Glioblastoma_mixomics_supervised

```
Loading required package: MASS

Loading required package: lattice

Loading required package: ggplot2


Loaded mixOmics 6.30.0
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```

```
load("~/PROJECTS_ALL/DATA_Glioblastoma/preprocessed/glioblastoma_data_no_caseid.RData")
```

```
X <- list(mRNA = glioblastoma_data$data.train$mrna,
          methylation = glioblastoma_data$data.train$methylation,
          protein = glioblastoma_data$data.train$protein
)

Y <- glioblastoma_data$data.train$class
```

```
Y[is.na(Y)] <- 0
Y <- factor(Y, levels = c(0, 1))
print(Y)
```

```
 [1] 1 0 1 0 1 1 0 1 1 1 1 1 0 0 0 1 1 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 1
[39] 0 0 0 1 0 0 1 0 0 1 1 1 1 1 1 0 0 1 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 0
[77] 1 1
Levels: 0 1
```

```
design <- matrix(0.1, ncol = length(X), nrow = length(X),
                 dimnames = list(names(X), names(X)))
diag(design) <- 0
design
```

```
            mRNA methylation protein
mRNA         0.0         0.1     0.1
methylation  0.1         0.0     0.1
protein      0.1         0.1     0.0
```

```r
res1.pls.gbm <- pls(X$mRNA, X$protein, ncomp = 1)
cor(res1.pls.gbm$variates$X, res1.pls.gbm$variates$Y)
```

```
          comp1
comp1 0.9464596
```

```r
res2.pls.gbm <- pls(X$mRNA, X$methylation, ncomp = 1)
cor(res2.pls.gbm$variates$X, res2.pls.gbm$variates$Y)
```

```
          comp1
comp1 0.4892087
```

```r
res3.pls.gbm <- pls(X$protein, X$methylation, ncomp = 1)
cor(res3.pls.gbm$variates$X, res3.pls.gbm$variates$Y)
```

```
          comp1
comp1 0.5068804
```

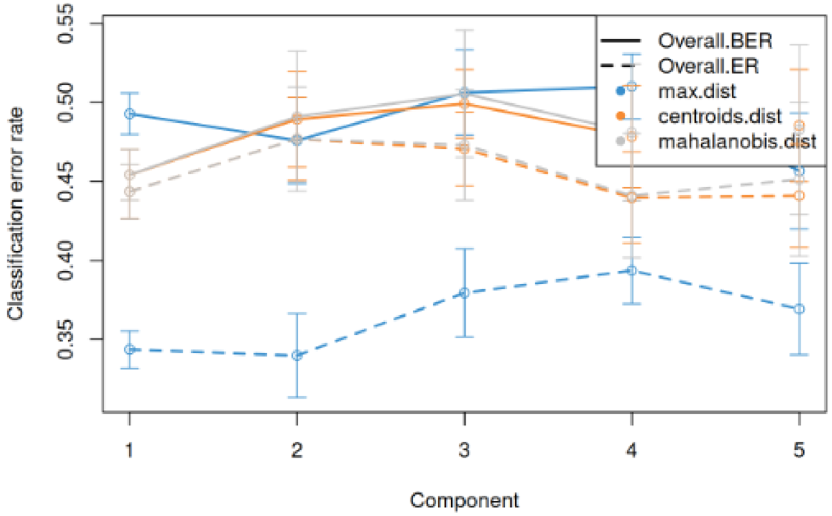
```r
diablo.gbm <- block.plsda(X, Y, ncomp = 5, design = design)
```

```
Design matrix has changed to include Y; each block will be
            linked to Y.
```

```r
set.seed(123)

perf.diablo.gbm = perf(diablo.gbm, validation = 'Mfold', folds = 10, nrepeat = 10)
```

```r
plot(perf.diablo.gbm)
```



```r
perf.diablo.gbm$choice.ncomp$WeightedVote
```

```
            max.dist centroids.dist mahalanobis.dist
Overall.ER         1              1                1
Overall.BER        5              1                1
```

```r
ncomp <- perf.diablo.gbm$choice.ncomp$WeightedVote["Overall.BER", "centroids.dist"]
```

