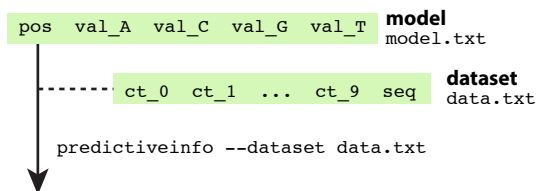


A



B

```
$ sortseq predictiveinfo --dataset data.txt \
  -i model.txt -o info.txt
```

C

datasets.txt	
dataset	file
full-wt	full-wt_data.txt
crp-wt	crp-wt_data.txt
full-0	full-0_data.txt
full-150	full-150_data.txt
full-500	full-500_data.txt

D

models.txt	
model	file
full-wt	full-wt_crp_model.txt
crp-wt	crp-wt_crp_model.txt
full-0	full-0_crp_model.txt
full-150	full-150_crp_model.txt
full-500	full-500_crp_model.txt

E

```
$ sortseq compare_predictive_information \
  --datasets datasets.txt \
  --models models.txt -s 3 -e 25 \
  -o comparison.txt
$ sortseq draw -i comparison.txt -o comparison.pdf
```

F

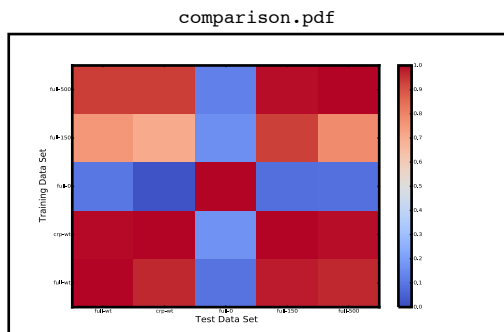


Figure 9