QUEEN'S UNIVERSITY BELFAST

SCHOOL OF ELECTRONICS, ELECTRICAL ENGNIEERING AND COMPUTER SCIENCE

Data Analysis & Visualisation

CSC3062

BEng (CS & SE), MEng (CS & SE), BIT & CIT

Dr Reza Rafiee

Semester 1 2019

Principal component analysis

PCA

Quick review on some technical terms

- Dataset (data set, cohort)
- Variables (or features) & feature space
- Observation (sample)
- Variation
- Dimension
- Pattern

Principal component analysis (PCA)

- A **linear** dimensionality-reduction technique
  - **Transforming** variables (or features) of a large dataset (i.e., multivariate data) into a smaller one that still contains most of the information in the large dataset

http://www.sthda.com/english/articles/31-principal-component-methods-in-r-practical-guide/112-pca-principal-component-analysis-essentials/

Principal component analysis (PCA)

Reducing data by **projecting** (geometrically) into a lower dimensions which called principal components (PCs)

http://www.sthda.com/english/articles/31-principal-component-methods-in-r-practical-guide/112-pca-principal-component-analysis-essentials/

PCA example

Let's look at
a question & analysis for better understanding of PCA

PCA example (17 dimensions)

Eating in the UK

Assume we have a dataset including 17 features/dimensions (Table 1). This table shows the average consumption of 17 types of food in grams per person per week for every country in the UK.

The table shows some interesting variations across different food types, but overall differences aren't so notable. Let's see if PCA can eliminate dimensions to emphasize how countries differ.

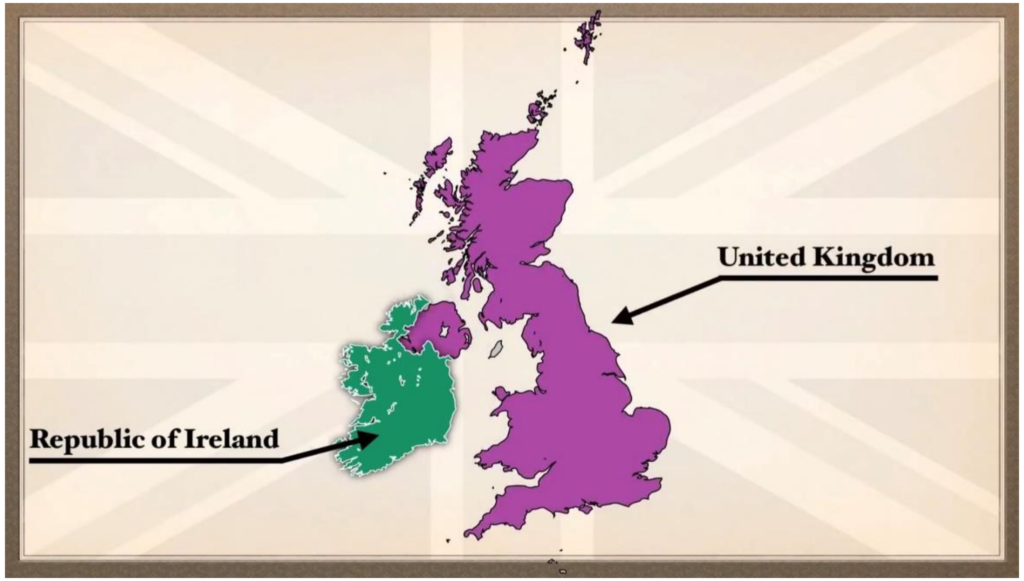
http://www.sdss.jhu.edu/~szalay/class/2016-oldold/SignalProcPCA.pdf

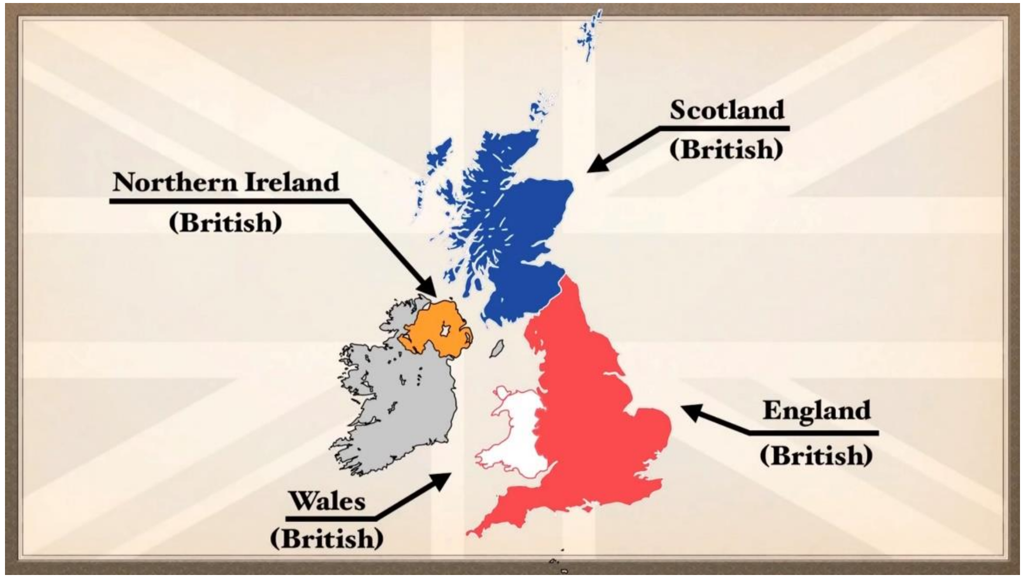
	England	N Ireland	Scotland	Wales
Alcoholic drinks	375	135	458	475
Beverages	57	47	53	73
Carcase meat	245	267	242	227
Cereals	1472	1494	1462	1582
Cheese	105	66	103	103
Confectionery	54	41	62	64
Fats and oils	193	209	184	235
Fish	147	93	122	160
Fresh fruit	1102	674	957	1137
Fresh potatoes	720	1033	566	874
Fresh Veg	253	143	171	265
Other meat	685	586	750	803
Other Veg	488	355	418	570
Processed potatoes	198	187	220	203
Processed Veg	360	334	337	365
Soft drinks	1374	1506	1572	1256
Sugars	156	139	147	175

Table 1: UK food consumption in 1997 (g/person/week). Source: DEFRA website

PCA example (17 dimensions)

Eating in the UK





PCA example (17 dimensions)

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The table shows some interesting **variations across different food types**, but overall differences aren't so notable. Let's see **if PCA can eliminate dimensions to emphasize how countries differ**.

