



Tutorial thesis

Author: Ludivine Morvan

Institute:

Date: June 7, 2020

Version: 3.09

Victory won't come to us unless we go to it.

Contents

1	Biology	1	7.2	Machine learning models	10
2	Imaging	2	7.3	Deep learning models	11
3	Datasets	3	8	Python programming	12
3.1	Imajem	3	8.1	OS system	12
3.2	Bologna	3	8.2	Numpy/arrays	12
4	Machine learning	4	8.3	plot graphics	12
4.1	Dimension reduction or se- lection	4	8.4	Images	12
4.2	Random Forest	5	8.5	Pandas	14
5	Deep Learning	6	8.6	Tensorflow and Keras	14
5.1	Definitions	6	9	R programming	16
5.2	Possible layers	6	9.1	Create a package	16
5.3	Losses	7	9.2	Open files	16
5.4	Others	7	9.3	Modify	16
5.5	models	8	9.4	PCA	16
6	Metrics	9	10	Latex programming	18
6.1	For classification	9	10.1	Design	18
6.2	For segmentation	9	10.2	special caracters	18
6.3	For regression	9	11	Software tips	21
6.4	For survival analysis	9	11.1	Visual Studio code	21
6.5	For ranking	9	11.2	Windows	21
7	Survival	10	11.3	Anaconda	22
7.1	Definitions	10	11.4	Docker	22
			11.5	Excel	23
			11.6	Slicer 3D	23
			11.7	Imajem Fidji	23

Chapter 1 Biology

1.0.1 Multiple Myeloma

(From article Morvan et al. (2020)) [[[Multiple myeloma (MM) is a bone marrow cancer that accounts for 10% of all hematological malignancies. It was reported that full-body FDG PET imaging provides prognostic information for both baseline and therapeutic follow-up of MM patients [an example of full-body FDG PET imaging is presented in Fig. 2b]. Quantitative imaging have a great importance for treatment protocol guidance.]]]

1.0.2 PET images

1.0.3 CT images

Chapter 2 Imaging



2.0.1 Radiomics

2.0.2 Mathematics morphology

2.0.3 Filters

Chapter 3 Datasets

Dataset	Input	task
Imajem	Images 3D (PET+CT) + clinical	Survival
Bologna	Images 3D (PET+CT) + clinical	Survival
Brats	Images 3D (MRI)	Segmentation + classification + survival
MNIST	Images 2D (handwritted digits)	classification

Table 3.1: List of the datasets

3.1 Imajem

Context: prospective multi-centric Multiple myeloma [Carlier et al. \(2017\)](#)

Number of patients: 134 in total

Input images: PET and CT images of whole body.

Input others: clinical data and radiomics and volumics

task: Survival (until 7 years). In days with censorship (...%)

masks: global polygon generated from Dosisoft and segmentation(majority vote between k-mean, 2.5suv and 40%)

3.2 Bologna

Context: prospective multi-centric Multiple myeloma [Nanni et al. \(2018\)](#)

Number of patients:

Input images: PET and CT images of whole body.

Input others: clinical data and radiomics and volumics

task: Survival. In days with censorship (...%)

masks: global polygon generated from Dosisoft

Chapter 4 Machine learning

4.1 Dimension reduction or selection

- PCA
- T-SNE
- Selection derived from Cox
- Selection derived from RSF

4.1.1 PCA

4.1.2 T-SNE

4.1.3 Selection derived from Cox

4.1.3.1 Lasso

4.1.3.2 Elastic Net

4.1.4 Selection derived from RSF

4.1.4.1 Variable importance (VIMP)

(From article Morvan et al. (2020)) [[[The *variable importance* (VIMP) measures for each variable, the increase in prediction error for the forest ensemble when random daughter nodes are assigned for this variable Ishwaran et al. (2018).]]]

4.1.4.2 Minimal depth

(From article Morvan et al. (2020)) [[[The *minimal depth* assesses the predictiveness of a variable by its depth relative to the root node of a tree Ishwaran et al. (2010).]]]

4.1.4.3 Variable Hunting (VH)

(From article Morvan et al. (2020)) [[[Variable-Hunting Ishwaran et al. (2010), was defined in the ultra-high dimensional problems, where minimal depth thresholding becomes ineffective. A forest is fit to a random number of variables and variables selected using minimal depth thresholding. Then, variables are added to the selected ones in order of minimal depth until the joint VIMP for the nested models stabilizes. This whole process is then repeated several times.]]]

4.2 Random Forest

Chapter 5 Deep Learning

5.1 Definitions

supervised/semi-supervised/unsupervised

Latent space, manifold

5.2 Possible layers

5.2.1 Convolutions

1. Basic convolution
2. Separable convolution

5.2.1.1 Basic convolution

5.2.1.2 Separable convolutions

5.2.2 Pooling

- Max-pooling
- Average pooling
- spacial pooling Fig.
- spacial pyramidal pooling (SPP)

5.2.2.1 Spatial pooling

Spatial pooling is represented in Fig. 5.1.