```r
set.seed(123)

test.keepX <- list(mRNA = c(5:9, seq(10, 25, 5)),
                   methylation = c(5:9, seq(10, 20, 2)),
                   proteomics = c(seq(5, 25, 5)))


tune.diablo.gbm <- tune.block.splsda(X, Y, ncomp = 2,
                              test.keepX = test.keepX, design = design,
                              validation = 'Mfold', folds = 10, nrepeat = 2,
                              BPPARAM = BiocParallel::SnowParam(workers = 2),
                              dist = "centroids.dist")
```

```
list.keepX <- tune.diablo.gbm$choice.keepX
```

```
list.keepX
```

```
$mRNA
[1] 5 8

$methylation
[1] 6 8

$protein
[1] 5 5
```

```
diablo.gbm <- block.splsda(X, Y, ncomp = 2,
                            keepX = list.keepX, design = design)
```

```
Design matrix has changed to include Y; each block will be
            linked to Y.
```

```
diablo.gbm$design
```

```
            mRNA methylation protein Y
mRNA         0.0         0.1     0.1 1
methylation  0.1         0.0     0.1 1
protein      0.1         0.1     0.0 1
Y            1.0         1.0     1.0 0
```

```
# mRNA variables selected on component 1
selectVar(diablo.gbm, block = 'mRNA', comp = 1)
```

```
$mRNA
$mRNA$name
[1] "ENSG00000183034.13" "ENSG00000176209.11" "ENSG00000172794.20"
[4] "ENSG00000140993.11" "ENSG00000006283.18"

$mRNA$value
                     value.var
ENSG00000183034.13  0.59703579
ENSG00000176209.11 -0.57171728
ENSG00000172794.20 -0.53451506
```

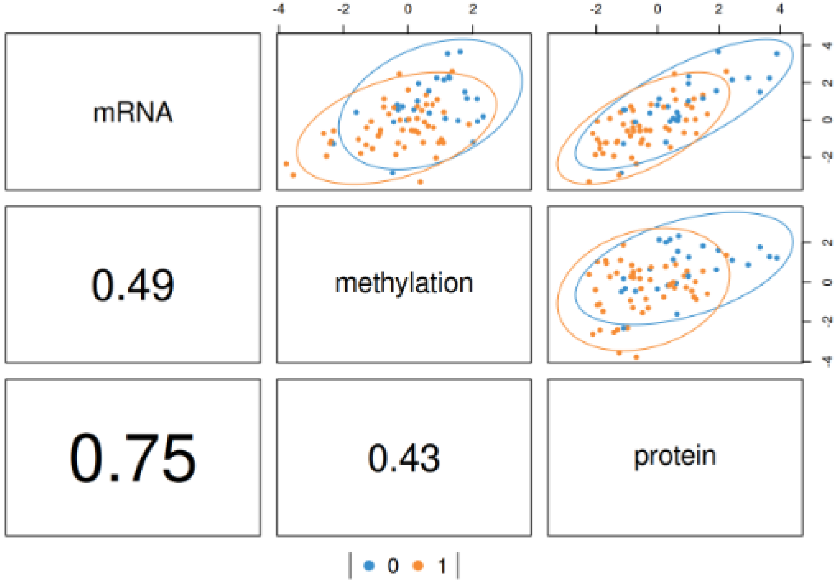
```
ENSG00000140993.11  0.16966791
ENSG00000006283.18 -0.04684085