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PCA example (17 dimensions)

Eating in the UK – Question?

Can PCA reduce the dimension of this dataset (i.e., eliminate dimensions) to highlight how countries differ?

PCA analysis using *prcomp()* package

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Input_dataset

?

	England	N Ireland	Scotland	Wales
PC1	-144.993	477.3916	-91.8693	-240.529
PC2	2.532999	58.90186	-286.082	224.6469
PC3	105.7689	-4.8779	-44.4155	-56.4756

Reduced dataset

Summarises of features

PCA analysis using *prcomp()* package

	England	N Ireland	Scotland	Wales
PC1	-144.993	477.3916	-91.8693	-240.529
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Reduced dataset

Question: how many new variables (PCs) will be acceptable when using this transformation (or projection)?

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PCA analysis using *prcomp()* package

Input_dataset

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 # scale =T is appropriate for high-dimensional data
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PCA analysis using *prcomp()* package

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summary(PCA_Model_prcomp)
# Importance of components:
#                              PC1      PC2      PC3       PC4
# Standard deviation     324.1502 212.7478 73.87622 3.828e-14
# Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
# Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
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```

```
PCA_Model_prcomp$x   # Showing the principle components
#                  PC1         PC2        PC3           PC4
# England   -144.99315    2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164   58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915  224.646925 -56.475555  7.770000e-13
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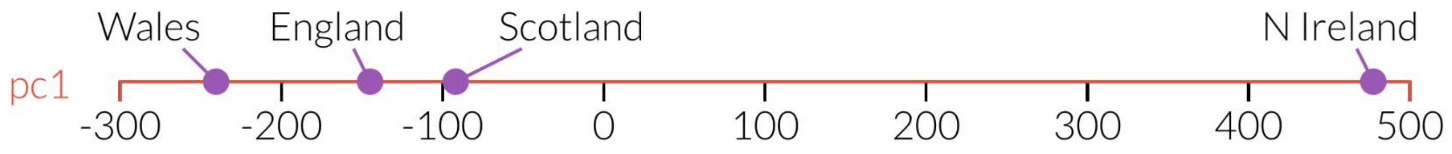
# Wales     -240.52915 224.646925 -56.475555  7.770000e-13
```

PCA analysis using *prcomp()* package

Eating in the UK

Here is the plot of the data along the first principal component (PCA).

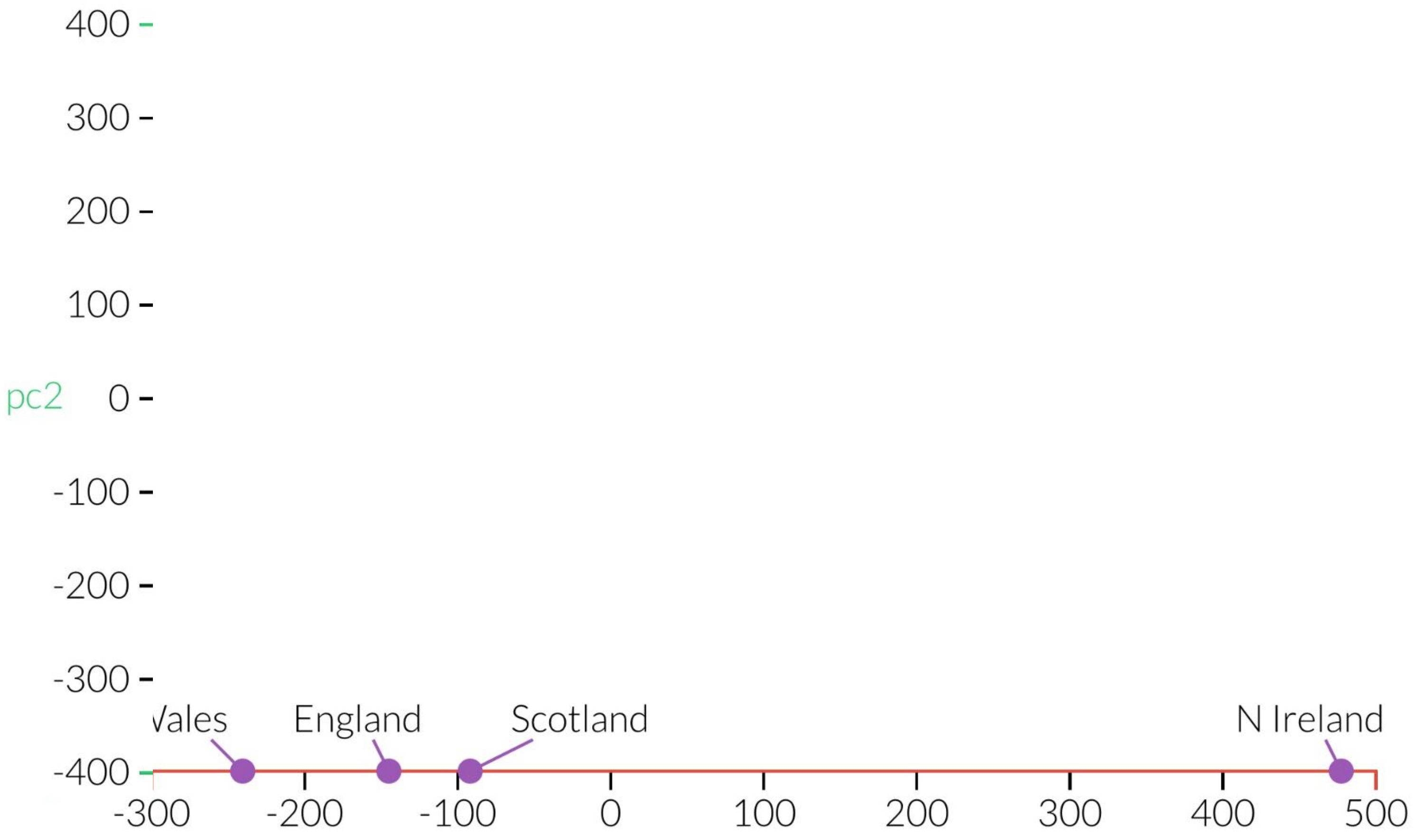
	PC1
# England	**-144.99315**
# N Ireland	**477.39164**
# Scotland	**-91.86934**
# Wales	**-240.52915**



PCA analysis using *prcomp()* package

Eating in the UK

Adding the second principal components (PCA).