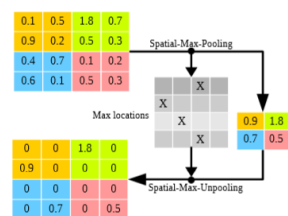


Fig. 1: Spatial Pooling and Unpooling operations.

Figure 5.1: Spatial pooling

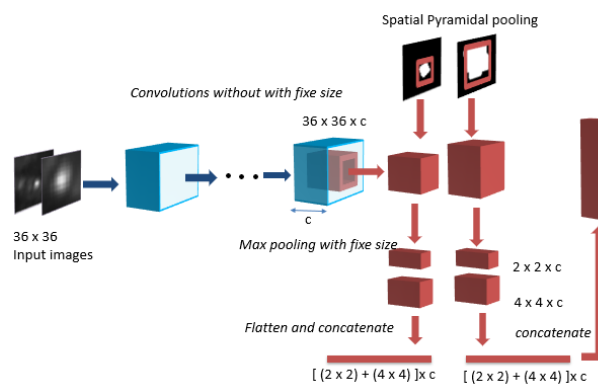


Figure 5.2: Figure of SPP from miccai 2020 article

5.2.2.2 Spatial Pyramidal Pooling

To handle different size images. (Fig.5.2)

5.2.3 normalisation

1. Batch normalisation
2. Instance normalisation

5.2.3.1 Batch normalisation

5.2.3.2 Instance normalisation

5.3 Losses

5.3.1 classification

5.3.2 regression

5.3.3 segmentation

5.3.4 survival

5.3.5 ranking

5.4 Others

5.4.1 Bilinear

5.4.2 Attention

(Fig. 5.3) Figs. 5.5 and 5.4 are examples of channel and spatial weight obtained from the

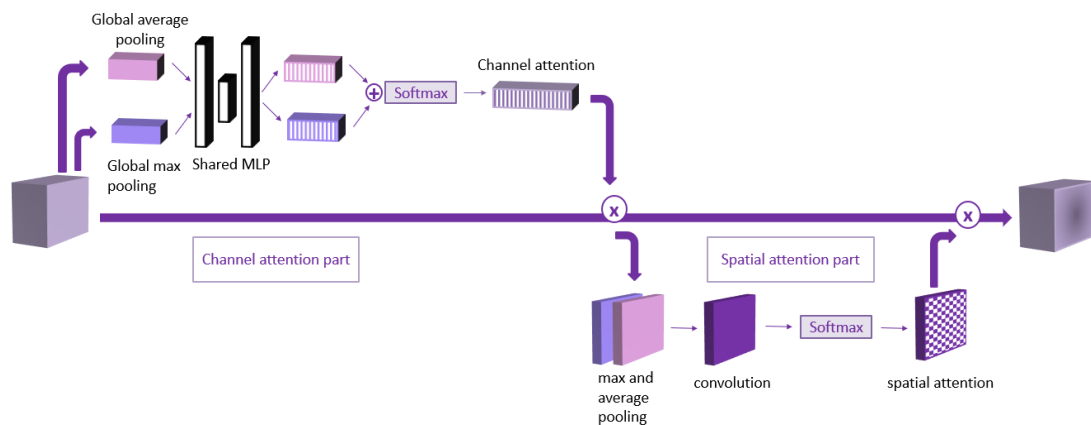


Figure 5.3: Attention block (figure from Miccai 2020 paper)

attention block.

Figure 5.4: Example of Channel attention weights (in columns) for a set of patients. Color varies from blue to red for increasing weight values.

Figure 5.5: For every 3-image block: left) Spatial attention weights. middle) Input image. right) Segmentation mask (used only for validation here).

5.4.2.1 Papers using it

- reconstruction [Huang et al. \(2019\)](#)
- segmentation and detection [Tong et al. \(2019\)](#)
- classification [Herent et al. \(2019\)](#) (with images)
- Survival [Kaji DA \(2019\)](#) (model clinical events in the intensive care unit, no images)

5.5 models

5.5.1 classification

5.5.2 regression

5.5.3 segmentation

u-net

5.5.4 survival

1. DeepSurv
2. DeepConvSurv
3. RankDeepSurv

5.5.5 ranking

1. RankDeepSurv [cf. survival losses]

Chapter 6 Metrics



6.1 For classification

6.2 For segmentation

6.3 For regression

6.4 For survival analysis

6.5 For ranking

Chapter 7 Survival

7.1 Definitions

7.2 Machine learning models

7.2.1 Kaplan Meier model

7.2.2 Cox model

7.2.3 Gradient boosting cox

7.2.4 Random Survival Forest

(From article Morvan et al. (2020)) [[[A *Random Forest* is a collection of N_{trees} decision trees $\mathcal{T} = \{f_1, \dots, f_{N_{\text{trees}}}\}$ trained to predict a target value y given an input feature vector $\mathbf{x} \in \mathbb{R}^D$ composed of the concatenation of D features. The target y can be a categorical or continuous variable. One decision tree f consists of a series of nodes, each characterized by a binary split decision function

