nn-vs-svm

AnhVu

2/18/2020

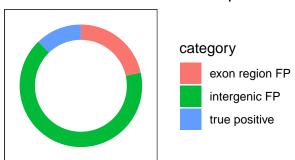
## Comparison of SVM and NN models ${\cal N}$

Thega1 splice site classification (SVM models)

### Classification metrics of donor

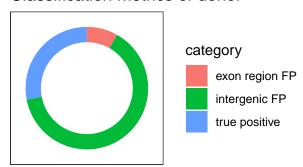
category
exon region FP
intergenic FP
true positive

### Classification metrics of acceptor

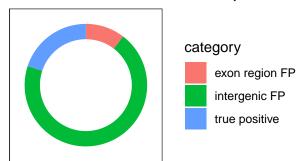


Thega1 splice site classification (NN models)

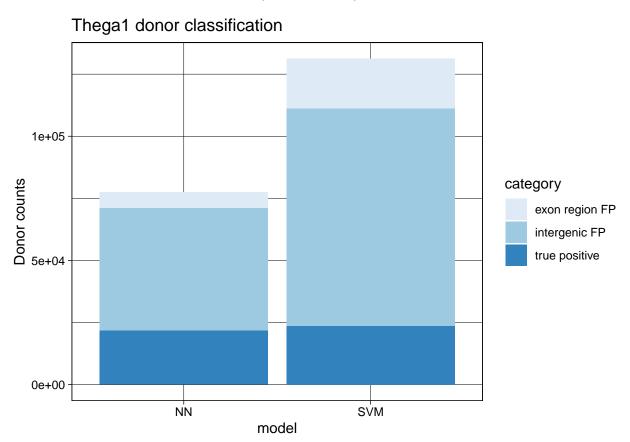
#### Classification metrics of donor



### Classification metrics of acceptor

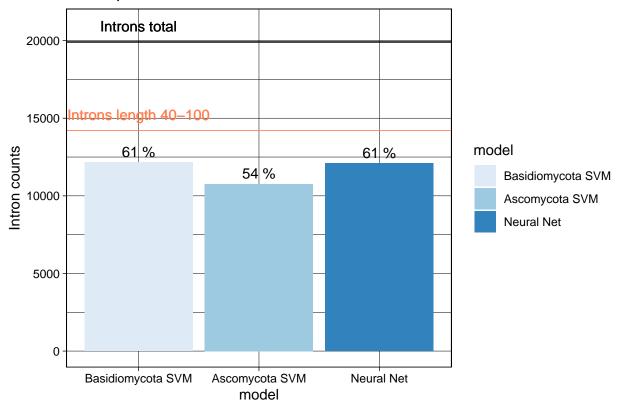


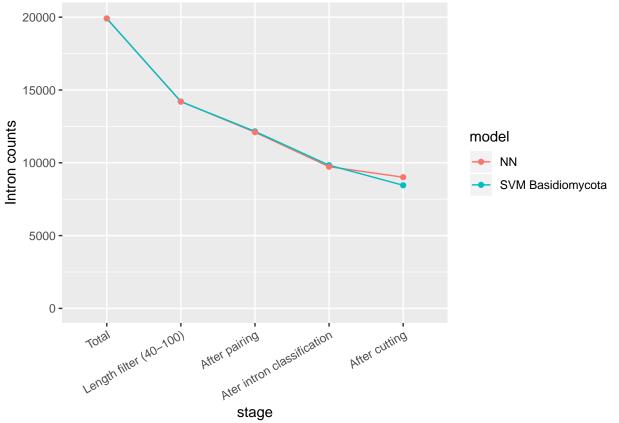
Thega1 splice site classification (comparison)



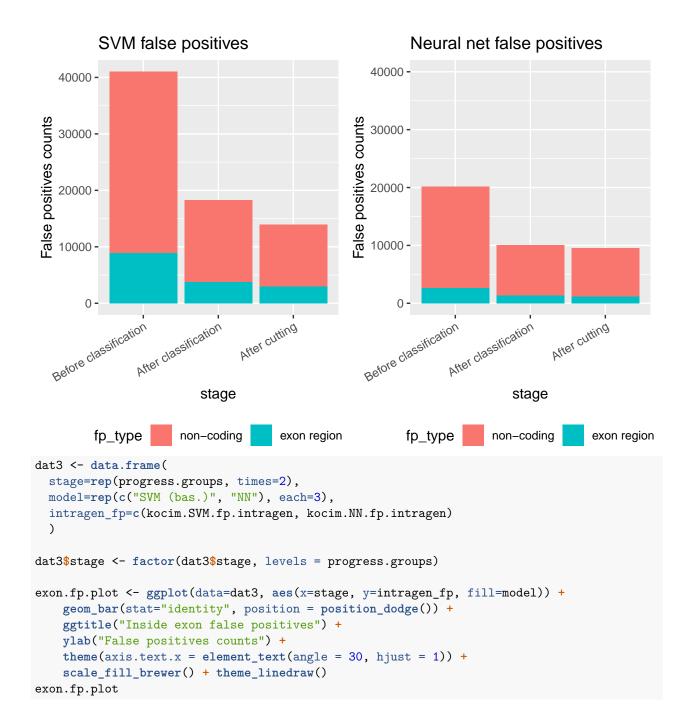
# Intron classification (Kocim1 and Thega1)