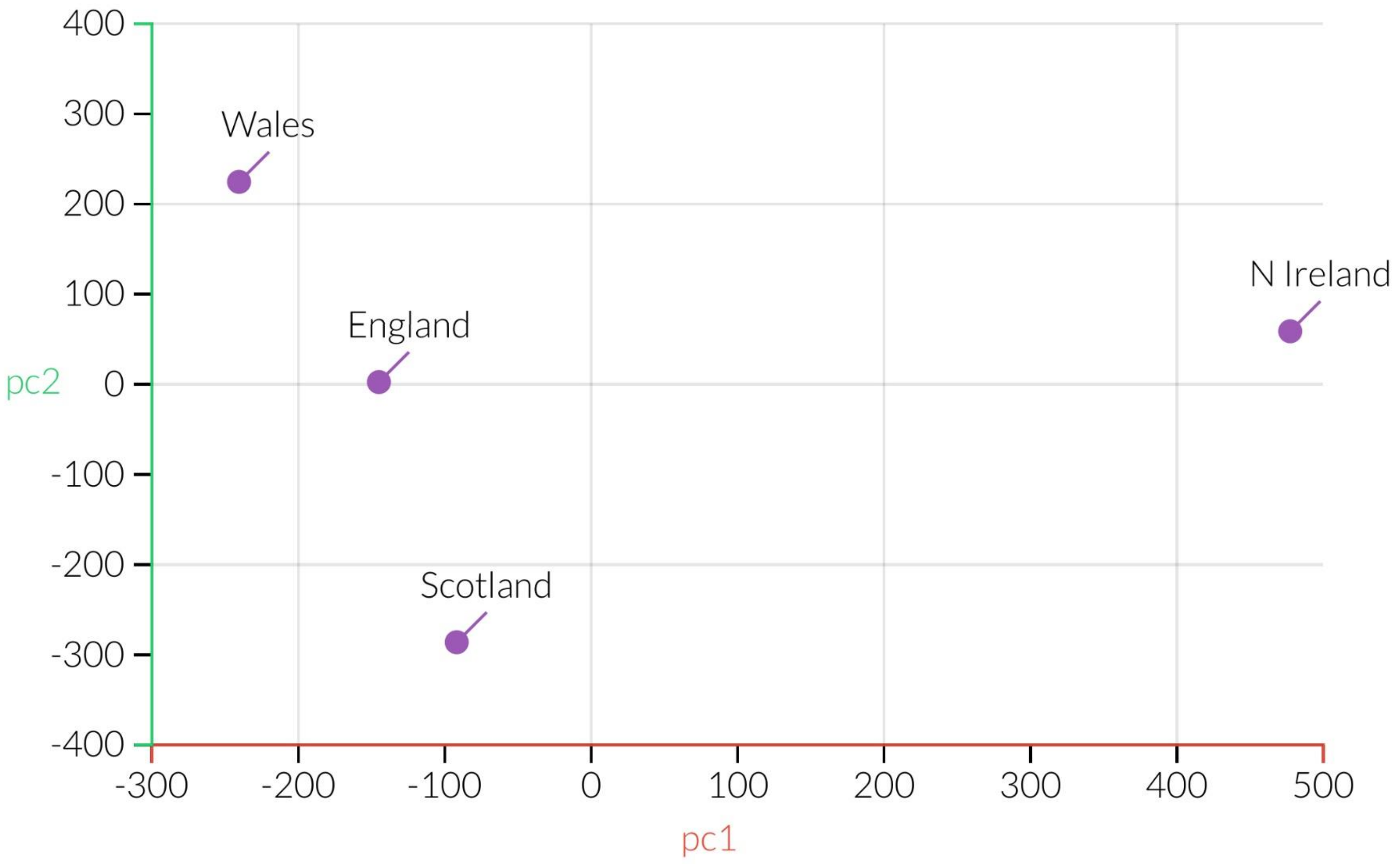


PCA analysis using *prcomp()* package

Eating in the UK

The first and second principal components (PCA).

#	PC1	PC2
# England	-144.99315	2.532999
# N Ireland	477.39164	58.901862
# Scotland	-91.86934	-286.081786
# Wales	-240.52915	224.646925



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Interpret the PCs

Eating in the UK

Assume we have a dataset including 17 features/dimensions (Table 1). This table shows the average consumption of 17 types of food in grams per person per week for every country in the UK.

The Northern Irish eat way more grams of fresh potatoes and way fewer of fresh fruits, cheese, fish and alcoholic drinks.

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Principal component analysis (PCA)

- A **linear** dimensionality-reduction technique
  - **Transforming** variables (or features) of a large dataset (i.e., multivariate data) into a smaller one that still contains most of the information in the large dataset
- By using PCA, we **reduce the number of features** of a dataset, while preserving as much information as possible.
- Reducing data by **projecting** (geometrically) into a lower dimensions which called principal components (PCs)

http://www.sthda.com/english/articles/31-principal-component-methods-in-r-practical-guide/112-pca-principal-component-analysis-essentials/

Directions with most variance

- Principal components are the underlying structure in the data.

- Principal components are **the directions** where there is the **most variance**, or the directions where the data is most spread out.

How to find the direction where there is most variance?

Directions with most **variance**

Standard deviation (SD) is a measure of how spread out numbers are

SD is the square root of the variance

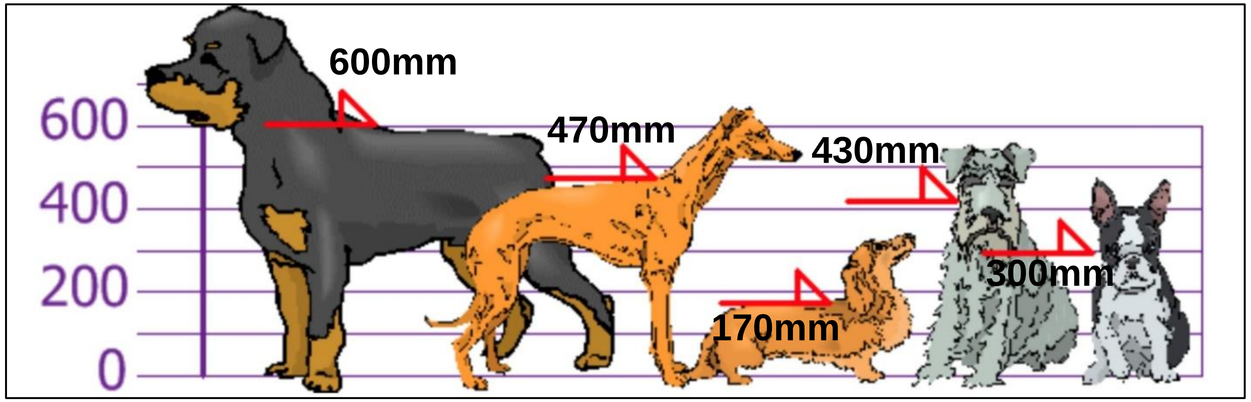
(Sigma: $\boldsymbol{\sigma}$) $\boldsymbol{\sigma}^2$

