

CNC Fly Food Dispenser

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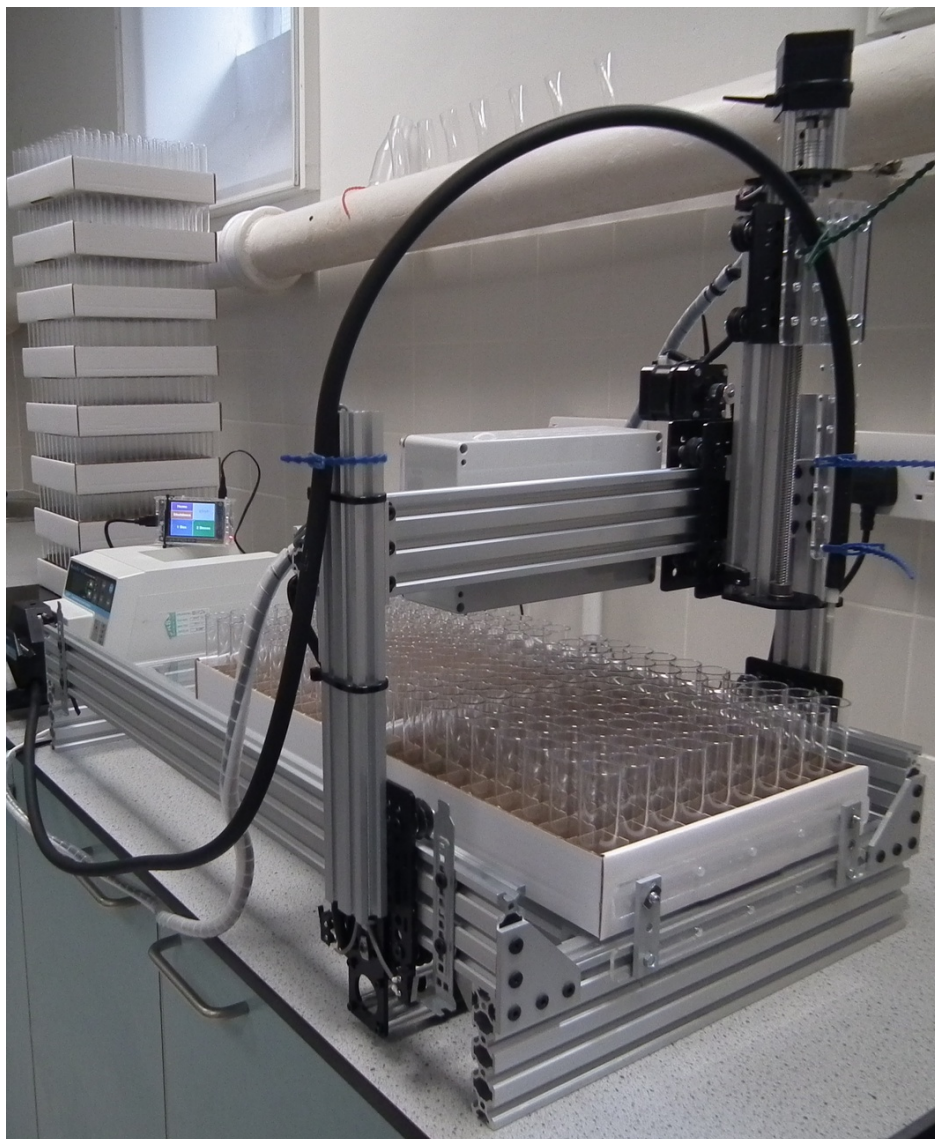
2017-06-05

Contents

1	About the course	5
1.1	Overview	6
1.2	Registration	6
1.3	Prerequisites	6
1.4	Github	6
1.5	Contact	6
1.6	Colophon	6
2	Introduction	7
3	Linear models and matrix algebra	9
4	Linear and non linear logistic regression	11
5	Nearest neighbours	13
5.1	Example one	13
5.2	Example two	13
6	Decision trees and random forests	15

Chapter 1

About the course



1.1 Overview

Machine learning gives computers the ability to learn without being explicitly programmed. It encompasses a broad range of approaches to data analysis with applicability across the biological sciences. Lectures will introduce commonly used algorithms and provide insight into their theoretical underpinnings. In the practicals students will apply these algorithms to real biological data-sets using the R language and environment.

During this course you will learn about:

- Some of the core mathematical concepts underpinning machine learning algorithms: matrices and linear algebra; Bayes' theorem.
- Classification (supervised learning): partitioning data into training and test sets; feature selection; logistic regression; support vector machines; artificial neural networks; decision trees; nearest neighbours, cross-validation.
- Exploratory data analysis (unsupervised learning): dimensionality reduction, anomaly detection, clustering.

After this course you should be able to:

- Understand the concepts of machine learning.
- Understand the strengths and limitations of the various machine learning algorithms presented in this course.
- Select appropriate machine learning methods for your data.
- Perform machine learning in R.

1.2 Registration

Bioinformatics Training: An Introduction to Machine Learning

1.3 Prerequisites

- Some familiarity with R would be helpful.
- For an introduction to R see An Introduction to Solving Biological Problems with R course.

1.4 Github

bioinformatics-training/intro-machine-learning

1.5 Contact

If you have any **comments**, **questions** or **suggestions** about the material, please contact the authors: Sudhakaran Prabakaran, Matt Wayland and Chris Penfold.

1.6 Colophon

This book was produced using the **bookdown** package (Xie, 2017), which was built on top of R Markdown and **knitr** (Xie, 2015).

Chapter 2

Introduction

```
knitr::include_graphics("images/system.jpg")
```

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 2. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter ??.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 2.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 2.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```



Figure 2.1: Here is a nice figure!

Table 2.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Chapter 3

Linear models and matrix algebra

Chapter 4

Linear and non linear logistic regression

Chapter 5

Nearest neighbours

5.1 Example one

5.2 Example two

Chapter 6

Decision trees and random forests

Bibliography

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2017). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.4.