# ECOLE NATIONALE DE LA STATISTIQUE ET DE L'ANALYSE DE L'INFORMATION



### PROJECT TITLE

Project Description

### **TITLE**

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#### Résumé

Lorem ipsum dolor sit amet. Ut expedita sunt est delectus quia ad nostrum delectus eum magni dolor. Eos nemo minima sit deleniti porro et necessitatibus minima ab quia necessitatibus in beatae autem et voluptas labore.

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#### contribution

si jamais vous apercevez des fautes dans le polycopié, merci de rédiger une *issue* sur Github à l'adresse :

correctif



LaTeX-Template/issues

contact



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## Chapitre 1

# Chapter 1

#### Contents

1.1	A	2
1.2	B	<b>2</b>
1.3	C	<b>2</b>

### 1.1 A

this is text

#### 1.2 B

this is more text

#### 1.3 C

and again

## Chapitre 2

# **Chapter 2**

Contents		
2.1	D	
2.2	E	
2.3	F	

### 2.1 D

this is an equation  $\int f \, d\mu$ 

- 2.2 E
- 2.3 F

## Chapitre 3

# **Chapter 3**

Contents		
3.1	G and subs	1
	3.1.1 a subsection	1
	3.1.2 yeah pretty cool	1
3.2	H	1
3.3	I	1

chapter 3 is awesome

#### 3.1 G and subs

- 3.1.1 a subsection
- 3.1.1  $\square$  A $\rangle$  da hell? custom subsub?
- 3.1.2 yeah pretty cool
- 3.2 H
- 3.3 I

### Annexe A

## **Some Appendix**

<b>A.1</b>	with subsection	5
<b>A.2</b>	which is really cool	5

#### A.1 with subsection

### A.2 which is really cool

#### **Annexe B**

### some code

#### données fonctionnelles pour le praticien

```
# --- install --- #
install.packages(c("fda", "fda.usc"))
# --- general packages --- #
library(data.table)
# --- FDA packages --- #
library(fda)
library(fda.usc)
```

```
/X_1 / X_2 / \cdots / X_p /
    # | Jan 1st 12:00 | : | : | | : |
2
    data <- fread("data.csv")</pre>
    # un individu = une ligne
6
    # donc pour une série temporelle, il faut transposer les observations et avoir la
    → suite des données disposées sur une ligne.
    fdata_standard_index <- fda.usc::fdata(</pre>
8
        mdata = t(X),
9
        argvals = to_unit_interval(
10
11
        # on doit ramener les dates dans l'intervalle [0,1]
12
            data[, .(date)]
13
14
15
```

```
type.CV = fda.usc::GCV.S,
W = NULL,
lambda = lambda_CV_look_list,
numbasis = num_basis__seq,
type.basis = "bspline",
verbose = TRUE

)
```

```
fda_optimal_basis <- ...
fdata_obj_temp <- fda_optimal_basis[["fdata.est"]]

fdata_obj <- fda.usc::fdata2fd(fdata_obj_temp)

fpca_result <- fda::pca.fd(

fdobj = fdata_obj,

nharm = 3,

# centrer les données

centerfns = TRUE

)</pre>
```

Regardons désormais à quoi ressemble la sortie :

```
\texttt{fpca\_result\$scores} = \\ \downarrow [X_i] \begin{bmatrix} \ddots & \dots & \vdots \\ \vdots & \xi_i^{[k]} = \langle X_i - \mu | \phi_k \rangle & \vdots \\ \dots & \dots & \ddots \end{bmatrix}
```

## **Bibliographie**

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