We aim to measure the average, SD and variance of the heights of following objects.

https://studylib.net/doc/6625962/standard-deviation-and-variance-explanation

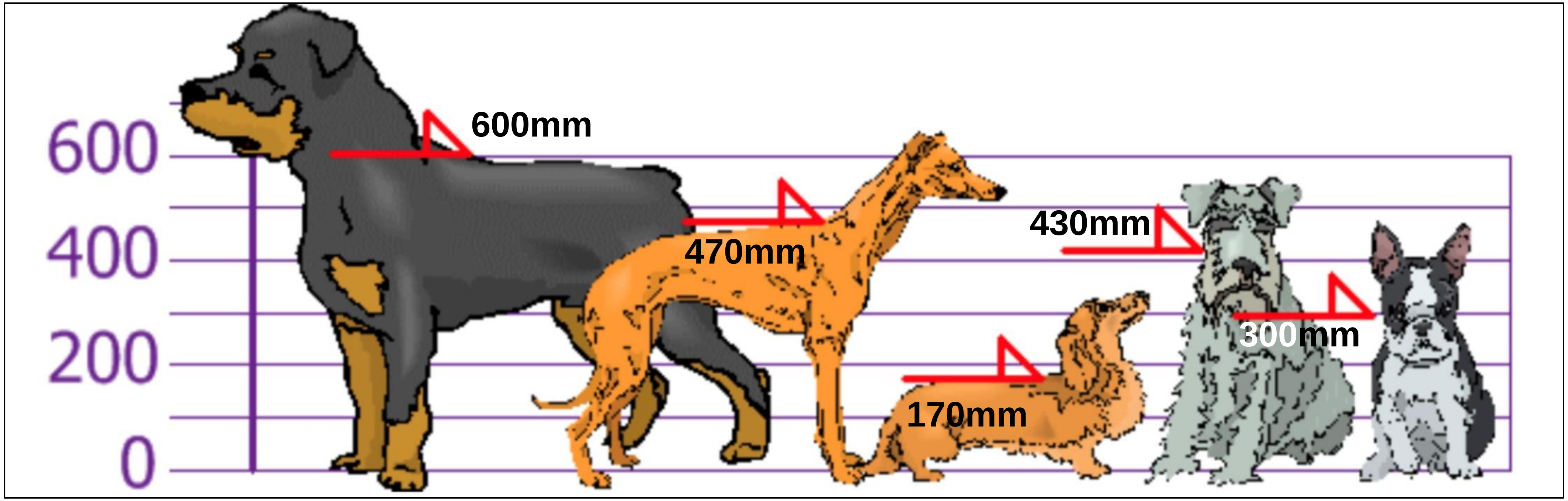
Directions with most **variance**

What is variance?



Directions with most **variance**

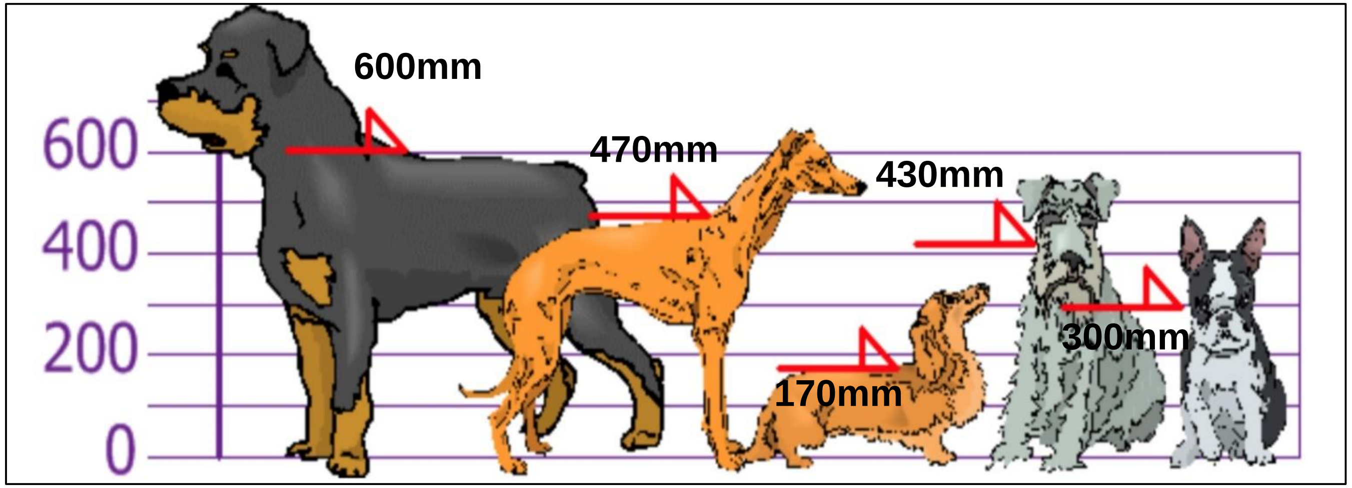
We aim to measure the average, SD and variance of the **heights** of following **dogs**



Sample (observation)
Variable or feature (i.e, random variable)
Statistical measurement

