mrr_project_bio

2025-11-10

Classification of Cancer outcome using Genetic and Clinical data

Introduction

This project investigates the effect of genetic and clinical variables on the survival outcome of breast cancer patients. The data contains records of more than 1000 breast cancer patients from several research institutions. Clinical data contains patient-related and tumor-related information. Additionally mRNA gene expression data is available for each patient. The gene expression data has been processed to include only the top 5000 most variable genes on the transformed scale (log2(counts + 1)).

We consider that the main outcome variable of interest is **vital_status**, which is defined in clinical data.

Load data

```
load("mrr_bio.Rdata")
```

Genes data

```
dim(GeneX)
```

```
## [1] 1231 5000
```

```
str(GeneX)
```

```
##  num [1:1231, 1:5000] 0 0 10.92 3.17 5 ...
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:1231] "EW-A2FS-01A-11R-A17B" "OL-A6VR-01A-32R-A33J" "E9-A226-01A-21R-A157" "A8-A08H-0
##   ..$ : chr [1:5000] "CLEC3A" "SCGB2A2" "CPB1" "GSTM1" ...
```

```
colnames(GeneX)[1:10]
```

```
##  [1] "CLEC3A"    "SCGB2A2"   "CPB1"      "GSTM1"     "TFF1"      "SCGB1D2"
##  [7] "KCNJ3"     "MUCL1"     "LINC00993" "ANKRD30A"
```

```
rownames(GeneX)[1:10]
```

```
##  [1] "EW-A2FS-01A-11R-A17B" "OL-A6VR-01A-32R-A33J" "E9-A226-01A-21R-A157"
##  [4] "A8-A08H-01A-21R-A00Z" "D8-A27H-01A-11R-A16F" "D8-A3Z6-01A-11R-A239"
##  [7] "B6-A1KN-01A-11R-A13Q" "BH-A0DL-01A-11R-A115" "A8-A09X-01A-11R-A00Z"
## [10] "BH-A2L8-01A-11R-A18M"
```

`GeneX` est un tableau de 1231 lignes par 5000 colonnes :

- Les lignes correspondent aux patients avec le nom de chaque ligne l'identifiant du patient comme `EW-A2FS-01A-11R-A17B`.
- Les colonnes correspondent aux gènes avec chaque nom de colonne un gène comme `CLEC3A`, qui sont les 5000 gènes les plus variables d'une personne à l'autre.
- Chaque case correspond à la valeur d'expression (un flottant) d'un certain gène (colonne) pour un certain patient (ligne) -> variables continues

Clinical data

```
load("mrr_bio.Rdata")
dim(clinical_data)
```

```
## Loading required namespace: S4Vectors
```

```
## NULL
```

```
head(clinical_data[, 0:5])
```

```
## DataFrame with 6 rows and 5 columns
##                      initial_weight tissue_type  laterality
##                           <numeric> <character> <character>
## EW-A2FS-01A-11R-A17B            110       Tumor        Left
## OL-A6VR-01A-32R-A33J            380       Tumor       Right
## E9-A226-01A-21R-A157            510       Tumor        Left
## A8-A08H-01A-21R-A00Z            250       Tumor        Left
## D8-A27H-01A-11R-A16F            170       Tumor       Right
## D8-A3Z6-01A-11R-A239             60       Tumor        Left
##                      tissue_or_organ_of_origin age_at_diagnosis
##                                    <character>        <integer>
## EW-A2FS-01A-11R-A17B               Breast, NOS            15302
## OL-A6VR-01A-32R-A33J               Breast, NOS            17702
## E9-A226-01A-21R-A157               Breast, NOS            16511
## A8-A08H-01A-21R-A00Z               Breast, NOS            24137
## D8-A27H-01A-11R-A16F               Breast, NOS            26588
## D8-A3Z6-01A-11R-A239               Breast, NOS            20629
```

```
colnames(clinical_data)
```

```
##  [1] "initial_weight"              "tissue_type"
##  [3] "laterality"                  "tissue_or_organ_of_origin"
##  [5] "age_at_diagnosis"            "primary_diagnosis"
##  [7] "prior_treatment"             "diagnosis_is_primary_disease"
```

```
##  [9] "ajcc_pathologic_t"            "morphology"
## [11] "classification_of_tumor"      "sites_of_involvement"
## [13] "days_to_last_follow_up"       "follow_ups_disease_response"
## [15] "race"                         "gender"
## [17] "ethnicity"                    "vital_status"
## [19] "age_at_index"                 "days_to_birth"
## [21] "age_is_obfuscated"            "bcr_patient_barcode"
## [23] "primary_site"                 "disease_type"
```

`clinical_data` est un tableau de 1231 lignes par 24 colonnes :

- Les lignes correspondent aux noms des patients comme pour `GeneX`.
- Les colonnes sont les noms des données cliniques, comme `initial_weight`, `sites_of_involvement` et `vital_status`.
- Chaque case correspond à la valeur de la donnée clinique pour chaque patient, donc ce peut être un entier ou une chaîne de caractères.