The *Random Survival Forest* is also an ensemble-tree method, introduced by Ishwaran in 2008 Ishwaran et al. (2018) to adapt the Random Forests to right-censored data and survival analysis. For survival, every input feature vector \mathbf{x}_i is accompanied by a censorship θ_i , which is equal to 1 if an event occurred during the study period and 0 if not. The target value y_i is the expected ensemble mortality, an interpretation in terms of the expected total number of deaths and derived from the ensemble cumulative hazard function (CHF). It is estimated from the given time to event data τ_i for the individuals i in the training set.

As before, tree growing is done through randomized node optimization, generating several candidates for feature (axis aligned split) and threshold $\{\phi, th\}$. However, instead of an information theoretic criteria, the split function and threshold are chosen to maximize the survival difference between the individuals going to the two daughter nodes. In particular, we use the *log-rank* criteria: Considering $t_1 < \dots < t_m$ the distinct times of events in the node h . $d_{k,l}$ and $Y_{k,l}$ respectively the numbers of event and the number of individuals at risk in the left daughter node without event at t_{k-1} ($d_{k,r}$ and $Y_{k,r}$ for the right daughter node). $Y_k = Y_{k,l} + Y_{k,r}$ and $d_k = d_{k,l} + d_{k,r}$.

$$L(\phi, th) = \frac{\sum_{k=1}^m (d_{k,l} - Y_{k,l}) \frac{d_k}{Y_k}}{\sqrt{\sum_{k=1}^m \frac{Y_{k,l}}{Y_k} (1 - \frac{Y_{k,l}}{Y_k}) \frac{Y_k - d_k}{Y_k - 1}} d_k} \quad (7.1)$$

to evaluate the best population separation. Finally, unlike class histogram or regression value in RF, each leaf in RSF stores the ensemble mortality and a survival curve. An example

of a survival tree is presented in Fig. ?? . The mortality is calculated with the Nelson-Aalen estimator for the Cumulative Hazard Function (CHF):

$$\hat{H}_h(t) = \sum_{t_{k,h} \leq t} \frac{d_{k,h}}{Y_{k,h}}, \quad (7.2)$$

with k the index of the event time between 1 and m , $\hat{H}_h(t)$ the CHF at the node h and time t ; while $d_{k,h}$ stands for the number of event at time $t_{k,h}$ and $Y_{k,h}$ is the number of individuals at risk at time $t_{k,h}$. It can be interpreted as the sum on each event time of rate of deaths. The ensemble mortality M_i of an individual i in the node h is the sum of CHF on each unique time:

$$M_i = \sum_{k=1}^m \hat{H}_h(t_k | X_i) \quad (7.3)$$

The ensemble mortality is the expected value for the CHF summed over time. It measures the number of deaths expected under a null hypothesis of similar survival behavior.]]]

7.3 Deep learning models

Chapter 8 Python programming

8.1 OS system

Check if a path exists

```
os.path.exists(pathCSV)
```

Check if a variable exists

```
try :  
    myVar  
except NameError:  
    myVar = 1
```

8.2 Numpy/arrays

To load a numpy file

```
data=np.load(doss+"data.npy")
```

To save a numpy file

```
data.save(doss+"data.npy")
```

8.3 plot graphics

How to use matplotlib colors : [Website](#)

8.3.1 Box Plot

```
lstlisting plt.subplot(121) plt.boxplot([[1, 2, 3, 4, 5, 13], [6, 7, 8, 10, 10, 11, 12], [1, 2, 3]])  
plt.ylim(0, 14) plt.title('boxplot avec sequence')  
plt.subplot(122) plt.boxplot(numpy.array([[1, 2, 3], [2, 7, 8], [1, 3, 10], [2, 5, 12]]))  
plt.ylim(0, 14) plt.title('boxplot avec array 2d')
```

