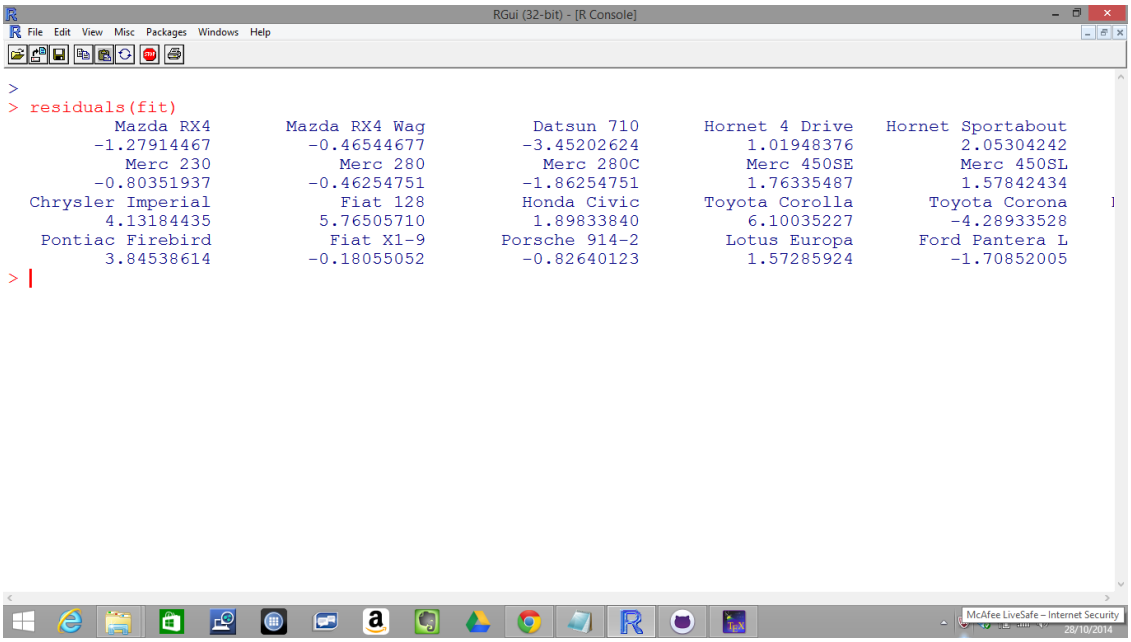

Figure 1:

```
> sum(residuals(fit))
[1] 1.096345e-15

> #Shapiro-Wilk Test for Normality
> shapiro.test(resid(fit))
```

```
Shapiro-Wilk normality test

data:  resid(fit)
W = 0.9375, p-value = 0.06341
```

Weighted Residuals

```
x <- 1:10
w <- 0:9
y <- rnorm(x)
weighted.residuals(lmxy <- lm(y ~ x, weights = w))
```