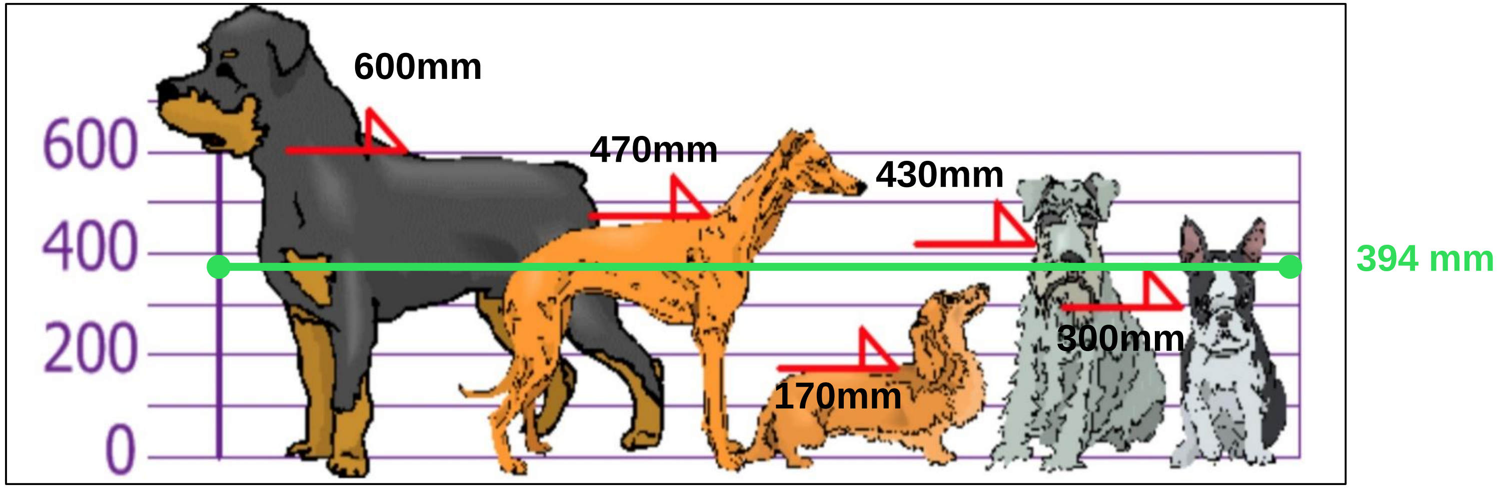
https://studylib.net/doc/6625962/standard-deviation-and-variance-explanation

Directions with most **variance**



$$Mean = \frac{600 + 470 + 170 + 430 + 300}{5} = \frac{1970}{5} = 394$$

Directions with most **variance**



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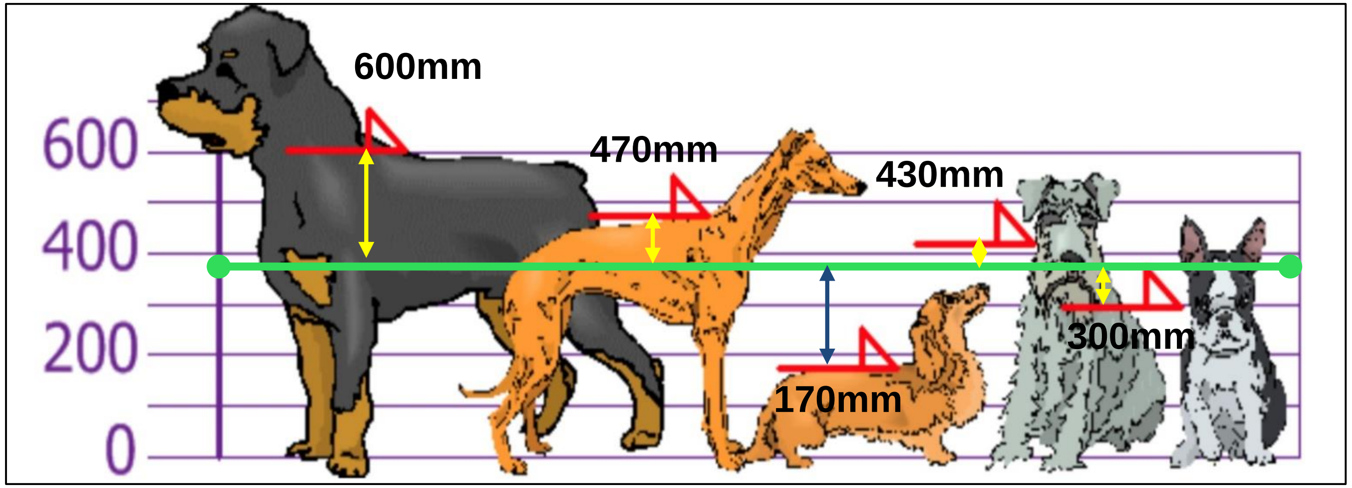
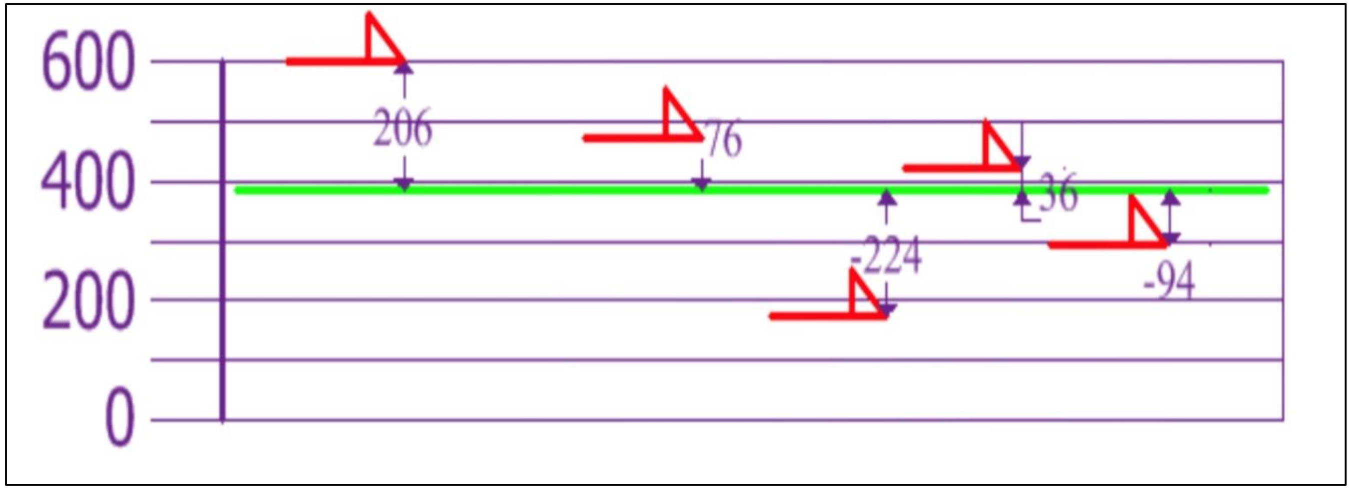
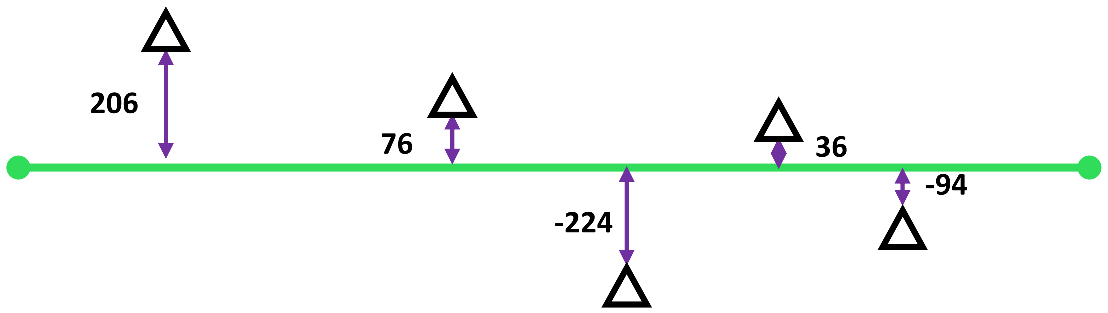
Directions with most **variance**