$comp
[1] 1
```

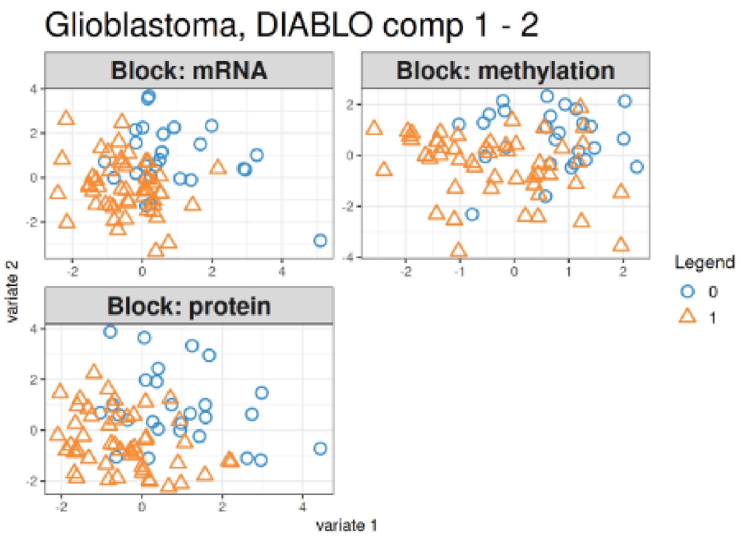
Plotting

`plotDiablo()` is a diagnostic plot to check whether the correlations between components from each data set were maximised as specified in the design matrix. We specify the dimension to be assessed with the `ncomp` argument

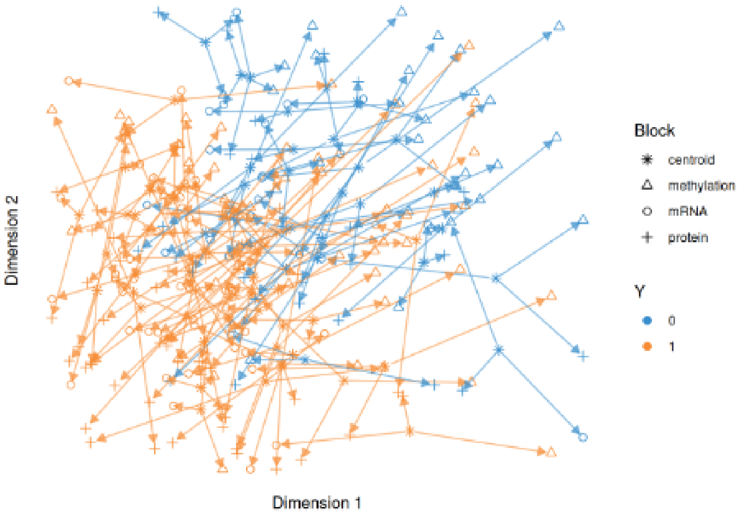
```
plotDiablo(diablo.gbm, ncomp = 2)
```



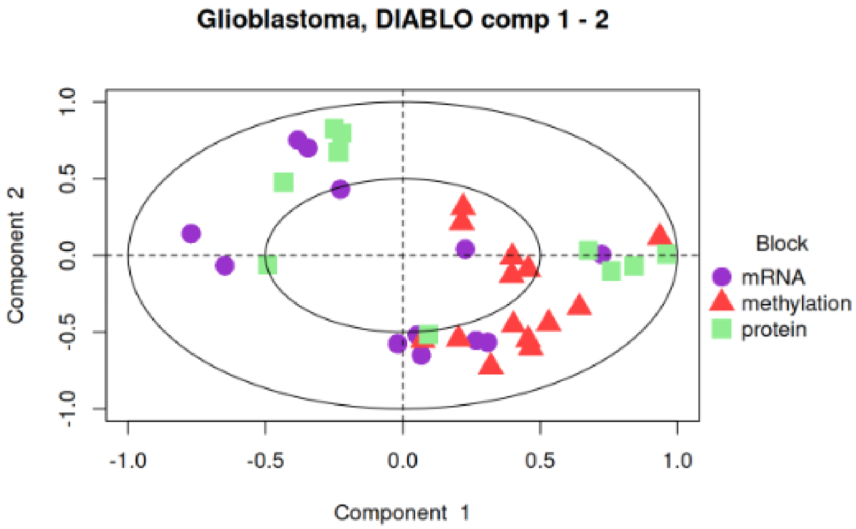
```
plotIndiv(diablo.gbm, ind.names = FALSE, legend = TRUE,
          title = 'Glioblastoma, DIABLO comp 1 - 2')
```



```r
plotArrow(diablo.gbm, ind.names = FALSE, legend = TRUE,
          title = 'Glioblastoma, DIABLO comp 1 - 2')
```

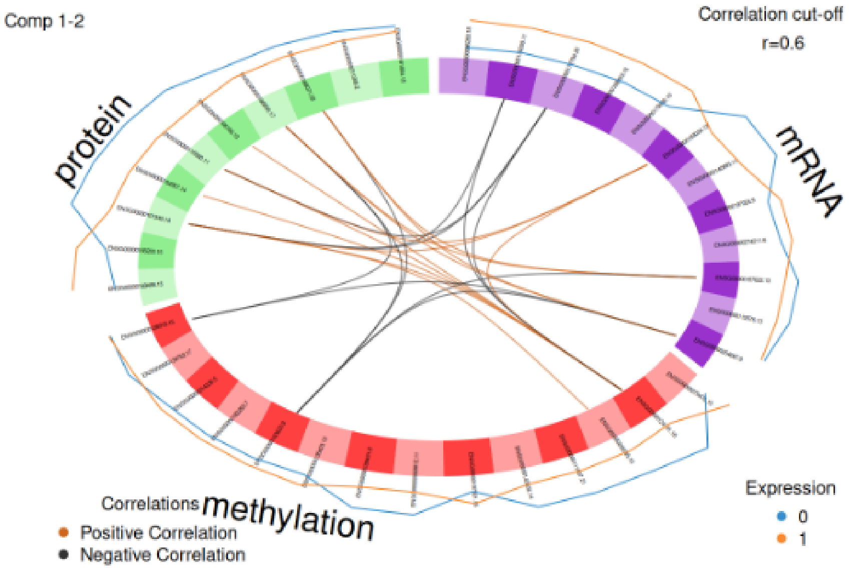


