

*The Power of GNU Make for
Building Anything*

3rd Edition
Completely Revised & Updated



*Managing
Projects with*

GNU Make

O'REILLY®

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GNU make



GNU Make is a tool which controls the workflow of generating target/result files from the dependencies (source files).

Target/result files may be text files, standalone programs, packages

Capabilities of Make

- Make is for more than just a tool for compiling software
- The path from raw data to final results
- Automates/documents a workflow
- Intelligently handles the dependencies among data files, code
- Accounts for the updates in data, code
- Re-runs only the necessary code, based on what has changed

Makefile structure

Makefile contains **recipes** in the form of:

```
target: dependencies
```

```
<code>
```

- **target** the outcome
 - **dependencies** the necessary parts to build the outcome
 - **code** outlines the rules to build target using
 dependencies
- All commands must be **tab**-indented
 - Dependencies, if more than one, must be **space**-separated

Makefile example

```
# An example of obtaining counts and types of the cytobands  
all: cytoband_counts.txt cytoband_types.txt
```

```
# Download the raw data
```

```
cytoBand.txt.gz:
```

```
    wget http://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/$@
```

```
# Obtain counts of the cytobands
```

```
cytoband_counts.txt:    cytoBand.txt.gz
```

```
    zcat < $< | cut -f1 | sort | uniq -c | awk '{OFS="\t"} {print $$2,$$1}' | sort -  
k2 -nr > $@
```

```
# Obtain types of the cytobands
```

```
cytoband_types.txt: cytoBand.txt.gz
```

```
    zcat < $< | cut -f5 | sort | uniq -c | awk '{OFS="\t"} {print $$2,$$1}' | sort -  
k2 -nr > $@
```

```
clean:
```

```
    rm *.gz
```



Makefile structure

Typical recipes

- `clean` – commands to clean up the working directory from temporary files
- `test` – runs a series of tests
- `install` – installs a software
 - `./configure`
 - `make`
 - `make install`



How to use make

- If you name your make file **Makefile**, then just go into the directory containing that file and type **make**
- If you name your make file **something.else**, then type **make -f something.else**
- By default, **make** builds the first target listed in the **Makefile**. Generally, the first target generates all other targets
all: target1 target2 target3
- To build a specific target, type **make target**. For example, **make cytoband_counts.txt**



Make variables

- A variable is a name defined in a makefile to represent a string of text, called the variable's value. Variables are used to simplify recipes

- Defining internal Makefile variable

```
DB = "/home/genomerunner/db_2.00_06.10.2014"
```

- Using a variable

```
${DB} or $(DB)
```



Using shell variables in Make

Shell variables, e.g. `$HOME`, need to be prefixed by `$`

<code>awk '{print \$0}'</code>	within shell variable use
<code>awk '{print \$\$0}'</code>	within Makefile variable use

Capturing output of shell commands into a variable:

```
TXT_FILES = $(shell find . -type f -name "*.txt")
```

TIP!

- The content of a Makefile runs in its own shell environment. The default shell environment is `/bin/sh`. To set shell environment to `bash`, use **`SHELL=/bin/bash`**

Why bother?

- Variable `$SECONDS` exists in `bash`, but not in `sh`
- Other syntax incompatibilities, e.g., `if-else-fi` syntax



Automatic variables

Makefile contains **recipes** in the form of:

```
target: dependencies
    <code>
```

<code>\$@</code>	the name of the target of the rule
<code>\$<</code>	the name of the first dependency
<code>\$?</code>	the names of all the dependencies
<code>\$(<F)</code>	the file part of the first dependency

Example:

```
COMPILER = g++          # Define compiler
COMPILER_FLAGS=-c -Wall # Define flags
```

```
hello.o: hello.c hello.h # Recipe
    $(COMPILER) $(COMPILER_FLAGS) $< -o $@
```

Patterns

A pattern rule allows “wildcard” matching between the target and the dependencies. The ‘%’ wildcard is similar to the ‘*’ wildcard in bash

- Existing files:
 - `module0_induction.Rmd`
 - `module1_basics.Rmd`
 - `module2_managingR.Rmd`
- Makefile recipe:

```
% .html: % .Rmd
    echo $(@)
    ./compile_slides $(basename $@)
```
- Results:
 - `module0_induction.html`
 - `module1_basics.html`
 - `module2_managingR.html`

Canned recipes (functions)

```
# Prefix for the `_snps.bed' and `_bkg.bed' file names
INP = chr22
```

```
# Path to the genomic background
BKG = background/snp138.bed.gz
```

```
# Types of analyses to run
AN1 = chromStates
AN2 = tfbsEncode
```

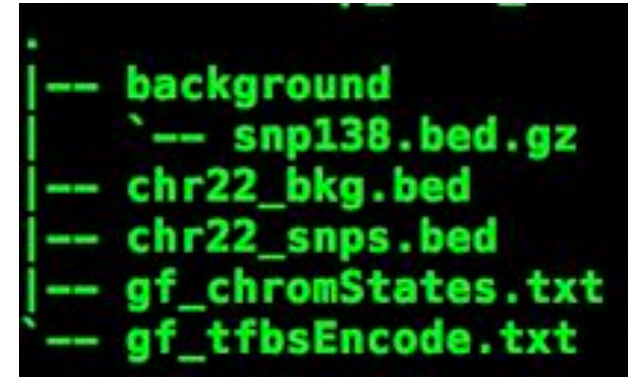
```
# Variable/function to execute the @$ analysis
```

```
define hypergeom4
python -m grsnp.hypergeom4 --output_dir @$ $(INP)_snps.bed gf_$.txt $
$(INP)_bkg.bed
endef
```

```
all:      .$(AN1) .$(AN2)
```

```
.$(AN1) :  $(INP)
           $(hypergeom4)
```

```
.$(AN2) :  $(INP)
           $(hypergeom4)
```



```
--- background
    |-- snp138.bed.gz
--- chr22_bkg.bed
--- chr22_snps.bed
--- gf_chromStates.txt
--- gf_tfbsEncode.txt
```