8.4 Images

8.4.0.1 Open an image

CSS Colors

black	bisque	forestgreen	slategrey
dimgray	darkorange	limegreen	lightsteelblue
dimgray	burlywood	darkgreen	cornflowerblue
gray	antiquewhite	green	royalblue
gray	tan	lime	ghostwhite
darkgray	navajowhite	seagreen	lavender
darkgray	blanchedalmond	mediumseagreen	midnightblue
silver	papayawhip	springgreen	navy
lightgray	moccasin	mintcream	darkblue
lightgray	orange	mediumspringgreen	mediumblue
gainsboro	wheat	mediumaquamarine	blue
whitesmoke	oldlace	aquamarine	slateblue
white	floralwhite	turquoise	darkslateblue
snow	darkgoldenrod	lightseagreen	mediumslateblue
rosybrown	goldenrod	mediumturquoise	mediumpurple
lightcoral	cornsilk	azure	rebeccapurple
indianred	gold	lightcyan	blueviolet
brown	lemonchiffon	paleturquoise	indigo
firebrick	khaki	darkslategray	darkorchid
maroon	palegoldenrod	darkslategrey	darkviolet
darkred	darkkhaki	teal	mediumorchid
red	ivory	darkcyan	thistle
mistyrose	beige	aqua	plum
salmon	lightyellow	cyan	violet
tomato	lightgoldenrodyellow	darkturquoise	purple
darksalmon	olive	cadetblue	darkmagenta
coral	yellow	powderblue	fuchsia
orangered	olivedrab	lightblue	magenta
lightsalmon	yellowgreen	deepskyblue	orchid
sienna	darkolivegreen	skyblue	mediumvioletred
seashell	greenyellow	lightskyblue	deeppink
chocolate	chartreuse	steelblue	hotpink
saddlebrown	lawngreen	aliceblue	lavenderblush
sandybrown	honeydew	dodgerblue	palevioletred
peachpuff	darkseagreen	lightslategray	crimson
peru	palegreen	lightslategrey	pink
linen	lightgreen	slategray	lightpink

Figure 8.1: Matplotlib colors

```
from PIL import Image
im = Image.open("data/image.jpeg")
plt.imshow(np.array(im))
```

```
from skimage import io
image = io.imread(os.path.join(PATH,patient,'image.tif')).T
```

Open a .nii.gz ([Lien](#))

```
import nibabel as nib
img = nib.load(os.path.join(data_path, 'example4d.nii.gz'))
img = np.array(img.get_fdata()) # pour passer de nifti a array
```

Open a .mha

```
from medpy.io import load
image_data, image_header = load('../data/image.mha')
```

8.4.0.2 show an image

```
plt.imshow(image)\textit {(image should be 2D, RGB or not, array)}
```

8.4.0.3 Save an image

To save in Tiff

```
from skimage.external import tiffle  
tiffle .imsave(im_Path, np_image.T)
```

8.5 Pandas

Read a csv

```
data = pd.read_csv(pathCSV, encoding='utf-8')
```

Take a value

```
data.iloc [0,1]. values #iloc: take a value thanks to the index. .loc: take thanks to the name
```

Pass from dataframe to array

```
data . values
```

From array to dataframe

```
fff = pd.DataFrame(rtrain )
```

Save a dataframe

```
data . to_csv (doss+"data . csv")
```

Change/obtain the row names

```
data . index
```

8.6 Tensorflow and Keras

8.6.1 Tensorboard

8.6.1.1 Sites

- <https://itnext.io/how-to-use-tensorboard-5d82f8654496>
- add hyperparams <https://github.com/tensorflow/tensorboard/issues/46>

8.6.1.2 Bases

Imports

```
from keras.callbacks import TensorBoard
import time
```

At the beginning

```
NAME = mode + "-{}".format(int(time.time()))
tensorboard = TensorBoard(log_dir='Resultats/logs/{}'.format(NAME))
```

In the model

```
fitting = model.fit(xtrain, ytrain, validation_data=(xval, yval), callbacks=[tensorboard])
```

In prompt

```
tensorboard --logdir="D:\Documents\thèse\simple_model\Resultats\logs\CNN_small-1565598264"
```

8.6.1.3 Tensorboard

- to view all scalars in the same time: write * in the search bar

Chapter 9 R programming

9.1 Create a package

Follow the following **tutorial**

9.2 Open files

Open numpy

```
library ( reticulate )  
np <- import("numpy")  
mat <- np$load("fmat.npy")
```

Open csv

```
data <- read.csv2(path ,header=T,sep=',',dec='.')  
#https :// pandas.pydata.org/pandas-docs/stable/reference/api/pandas.read_csv.html
```