Now, we calculate each dogs **difference from the Mean**



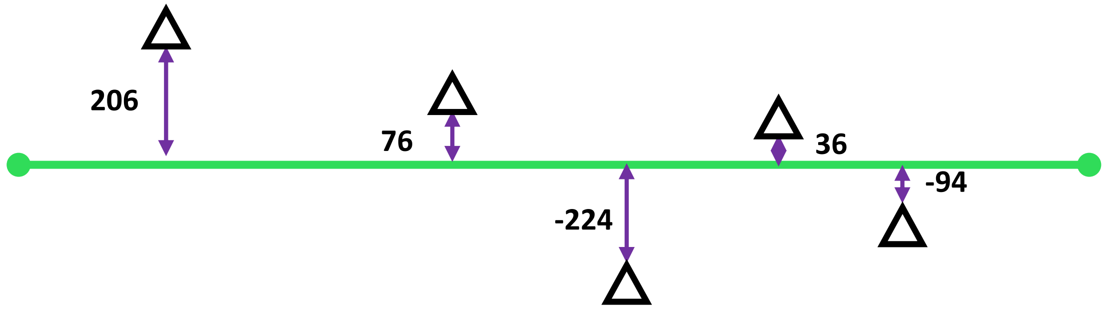
Directions with most **variance**



$$\mu = Mean = \frac{600 + 470 + 170 + 430 + 300}{5} = \frac{1970}{5} = 394$$

$$\sigma^2 = \frac{206^2 + 76^2 + (-224)^2 + 36^2 + (-94)^2}{5} = \frac{108{,}520}{5} = 21{,}704$$

Directions with most **variance**



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$$\sigma^2 = \frac{206^2 + 76^2 + (-224)^2 + 36^2 + (-94)^2}{5} = \frac{108{,}520}{5} = 21{,}704$$

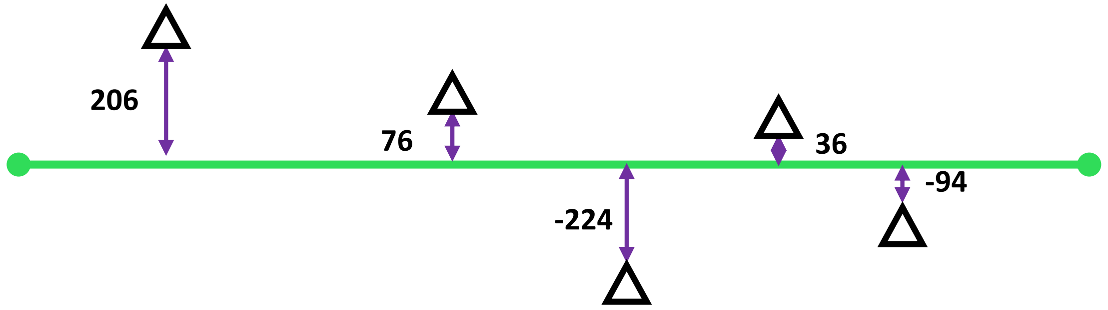
$$\sigma = \sqrt{21{,}704} = 147.32 \approx 147\, mm$$