```
plotVar(diablo.gbm, var.names = FALSE, style = 'graphics', legend = TRUE,
        pch = c(16, 17, 15), cex = c(2,2,2),
        col = c('darkorchid', 'brown1', 'lightgreen'),
        title = 'Glioblastoma, DIABLO comp 1 - 2')
```



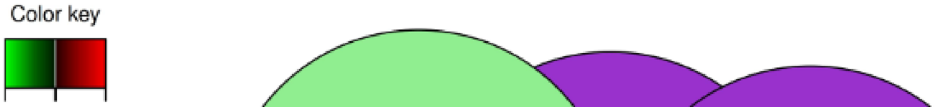
Correlation circle plot from multiblock sPLS-DA performed on the `glioblastoma` data. The variable coordinates are defined according to their correlation with the first and second components for each data set. Variable types are indicated with different symbols and colours, and are overlaid on the same plot. The plot highlights the potential associations within and between different variable types when they are important in defining their own component.

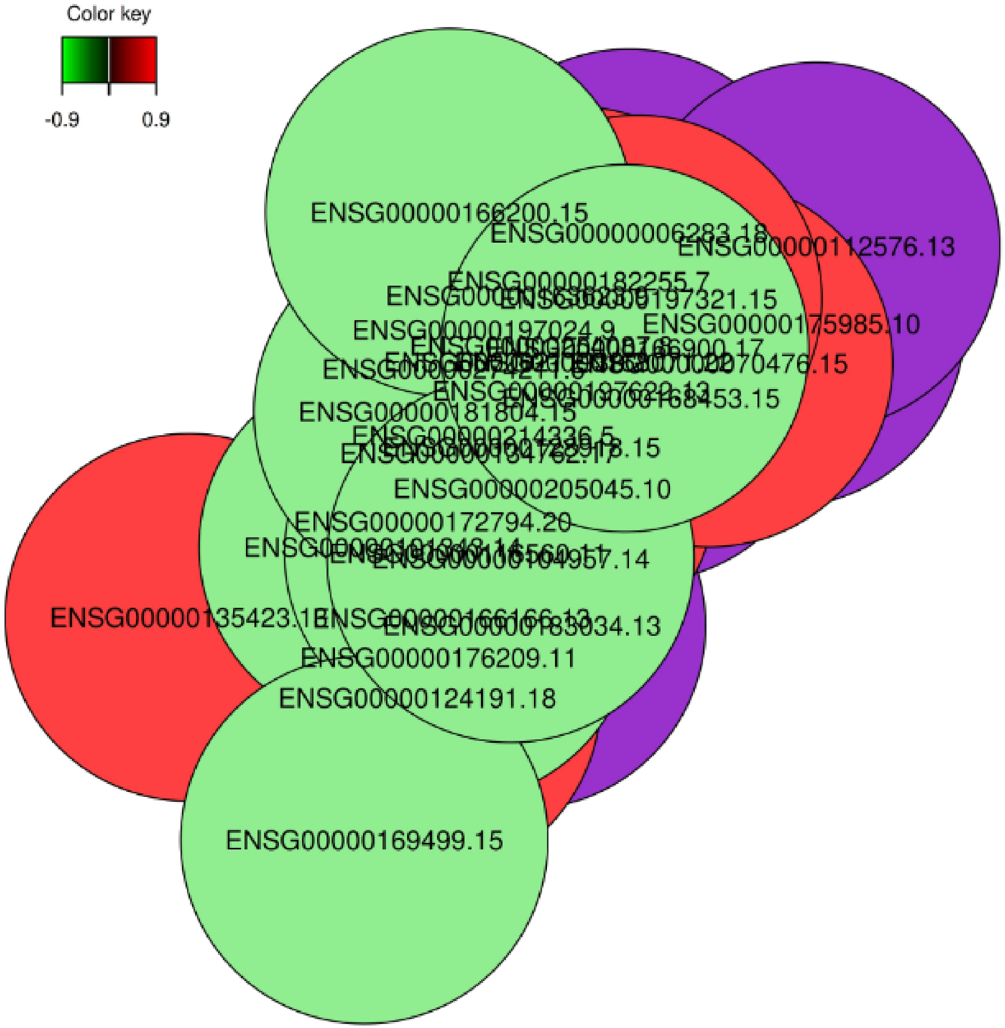
```
circosPlot(diablo.gbm, cutoff = 0.6, line = TRUE,
           color.blocks = c('darkorchid', 'brown1', 'lightgreen'),
           color.cor = c("chocolate3","grey20"), size.labels = 1.5)
```



Circos plot from multiblock sPLS-DA performed on the `glioblastoma` data. The plot represents the correlations greater than 0.6 between variables of different types, represented on the side quadrants. The internal connecting lines show the positive (negative) correlations. The outer lines show the expression levels of each variable in each sample group.