9.3 Modify

Concatenate

```
a= rbind(b,c) #for rows  
b= cbind(a,c) #for columns
```

Rename Columns

```
colnames(x) <- c("col1","col2")
```

9.4 PCA

```
library ("FactoMineR")  
library (" factoextra ")  
#http :// www.sthda.com/french/ articles /38-methodes-des-composantes-principales-dans-r-guide-pratique  
/73-acp-analyse-en-composantes-principales-avec-r-l-essentiel/
```

```
pca <- PCA(features, graph = FALSE,scale.unit = TRUE,ncp=100)  
# graph : Show or not the graph. ncp: number of dim to keep. Si scale.unit = True normalisation  
eig.val <- get_eigenvalue(pca) #Extraction des valeurs propres  
fviz_eig(res.pca) # Visualisation des valeurs propres
```

```

get_pca_ind(res.pca), get_pca_var(res.pca) # Extraction des résultats pour les individus et les
variables , respectivement .
fviz_pca_ind(res.pca), fviz_pca_var(res.pca) # visualisez les résultats des individus et des variables ,
respectivement .
fviz_pca_biplot (res.pca) # Création dun biplot des individus et des variables

```

```

NewXtrain <- pca$ind$coord #to obtain the features in the new dimensions. number of features = ncp de
PCA.

```

```

NewXtest = predict (pca,XTEST)$coord #to obtain the features in the new dimensions of a new dataset

```

To print cumulative information according to the number of kept dimensions.

```

eig.val <- get_eigenvalue(pca)
barplot(eig.val$cumulative.variance.percent[1:100], names.arg=c(1:100))
abline(h=80, col = "Red") # horizontal line
abline(v=56, col = "Red") # vertical line

```

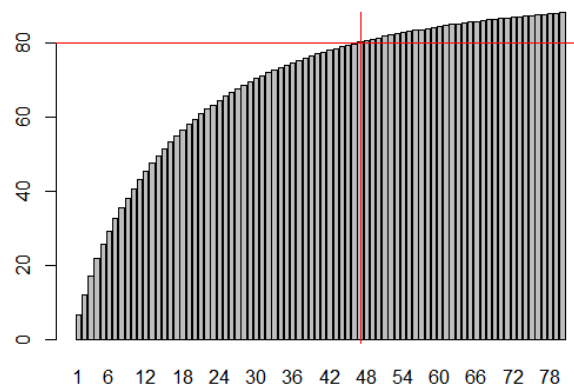


Figure 9.1: Cumulative information of PCA

Chapter 10 Latex programming



Aide mémoire

10.1 Design

Put a line

```
\headrule #full line
```

10.2 special characters

Alphabet grec

α \alpha	ζ \zeta	\varkappa \varkappa	ϖ \varpi	υ \upsilon	\digamma \digamma	Π \Pi
β \beta	η \eta	λ \lambda	ρ \rho	ϕ \phi	Γ \Gamma	Σ \Sigma
γ \gamma	θ \theta	μ \mu	ρ \rho	φ \varphi	Δ \Delta	Υ \Upsilon
δ \delta	ϑ \vartheta	ν \nu	σ \sigma	χ \chi	Θ \Theta	Φ \Phi
ϵ \epsilon	ι \iota	ξ \xi	ς \varsigma	ψ \psi	Λ \Lambda	Ψ \Psi
ε \varepsilon	κ \kappa	π \pi	τ \tau	ω \omega	Ξ \Xi	Ω \Omega

Symboles alphanumériques

\aleph \aleph	\beth \beth	ℓ \ell	∂ \partial	\forall \forall	$\exists!$ \exists!	\neg \neg
\beth \beth	\daleth \daleth	∞ \infty	\wp \wp	\exists \exists	\varnothing \varnothing	∇ \nabla

Lois de composition

$+$ +	\times \times	\star \star	\sqcup \sqcup	\oplus \oplus	\lhd \lhd	\amalg \amalg
$-$ -	\cdot \cdot	\circ \circ	\sqcap \sqcap	\otimes \otimes	\rhd \rhd	\wr \wr
\pm \pm	\div \div	\cup \cup	\amalg \amalg	\wedge \wedge	\rtimes \rtimes	\bot \bot
\mp \mp	$*$ *	\cap \cap	\vartriangle \vartriangle	\vee \vee	\ltimes \ltimes	\top \top

Symboles de relation**Égalités.**

$=$ =	\neq \neq	\propto \propto	$\not\propto$ \not\propto	\simeq \simeq	$\not\simeq$ \not\simeq	\approx \approx	$\not\approx$ \not\approx
\coloneqq \coloneqq	$\vcntcolon\neq$ \vcntcolon\neq	\asymp \asymp	$\not\asymp$ \not\asymp	\approx \approx	$\not\approx$ \not\approx	\cong \cong	$\not\cong$ \not\cong
\equiv \equiv	$\not\equiv$ \not\equiv	\sim \sim	$\not\sim$ \not\sim				

Inclusions.

