

# [PROGRAM NAME]

Install/load packages

```
#call another setup program
#source("~/GitHub/template/RunScript.R")#comment out (after running) if knitting
load("meta.RData")
project<-print(project)
```

```
## [1] "template"
```

```
#setwd("ad.bu.edu/bumcfiles/SPH/DCC/Dept")
pacman::p_load(rmarkdown,readxl,haven,Hmisc,foreign,lattice,janitor,dplyr,rstudioapi,stringr)
#p_load command installs packages in list not previously installed
```

## Header:

PROJECT: template SPONSOR/PI:

PROGRAM NAME: skeleton

LOCATION: C:/Users/maggi/Documents/GitHub/template/inst/rmarkdown/templates/ms\_template/skeleton

DESCRIPTION:

SPEC NAME:

SPEC LOC:

PROGRAMMER: Maggie Shea (Username: maggi )

DATE WRITTEN: YYYY.MM.DD (Last compiled on 2021-06-29 )

GENERAL NOTES:

### NOTES FOR QC

QC PROGRAMMER:

QC DATE:

QC STATUS:

QC NOTES:

### INPUT/OUTPUT

DATA IN:

DATA OUT:

REPORTS OUT:

### MODIFICATION #

DATE:

PROGRAMMER:

DESCRIPTION: NOTES FOR QC:

QC PROGRAMMER:

QC DATE:

QC STATUS:

QC NOTES:

## Setup

*Note: remove "eval=FALSE" from top of code chunks to run*  
Import data

```
#Haven package read_sas command  
#Data reads in with labels from SAS  
data <- read_sas("[file path]/[data file name].sas7bdat")  
#View(data)
```

Clean variable names

```
#Use Janitor package clean_names command to clean variable name  
#by making all lowercase, changing spaces and punctuation to underscores  
data_clean<-clean_names(data)  
#names(data_clean)
```

Add/edit labels

```
#View labels using Hmisc package label command  
label(data_clean)  
#Set labels with same command  
label(data_clean$id)<-"ID Label"  
#View(data_clean)
```

## Macros/Functions

### Data Manipulation

### Permanent Dataset

### Statistical Procedures

### Output Manipulation

### Formatted Output (TFLs)