```r
network(diablo.gbm, blocks = c(1,2,3),
        cutoff = 0.4,
        color.node = c('darkorchid', 'brown1', 'lightgreen'),
        save = 'png', name.save = 'diablo-network'
        )
```





Relevance network for the variables selected by multiblock sPLS-DA performed on the `glioblastoma` data on component 1. Each node represents a selected variable with colours indicating their type. The colour of the edges represent positive or negative correlations.

Model performance and prediction

```
set.seed(123)

perf.diablo.gbm <- perf(diablo.gbm,  validation = 'Mfold', folds = 10,
                        nrepeat = 10, dist = 'centroids.dist')
```

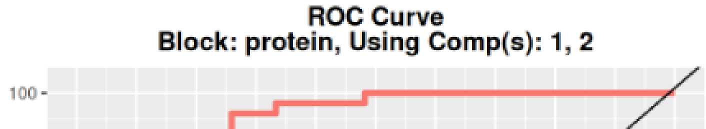
```
# Performance with Majority vote
perf.diablo.gbm$MajorityVote.error.rate
```

```
$centroids.dist
                comp1     comp2
0           0.6222222 0.5851852
1           0.3882353 0.3450980
Overall.ER  0.4692308 0.4282051
Overall.BER 0.5052288 0.4651416
```

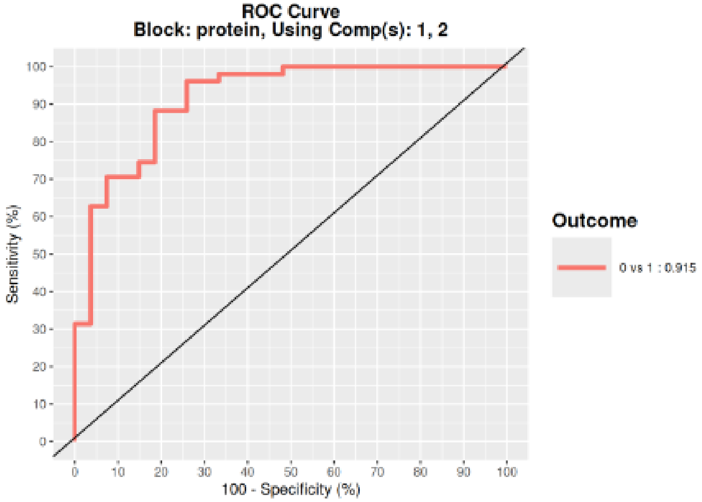
```
# Performance with Weighted vote
perf.diablo.gbm$WeightedVote.error.rate
```

```
$centroids.dist
                comp1     comp2
0           0.6222222 0.5851852
1           0.3882353 0.3450980
Overall.ER  0.4692308 0.4282051
Overall.BER 0.5052288 0.4651416
```

```
auc.diablo.gbm <- auroc(diablo.gbm, roc.block = "protein", roc.comp = 2,
                  print = TRUE)
```