\subset \subset	\subseteq \subseteq	\subsetneq \subsetneq	\subseteq \subseteq	\subsetneqq \subsetneqq	\sqsubset \sqsubset	\sqsubseteq \sqsubseteq
$\not\subset$ \not\subset	\nsubseteq \nsubseteq	\supsetneq \supsetneq	\nsubseteq \nsubseteq	\supsetneqq \supsetneqq	$\not\sqsubset$ \not\sqsubset	$\not\sqsubseteq$ \not\sqsubseteq
\supset \supset	\supseteq \supseteq	\varsubsetneq \varsubsetneq	\supseteq \supseteq	\varsubsetneqq \varsubsetneqq	\sqsupset \sqsupset	\sqsupseteq \sqsupseteq
$\not\supset$ \not\supset	$\not\supseteq$ \not\supseteq	\varsupsetneq \varsupsetneq	$\not\supseteq$ \not\supseteq	\varsupsetneqq \varsupsetneqq	$\not\sqsupset$ \not\sqsupset	$\not\sqsupseteq$ \not\sqsupseteq

Inégalités.

$<$ <	$>$ >	\leq \leq	\geq \geq	\leqslant \leqslant	\geqslant \geqslant	\ll \ll	\gg \gg
-------	-------	-------------	-------------	-----------------------	-----------------------	-----------	-----------

Flèches

\rightarrow \to	\Rightarrow \implies	\nearrow \nearrow	\rightarrowtail \rightarrowtail
\mapsto \mapsto	\Leftrightarrow \iff	\swarrow \swarrow	$\mapstochar\rightarrowtail$ \mapstochar\rightarrowtail
\hookrightarrow \hookrightarrow	$\not\Rightarrow$ \centernot\implies (pkg centernot)	\rightleftarrows \rightleftarrows	\rightsquigarrow \rightsquigarrow
\twoheadrightarrow \twoheadrightarrow	$\not\Leftrightarrow$ \centernot\iff (pkg centernot)	\Rightarrow \Rightarrow	\dashrightarrow \dashrightarrow

Flèches extensible. \xrightarrow{f} donne \xrightarrow{f} et $\xrightarrow[\text{dessous}]{\text{dessus}}$ donne $\xrightarrow[\text{dessous}]{\text{dessus}}$.

\leftarrow \leftarrow	\Rightarrow \Rightarrow	\rightarrowtail \rightarrowtail	\leftrightharpoons \leftrightharpoons
\rightarrow \rightarrow	\Leftarrow \Leftarrow	\rightarrowtail \rightarrowtail	\leftrightharpoons \leftrightharpoons
\mapsto \mapsto	\Leftrightarrow \Leftrightarrow	\leftarrowtail \leftarrowtail	\hookleftarrow \hookleftarrow
\leftrightarrow \leftrightarrow		\leftarrowtail \leftarrowtail	\hookrightarrow \hookrightarrow

Fonctions usuelles

<code>\ln</code>	ln	<code>\cos</code>	cos	<code>\arctan</code>	arctan	<code>\deg</code>	deg	<code>\hom</code>	hom	<code>\varlimsup</code>	$\overline{\lim}$
<code>\exp</code>	exp	<code>\sin</code>	sin	<code>\sinh</code>	sinh	<code>\det</code>	det	<code>\lg</code>	lg	<code>\projlim</code>	proj lim
<code>\lim</code>	lim	<code>\tan</code>	tan	<code>\cosh</code>	cosh	<code>\dim</code>	dim	<code>\log</code>	log	<code>\varprojlim</code>	\varprojlim
<code>\max</code>	max	<code>\cot</code>	cot	<code>\tanh</code>	tanh	<code>\ker</code>	ker	<code>\liminf</code>	lim inf	<code>\injlim</code>	\varinjlim
<code>\sup</code>	sup	<code>\arccos</code>	arccos	<code>\coth</code>	coth	<code>\arg</code>	arg	<code>\varliminf</code>	\varliminf	<code>\varinjlim</code>	\varinjlim
<code>\min</code>	min	<code>\arcsin</code>	arcsin	<code>\inf</code>	inf	<code>\gcd</code>	gcd	<code>\limsup</code>	lim sup		

Pour définir de nouvelles fonctions : `\DeclareMathOperator{\Vect}{Vect}`

Délimiteurs

délimiteurs ouvrants et fermants

<code>(x)</code>	<code>(x)</code>	<code> x </code>	<code>\lvert x\rvert</code>	<code>\langle x \rangle</code>	<code>\langle x \rangle</code>						
<code>[x]</code>	<code>[x]</code>	<code>\ x\ </code>	<code>\lVert x\rVert</code>	<code>\llbracket x \rrbracket</code>	<code>\llbracket x \rrbracket</code>	<code>(stmaryrd)</code>	<code>\backslash</code>	<code>\ </code>	<code>\ </code>		
<code>\{x\}</code>	<code>\{x\}</code>	<code>\lfloor x \rfloor</code>	<code>\lfloor x \rfloor</code>	<code>\lceil x \rceil</code>	<code>\lceil x \rceil</code>						

délimiteurs médians

Pour $] - 1 ; 1[$, utiliser la commande `\intervalleoo` ci-dessous.