Voici chaque type correspondant à chaque donnée :

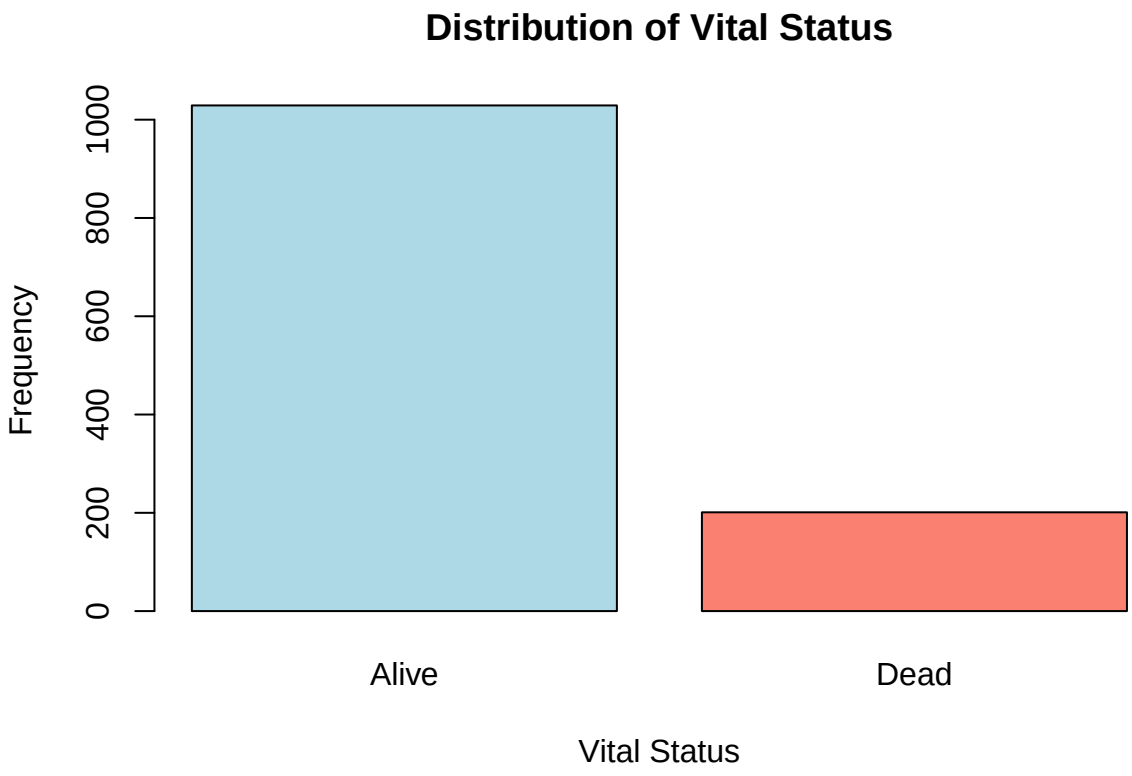
Outcome variable

The outcome variable is the vital status of the patient (dead or alive) :

```r
y <- clinical_data$vital_status
table(y)
```

```
## y
## Alive  Dead
##  1029   201
```

```r
# Visualize the outcome variable
barplot(table(y),
    main = "Distribution of Vital Status",
    xlab = "Vital Status",
    ylab = "Frequency",
    col = c("lightblue", "salmon"))
```



Exploratory data analysis: example

```
# summary statistics of first 10 genes
apply(GeneX[,1:10],2, summary)
```

```
##            CLEC3A  SCGB2A2      CPB1     GSTM1      TFF1   SCGB1D2     KCNJ3
## Min.     0.000000  0.00000  0.000000  0.000000  0.000000  0.000000  0.000000
## 1st Qu.  1.000000  7.48779  4.523562  0.000000  6.679463  5.614710  2.807355
## Median   4.523562 11.70434  7.686501  5.491853 10.796040  9.273796  5.930737
## Mean     5.925758 11.12788  8.313829  5.357693  9.712977  9.026789  6.687515
## 3rd Qu. 10.175539 15.06285 11.151939 10.344845 13.207240 12.274950 10.321917
## Max.    19.455835 22.36921 22.745581 15.874141 18.927850 21.479643 16.672715
##             MUCL1 LINC00993  ANKRD30A
## Min.     0.000000  0.000000  0.000000
## 1st Qu.  5.894767  5.643856  5.554589
## Median   8.945444 10.512740 10.338736
## Mean     9.151482  8.864887  8.650306
## 3rd Qu. 12.404866 12.230770 11.990273
## Max.    20.547814 15.914922 16.758184
```

```
# clinical variables: gender
unique(clinical_data$gender) # unique values
```

```
## [1] "female" "male"   NA
```

```r
table(clinical_data$gender) # frequency
```

```
##
## female   male
##   1217     13
```

Data analysis

But : prédire la donnée clinique vie/mort. Donc on veut utiliser des modèles de classification : - KNN avec $k = 2$ - kmeans avec $k = 2$ - régression logistique - groupe-lasso ? - elastic net ? - lasso, ridge ? - stepwise

Genes

Pour la tableau de gènes, traçons un premier plot pour chaque gène avec la distribution gaussienne de mort/vivant pour chaque gène. Ensuite nous pouvons prendre la moyenne de ce graphe. Et ensuite tracer toutes les moyennes correspondant à chaque gène dans un graphe commun et vérifier lesquels varient fortement de la médiane (la médiane des moyennes)

Et ensuite LASSO pour réduire la dimension