**diag.plt.r**

**Purpose**  This generates residual plots from the model for standardized residuals and/or the raw residuals. Plots are produced for any parameter output from the model that includes the name “resid” . Currently these include process residuals, fully recruited biomass residuals, recruit biomass residuals, clapper recruit residuals, and clapper fully recruited residuals.

**Version Control**  Likely several versions of this exist, obviously you love this version the most..

**Required packages** None

**Locally Derived Functions** None

**Section 1**

Takes the results of a model run and plots the residuals. Options to pull in both the standardized and raw residuals. The model will produce a plot for any variable name that includes “resid” in it and has been output from the model run. Any standardized or raw residuals will each be plotted together on their own page.

***Argument(s)***

1. data Data from the MCMC model.
2. years The years of interest, this must align with the model years. Default = missing,

must be supplied

1. graphic Plot to screen or a pdf. Default = "screen", option is "pdf".
2. path The path to put the pdf output if graphic ='pdf'. Default is blank ""
3. wd The width of the figure, default = 8.5
4. ht The height of the figure, default = 11