```
                print = TRUE)
```



```
$mRNA
$mRNA$comp1
          AUC   p-value
0 vs 1 0.7887 2.981e-05

$mRNA$comp2
          AUC   p-value
0 vs 1 0.8802 3.835e-08


$methylation
$methylation$comp1
         AUC   p-value
0 vs 1 0.764 0.0001346

$methylation$comp2
          AUC   p-value
0 vs 1 0.8722 7.335e-08


$protein
$protein$comp1
          AUC   p-value
0 vs 1 0.8134 5.842e-06

$protein$comp2
         AUC   p-value
0 vs 1 0.915 1.944e-09
```

```
# Prepare test set data: here one block (proteins) is missing
data.test.gbm <- list(mRNA = glioblastoma_data$data.test$mrna,
                      protein = glioblastoma_data$data.test$protein)

predict.diablo.gbm <- predict(diablo.gbm, newdata = data.test.gbm)
```

```
Warning in predict.block.spls(diablo.gbm, newdata = data.test.gbm): Some blocks
are missing in 'newdata'; the prediction is based on the following blocks only:
mRNA, protein
```

```
confusion.mat.gbm <- get.confusion_matrix(truth = glioblastoma_data$data.test$class,
                     predicted = predict.diablo.gbm$WeightedVote$centroids.dist[,2])
confusion.mat.gbm
```

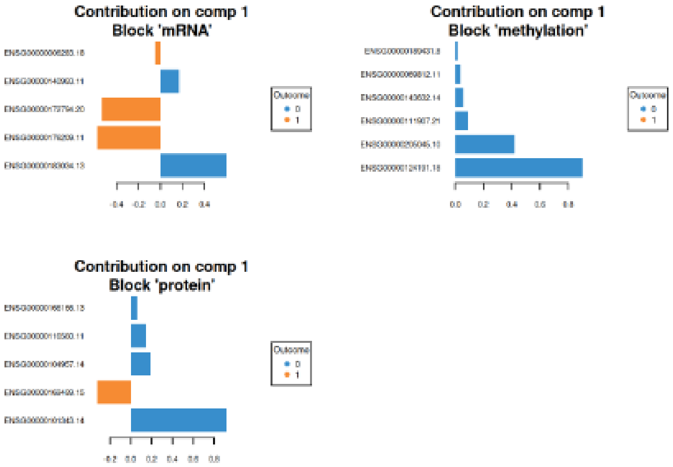
```
  predicted.as.0 predicted.as.1
0              2              1
1              6             10
```

```
get.BER(confusion.mat.gbm)
```

```
[1] 0.3541667
```

`plotLoadings()` visualises the loading weights of each selected variable on each component and each data set. The colour indicates the class in which the variable has the maximum level of expression (`contrib = 'max'`) or minimum (`contrib = 'min'`), on average (`method = 'mean'`) or using the median (`method = 'median'`)

```
plotLoadings(diablo.gbm, comp = 1, contrib = 'max', method = 'median')
```



```
$mRNA
$mRNA$comp1
          AUC   p-value
0 vs 1 0.7887 2.981e-05

$mRNA$comp2
          AUC   p-value
0 vs 1 0.8802 3.835e-08


$methylation
$methylation$comp1
         AUC   p-value
0 vs 1 0.764 0.0001346

$methylation$comp2
          AUC   p-value
0 vs 1 0.8722 7.335e-08


$protein
$protein$comp1
          AUC   p-value
0 vs 1 0.8134 5.842e-06

$protein$comp2
         AUC   p-value
0 vs 1 0.915 1.944e-09
```

```
data.test.gbm <- list(protein = glioblastoma_data$data.test$protein,
                      methylation = glioblastoma_data$data.test$methylation)

predict.diablo.gbm <- predict(diablo.gbm, newdata = data.test.gbm)
```

```
Warning in predict.block.spls(diablo.gbm, newdata = data.test.gbm): Some blocks
are missing in 'newdata'; the prediction is based on the following blocks only:
methylation, protein
```

```
confusion.mat.gbm <- get.confusion_matrix(truth = glioblastoma_data$data.test$class,
                     predicted = predict.diablo.gbm$WeightedVote$centroids.dist[,2])
confusion.mat.gbm
```

```
  predicted.as.0 predicted.as.1
0              2              1
1              6             10
```

```
get.BER(confusion.mat.gbm)
```

```
[1] 0.3541667
```