Pour changer la taille : `\left`, `\right`, `\middle`, `\big`, `\bigl`, `\bigr`, `\bigm`, `\bigr` (ainsi que `Big`, `bigg` et `Bigg`)

`\left` et `\right` sont certaines fois trop grands : $\left[\sum_i a_i \left| \sum_j x_{i,j} \right|^p \right]^{1/p}$ contre $\left[\sum_i a_i \left| \sum_j x_{i,j} \right|^p \right]^{1/p}$.

Grands opérateurs

<code>\int</code>	\int	<code>\iint</code>	\iint	<code>\iiint</code>	\iiint	<code>\idotsint</code>	$\int \dots \int$	<code>\oint</code>	\oint
<code>\sum</code>	\sum	<code>\coprod</code>	\coprod	<code>\bigcap</code>	\bigcap	<code>\bigoplus</code>	\bigoplus	<code>\bigwedge</code>	\bigwedge
<code>\prod</code>	\prod	<code>\bigcup</code>	\bigcup	<code>\bigsqcup</code>	\bigsqcup	<code>\bigotimes</code>	\bigotimes	<code>\bigvee</code>	\bigvee

Utilisation de `\limits`, `\nolimits` et `\displaystyle` ainsi que `\sideset`

$$\prod_{k=1}^n$$

Accents mathématiques

<code>\bar</code>	\bar{a}	<code>\tilde</code>	\tilde{a}	<code>\hat</code>	\hat{a}	<code>\check</code>	\check{a}	<code>\acute</code>	\acute{a}	<code>\grave</code>	\grave{a}	<code>\dot</code>	\dot{a}	<code>\ddot</code>	\ddot{a}	<code>\ddd</code>	\dddot{a}	<code>\mathring</code>	\mathring{a}
<code>\vec</code>	\vec{a}	<code>\breve</code>	\breve{a}																

Flèches extensibles. `\underbrace{ABC}_{bas}` donne \underbrace{ABC}_{bas} et `\overbrace{ABC}^{haut}` donne \overbrace{ABC}^{haut} .

<code>\overbrace</code>	$\overbrace{ABC\dots}$	<code>\underbrace</code>	$\underbrace{ABC\dots}_{bas}$	<code>\widetilde</code>	$\widetilde{ABCDEFG}$
<code>\overline</code>	$\overline{ABC\dots}$	<code>\underline</code>	$\underline{ABC\dots}$	<code>\widehat</code>	$\widehat{ABCDEFG}$
<code>\overrightarrow</code>	$\overrightarrow{ABC\dots}$	<code>\underrightarrow</code>	$\underrightarrow{ABC\dots}$	<code>\widetriangle</code>	$\widetriangle{ABCDEFG}$
<code>\overleftarrow</code>	$\overleftarrow{ABC\dots}$	<code>\underleftarrow</code>	$\underleftarrow{ABC\dots}$	<code>\wideparen</code>	$\wideparen{ABCDEFG}$
<code>\overleftrightarrow</code>	$\overleftrightarrow{ABC\dots}$	<code>\underleftrightarrow</code>	$\underleftrightarrow{ABC\dots}$	<code>\widering</code>	$\widering{ABCDEFG}$
<code>\overbracket</code>	$\overbracket{ABC\dots}$	<code>\underbracket</code>	$\underbracket{ABC\dots}$		

Chapter 11 Software tips

11.1 Visual Studio code

11.1.1 ShortCut

ctl+k ctrl+à : Fold All
ctl+k ctrl+j : Unfold all
ctrl S puis ctrl p : Split
ctrl+shift+(: Fold
ctrl+shift+ ^ : Unfold
F : walk in errors
shift + enter : Run a ligne in interactive terminal
ctrl+k puis ctrl+ T : Choose colors
ctrl+ù : Terminal
ctrl+shift+m : Problem
ctrl+B : Remove/add left barre
ctrl+K z : Zen mode
**ctrl+ ** : Side by side
ctrl K + ctrl S : Key map

11.2 Windows

11.2.1 ShortCut

CMD+P : Impression
Alt+tab : Navigation
Ctrl+tab : Navigation in onglets
Ctrl+del : Delete the entier word
ctrl + Fleche D/G : Deplace word by word
ctrl+G : I and U mis en forme
F2 : Rename
F5 : Actualise
alt + F4 : Close the window
ctrl + F4 : close the doc in software or onglet
alt+enter : Show properties of the doc
ctrl+o : open file in software

wind+fleche : diminish, increase, deplace window

wind+tab : new desk and see all windows

wind+i : parameters of the computer

wind+impr screen : register a screenshot

wind+shift+fleche G/D : deplace window on the other screen

wind+p : change affichage of the screen

11.3 Anaconda

11.3.1 In anaconda prompt

To list all the packages and versions

```
conda list
```

To list the available versions of a packages (ex. with numpy)

```
conda search -f numpy
```

