

## A - Example Project Flow using *build\_blast\_atlas.sh*

1) Create a new project called `my_project` with the directory structure seen in **B**:

```
[CCT]$ build_blast_atlas.sh -p my_project
```

2) Download the *R. norvegicus* mitochondrial sequence (AC: AC\_000022) into the `reference_genome` directory:

```
[CCT]$ fetch_genome_by_accession.sh -a AC_000022 -o my_project/reference_genome
```

3) Download all mitochondrial genome sequences in GenBank into the `comparison_genomes` directory:

```
[CCT]$ fetch_all_refseq_mitochondrial_genomes.sh -o my_project/comparison_genomes
```

4) Run *build\_blast\_atlas.sh* again to generate maps of both nucleotide (blastn) comparisons and translated coding sequence (blastp) comparisons (shown in Figure 3):

```
[CCT]$ build_blast_atlas.sh -p my_project \  
  --custom "global_label=T labelFontSize=50 draw_divider_rings=F \  
           legend=F featureSlotSpacing=0.1"
```

*--custom*: settings used to customize the appearance of the map.

## B - BLAST Atlas Project Directory Structure

```
my_project/  
├── reference_genome           - directory to place reference genome  
├── comparison_genomes       - directory to place multiple comparison genomes  
├── maps_for_cds_vs_cds      - directory for final CDS maps  
├── maps_for_dna_vs_dna     - directory for final DNA maps  
├── analysis                 - directory to place optional analysis GFF files  
├── features                 - directory to place optional feature GFF files  
├── cct_projects             - directory of CCT sub projects for DNA and CDS  
│   ├── cds_vs_cds          - CDS CCT sub project  
│   └── dna_vs_dna          - DNA CCT sub project  
├── project_settings_cds_vs_cds.conf - alter to modify CDS project  
└── project_settings_dna_vs_dna.conf - alter to modify DNA project
```