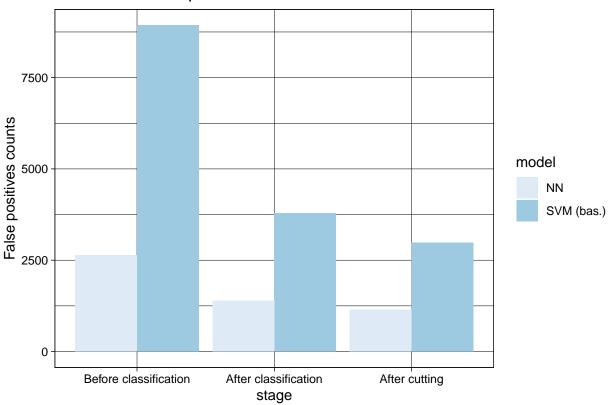




```
kocim.NN.fp.all \leftarrow c(20141, 10103, 9495)
kocim.NN.fp.intragen <- c(2640, 1383, 1143)
kocim.NN.fp.intergen <- kocim.NN.fp.all - kocim.NN.fp.intragen</pre>
kocim.SVM.fp.all <- c(41001, 18228, 13934)
kocim.SVM.fp.intragen <- c(8927, 3792, 2975)
kocim.SVM.fp.intergen <- kocim.SVM.fp.all - kocim.SVM.fp.intragen
dat_svm <- build_plot_df(kocim.SVM.fp.intergen, kocim.SVM.fp.intragen)</pre>
svm.plot <- ggplot(data=dat_svm, aes(x=stage, y=fp_counts, fill=fp_type)) +</pre>
    geom_bar(stat="identity") +
    ggtitle("SVM false positives") +
    ylab("False positives counts") +
    theme(legend.direction="horizontal", legend.position="bottom", axis.text.x = element_text(angle = 3
dat_nn <- build_plot_df(kocim.NN.fp.intergen, kocim.NN.fp.intragen)</pre>
nn.plot <- ggplot(data=dat_nn, aes(x=stage, y=fp_counts, fill=fp_type)) +
    geom_bar(stat="identity") +
    ggtitle("Neural net false positives") +
    ylab("False positives counts") +
    ylim(0,40000) +
    theme(legend.direction="horizontal", legend.position="bottom", axis.text.x = element_text(angle = 3
grid.arrange(svm.plot, nn.plot, ncol = 2)
```



### Inside exon false positives



#### Thega1 experiments

```
thega.NN.fp.all <- c(50331, 25251, 20008)
thega.NN.fp.intragen <- c(5071, 2759, 2195)
thega.NN.fp.intergen <- thega.NN.fp.all - thega.NN.fp.intragen
thega.SVM.fp.all <-c(86685, 41416, 29680)
thega.SVM.fp.intragen <- c(14131, 6204, 4577)
thega.SVM.fp.intergen <- thega.SVM.fp.all - thega.SVM.fp.intragen
dat_svm_thega <- build_plot_df(thega.SVM.fp.intergen, thega.SVM.fp.intragen)</pre>
svm.plot <- ggplot(data=dat_svm_thega, aes(x=stage, y=fp_counts, fill=fp_type)) +</pre>
    geom_bar(stat="identity") +
   ggtitle("SVM false positives") +
   ylab("False positives counts") +
   theme(legend.direction="horizontal", legend.position="bottom", axis.text.x = element_text(angle = 3
dat_nn_thega <- build_plot_df(thega.NN.fp.intergen, thega.NN.fp.intragen)
nn.plot <- ggplot(data=dat_nn_thega, aes(x=stage, y=fp_counts, fill=fp_type)) +
   geom_bar(stat="identity") +
   ggtitle("Neural net false positives") +
   ylab("False positives counts") +
   ylim(0,87000) +
```