Directions with most **variance**

$\mu = 394$

$\sigma^2 = 21{,}704$

$\sigma \approx 147\ mm$



Directions with most **variance**

$$\mu = 394$$

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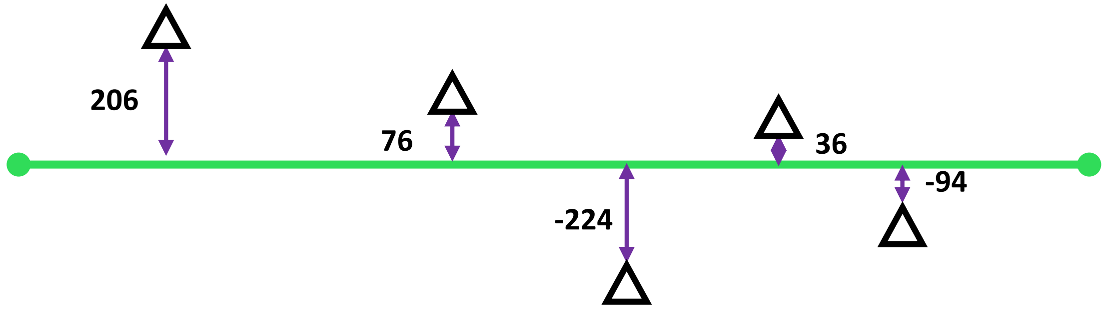
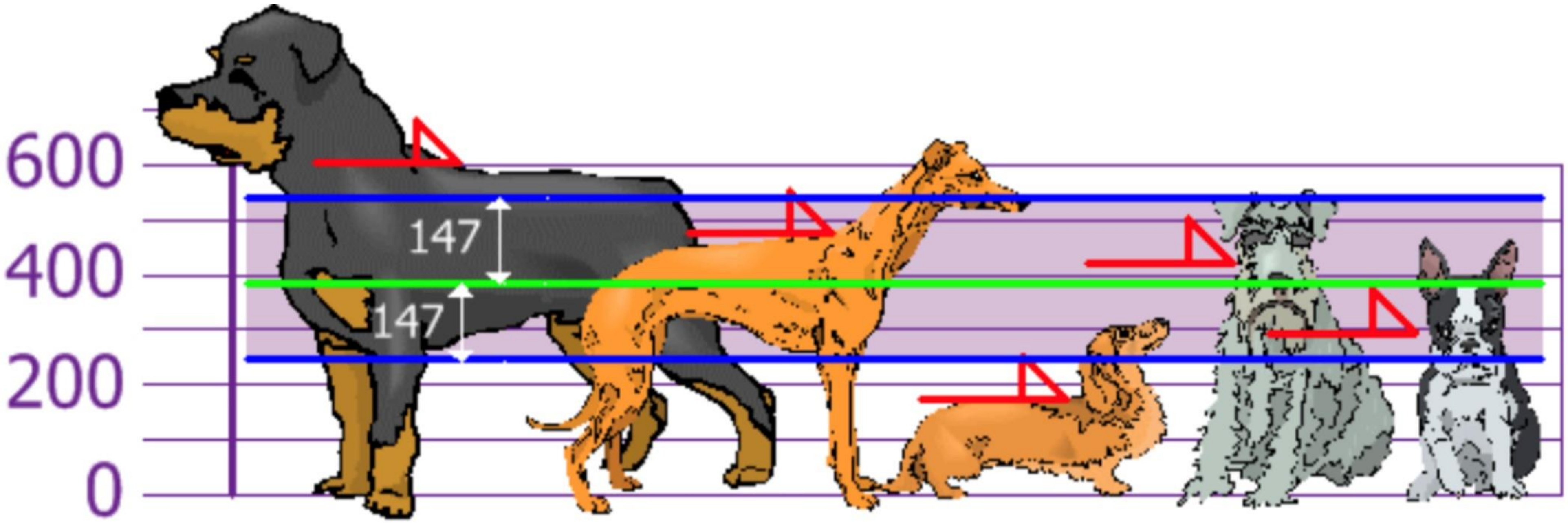
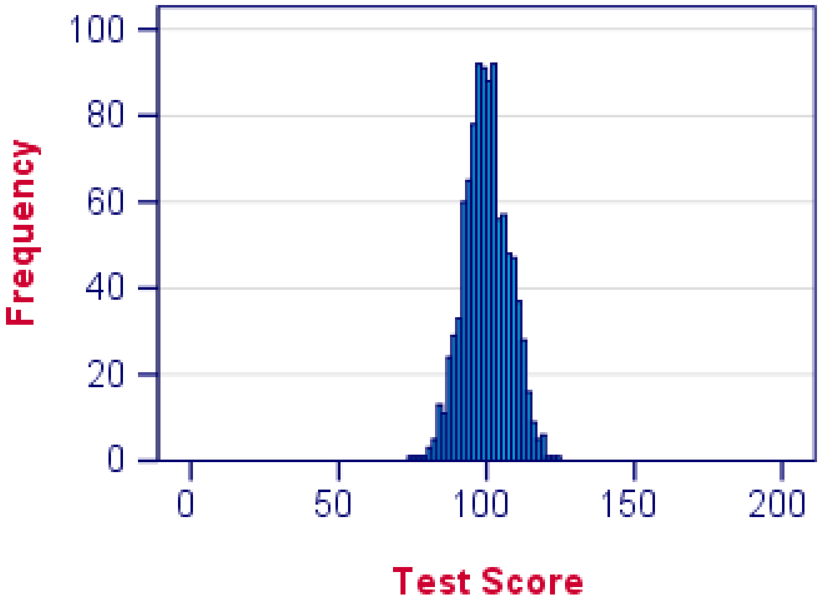
$$\sigma \approx 147\ mm$$