To clean tarballs and cache

```
conda clean -a
```

11.4 Docker

To open pc-milcom

```
ssh ludivine@pc-milcom or ludivine@130.66.84.51
```

To Run command

```
>> docker run -it --rm -u $(id -u):$(id -g) -v /PATH bash
* -it    interactive
* --rm   remove at the end
* -u $(id -u):$(id -g)
* -v /PATH bash
* ls2n/ ludivine    name of image
* --name ContainerName give a specific name to a container
* bash: launch to install things and modify
```

Install a package (Windows)

In the first CMD:

```
>> docker run --rm -it -v $PATH bash (If there is a problem of permission, add: -u 0:0)
```

```
>> pip install packagename
```

In a second CMD

```
>> ssh name@pc-milcom
```

```
>> docker ps -a    ContainerID
```

```
>> docker commit ContainerID ls2n/ ludivine
```


Useful commands (windows/linux)

```
>> who who have an open session
>> nvidia -smi information about the gpu
>> top
>> watch -n 1 nvidia-smi information about the gpu in real time
>> docker image ls see all docker images
```

Handle containers

```
docker container attach ContainerName (obtained with docker ps -a) to see in the shell the running
container
CTRL-p CTRL-q key combination Quit the container without stopping it .
CTRL-c Stop the container
Open PortNumber in the browser watch the output of the container process in real time.
docker logs containerID get acces to the logs
docker container exec -it containerName /bin/bash run a bash shell inside a running container
```

11.5 Excel

11.5.1 Small hints

Fuse the text from cells A1 and B1

```
=A1&B1
```

Keep 4 first letters of the A1 cell

```
=LEFT(A1, 4)/ GAUCHE(A1,4)
```

11.5.2 Analyse data

- You can do a dynamic Table (tableau croisé dynamique) when you have several parameters, to compare the combination of parameters

11.6 Slicer 3D

11.7 Imagem Fidji

Bibliography

- Carlier, Thomas, Clement Bailly, Rodolphe Leforestier, Cyrille Touzeau, Philippe Moreau, Francoise Bodere, and Caroline Bodet-Milin**, “Prognostic added value of PET textural features at diagnosis in multiple myeloma,” *Journal of Nuclear Medicine*, 2017, 58 (supplement 1), 111.
- et al. Kaji DA Zech JR, Kim JS**, “An attention based deep learning model of clinical events in the intensive care unit.,” *PLoS One*, 2019, 14 (2:e0211057).
- Herent, P., B. Schmauch, P. Jehanno, O. Dehaene, C. Saillard, C. Balleyguier, J. Arfi-Rouche, and S. Jégou**, “Detection and characterization of MRI breast lesions using deep learning,” *Diagnostic and Interventional Imaging*, 2019, 100 (4), 219 – 225.
- Huang, Q., D. Yang, P. Wu, H. Qu, J. Yi, and D. Metaxas**, “MRI Reconstruction Via Cascaded Channel-Wise Attention Network,” in “2019 IEEE 16th International Symposium on Biomedical Imaging (ISBI 2019)” April 2019, pp. 1622–1626.
- Ishwaran, H., U. Kogalur, E. Blackstone, and M. Lauer**, “Random Survival Forest,” *The annals of applied statistics*, 2018, 2 (3), 841–860.
- Ishwaran, Hemant, Udaya B. Kogalur, Eiran Z. Gorodeski, Andy J. Minn, and Michael S. Lauer**, “High-Dimensional Variable Selection for Survival Data,” *Journal of the American Statistical Association*, 2010, 105 (489), 205–217.
- Morvan, L, T Carlier, B. Bailly C.and Jamet, C Bodet-Milin, P. Moreau, C Touzeau, F Kraeber-Bodere, and D Mateus**, “Leveraging RSF and PET images for prognosis of multiple myeloma at diagnosis,” *International Journal of Computer Assisted Radiology and Surgery*, 2020, p. 129139.
- Nanni, C., A. Versari, S. Chauvie, and et al.**, “Interpretation criteria for FDG PET/CT in multiple myeloma (IMPeTUs): final results. IMPeTUs (Italian myeloma criteria for PET USE).,” *European Journal of Nuclear Medicine and Molecular Imaging*, 2018, 45, 712719.
- Tong, Qianqian, Caizi Li, Weixin Si, Xiangyun Liao, Yaliang Tong, Zhiyong Yuan, and Pheng Ann Heng**, “RIANet: Recurrent interleaved attention network for cardiac MRI segmentation,” *Computers in Biology and Medicine*, 2019, 109, 290 – 302.