A

ct_0 ct_1 ct_2 seq   **DNA sequence data**
                             dnadata.txt

↓ `convertseqs --protein`

ct_0 ct_1 ct_2 seq_pro   **protein sequence data**
                             proteindata.txt

↓ `profile_enrichment --bin 2 --lib 0`

pos wt le_A le_C le_D ... le_Y   **enrichment profile**
                                        enrichment.txt
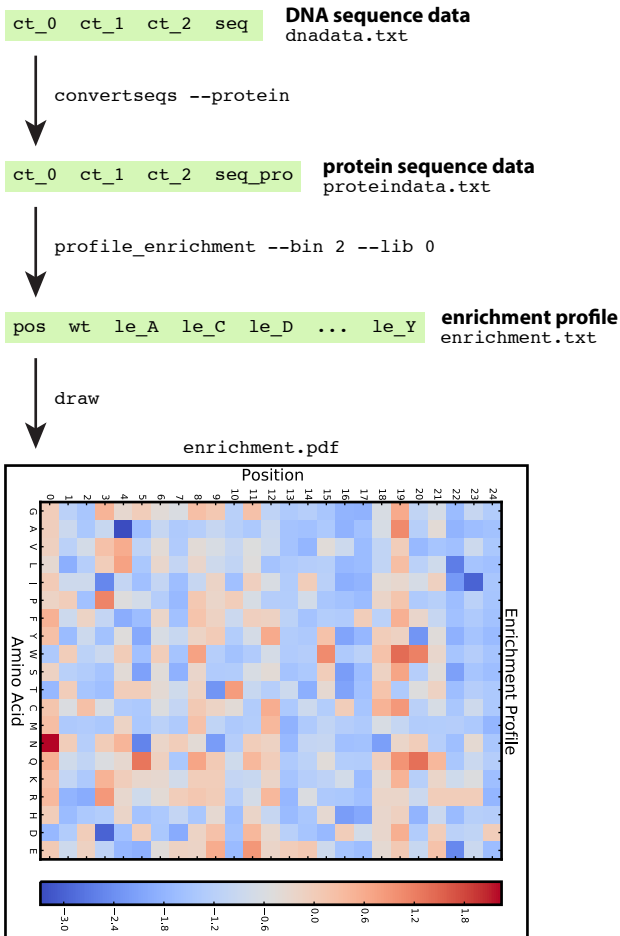
↓ `draw`

enrichment.pdf

B

```
$ sortseq convertseqs --protein \
    -i dnadata.txt -o proteindata.txt
$ sortseq profile_enrichment --bin 2 --lib 0 \
    -i proteindata.txt -o enrichment.txt
$ sortseq draw -i enrichment.txt -o enrichment.pdf
```

Figure 6