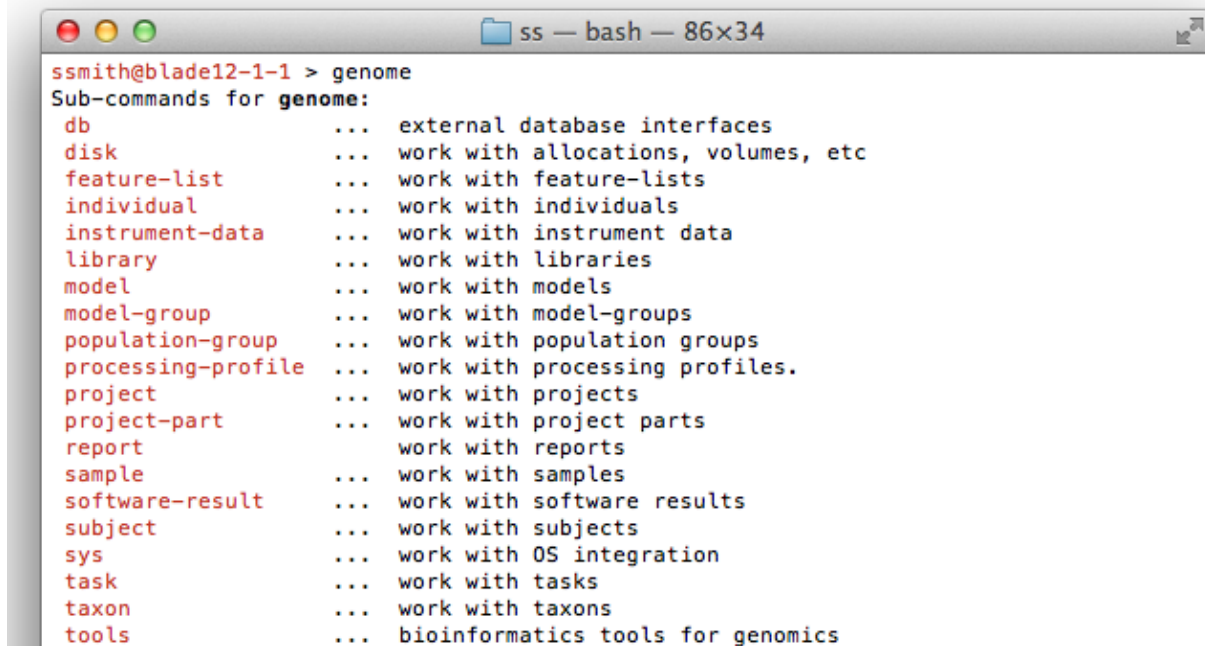
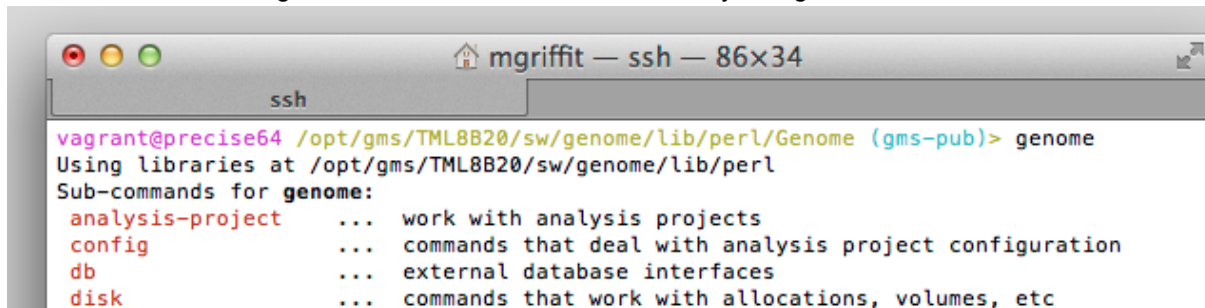


A. The top-level command tree of 'genome'



```
ssmith@blade12-1-1 > genome
Sub-commands for genome:
db          ... external database interfaces
disk       ... work with allocations, volumes, etc
feature-list ... work with feature-lists
individual ... work with individuals
instrument-data ... work with instrument data
library    ... work with libraries
model     ... work with models
model-group ... work with model-groups
population-group ... work with population groups
processing-profile ... work with processing profiles.
project    ... work with projects
project-part ... work with project parts
report     work with reports
sample    ... work with samples
software-result ... work with software results
subject   ... work with subjects
sys       ... work with OS integration
task     ... work with tasks
taxon    ... work with taxons
tools    ... bioinformatics tools for genomics
```

B. Modifications of the genome source code are automatically recognized and used



```
mgriffit — ssh — 86x34
ssh
vagrant@precise64 /opt/gms/TML8B20/sw/genome/lib/perl/Genome (gms-pub)> genome
Using libraries at /opt/gms/TML8B20/sw/genome/lib/perl
Sub-commands for genome:
analysis-project ... work with analysis projects
config          ... commands that deal with analysis project configuration
db             ... external database interfaces
disk          ... commands that work with allocations, volumes, etc
```