

Deep learning Augmented RNA-seq analysis of Transcript Splicing

Demo 1: Installation & Basic Usage

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1. Installation

- Download the Darts software
 - > `git clone git@github.com:zj-zhang/DARTS.git`
- Install Darts_BHT and Darts_DNN
 - > `cd Darts_BHT`
 - > `make install`
 - > `cd ../Darts_DNN`
 - > `make install`
- Install Keras and Theano (recommend Anaconda)
 - > `conda install -c conda-forge keras`

1. Installation

- Add Darts to your environment variables
 - > `vim ~/.bash_profile`
- .. paste the following code to the end of the file:
`export PATH=$HOME/.darts:$PATH`
- Then source it
 - > `source ~/.bash_profile`

2. Using Darts_BHT

- Download the demo data to local folder (11M) and unzip it
 - > `wget https://master.dl.sourceforge.net/project/rna-darts/demo/darts_demo_1.tar.gz`
 - > `tar -xvzf darts_demo_1.tar.gz`
- Run Darts-flat inference on the read count file `input.read_count.txt`; for the sake of time, let's only run the first 200 events:
 - > `head -n 201 input.read_count.txt > input.read_count.200.txt`
 - > `mkdir darts_out`
 - > `Darts_BHT -i input.read_count.200.txt -o darts_out/ -k 1 -v`

2. Using Darts_BHT

- This will prompt a progress bar for showing the inference progress. Once finished, the output file will be generated in folder `darts_out`; for now, let's use the pre-computed file you just downloaded, which you can check the first 200 rows are identical:
 > less darts_flat.out.txt

3. Using Darts_DNN

- Build the feature set for our target exon events:
 > Darts_DNN build_feature -i darts_flat.out.txt \
 -c cisFeature_absmax_normalized.h5 \
 -e kallisto/PC3E/ kallisto/GS689/ \
 -o data.h5
- Note: the backslash “\” separates different arguments for readability; in practice it can be omitted.
- This step will generate the output feature set “data.h5”, using the cis-feature stored in “cisFeature_absmax_normalized.h5” and the Kallisto abundance results stored under “kallisto” directory.

3. Using Darts_DNN

- Now run the prediction:

```
> Darts_DNN predict -i data.h5 -o pred.txt -m model_param.h5
```

- If configured correctly, you should see:

```
2018-03-17 16:43:09,112 - Darts_DNN.predict - INFO -  
pos=810  
2018-03-17 16:43:09,114 - Darts_DNN.predict - INFO -  
neg=38963  
2018-03-17 16:43:09,114 - Darts_DNN.predict - INFO -  
AUROC=0.799907525436  
2018-03-17 16:43:09,114 - Darts_DNN.predict - INFO -  
AUPR=0.159964942402
```

4. Visualizing Darts_DNN prediction

- We can do a quick check on the prediction in R. We should see a clear separation between differential splicing events vs. unchanged events:

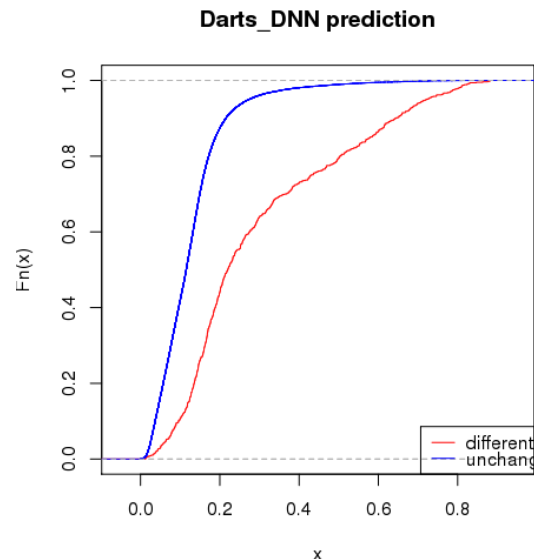
```
%%R
```

```
> data=read.table('pred.txt', header=T)
```

```
> plot(ecdf(data$Y_pred[data$Y_true>0.9]), col='red', do.points=F, main='Darts_DNN prediction',  
ylim=c(0,1))
```

```
> lines(ecdf(data$Y_pred[data$Y_true<0.1]), col='blue')
```

```
> legend('bottomright', col=c('red','blue'), legend=c('different', 'unchanged'), lty=1)
```



5. Run Darts_BHT with informative prior

- Since the prediction AUROC for this data is 0.80, this prediction can be utilized as an informative prior in Darts_BHT to boost the biological discovery in lowly expressed genes.
- Here is how to do it. We will use the first 200 events again as an example:
 > `Darts_BHT -i input.read_count.200.txt -o darts_out/ -r pred.txt -k 1 -v`
- This time, the output file name will be “Sp_out.prior.txt”. You can check the difference by incorporation of informative prior to the Darts-flat generated “Sp_out.txt” previously.