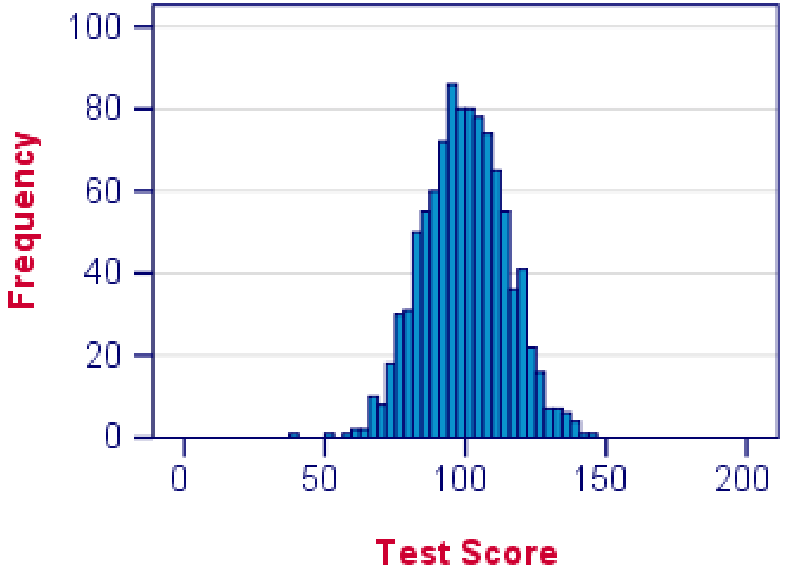


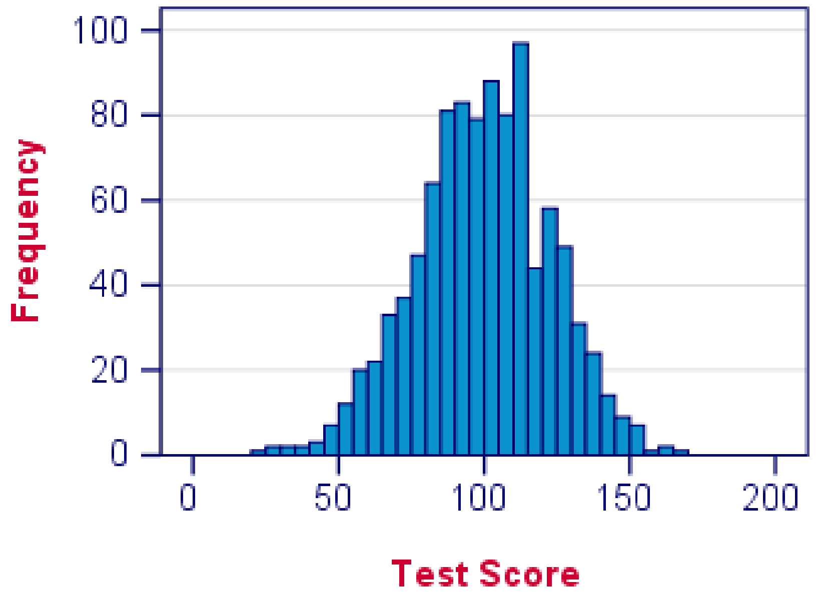


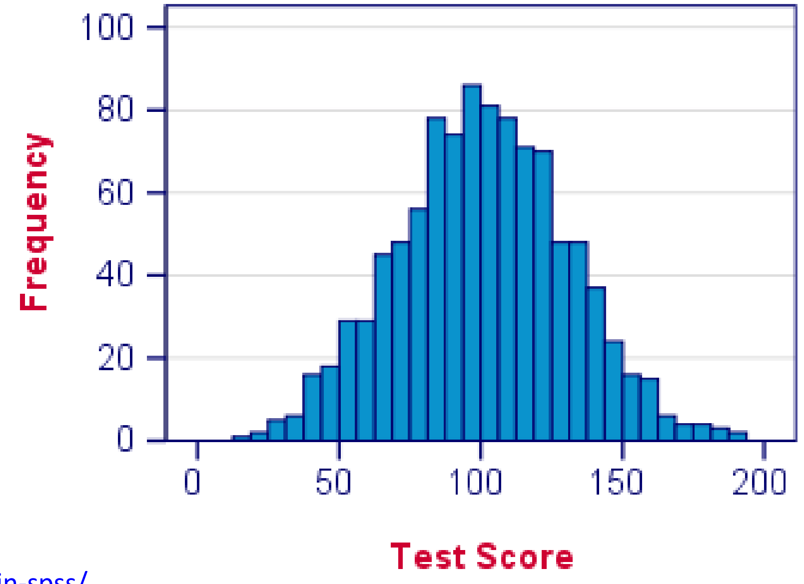
So, using the Standard Deviation we have a **"standard"** way of knowing what is **normal**, and what is **extra large** or **extra small**

Directions with most **variance**



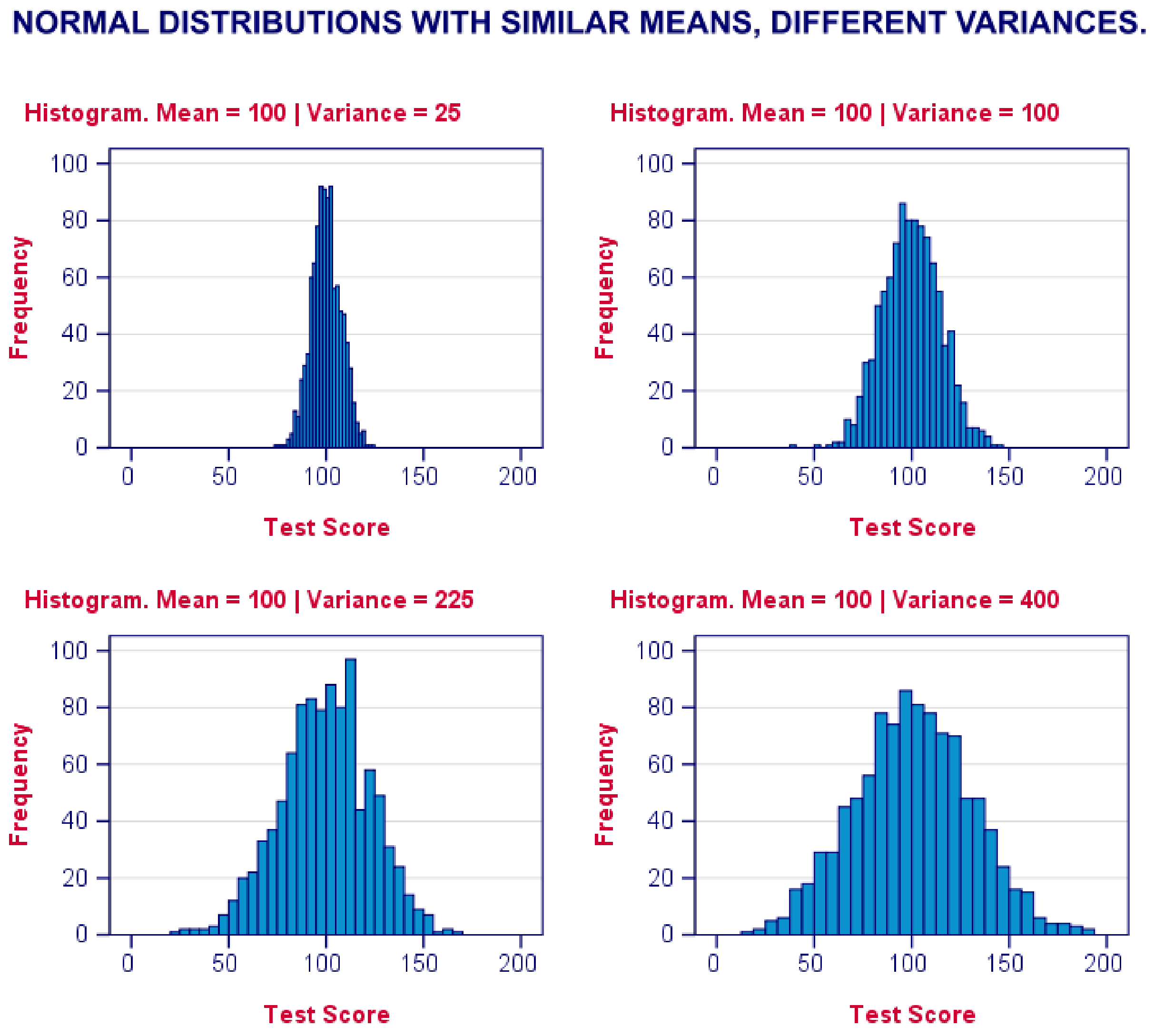






https://www.spss-tutorials.com/levenes-test-in-spss/

Directions with most **variance**



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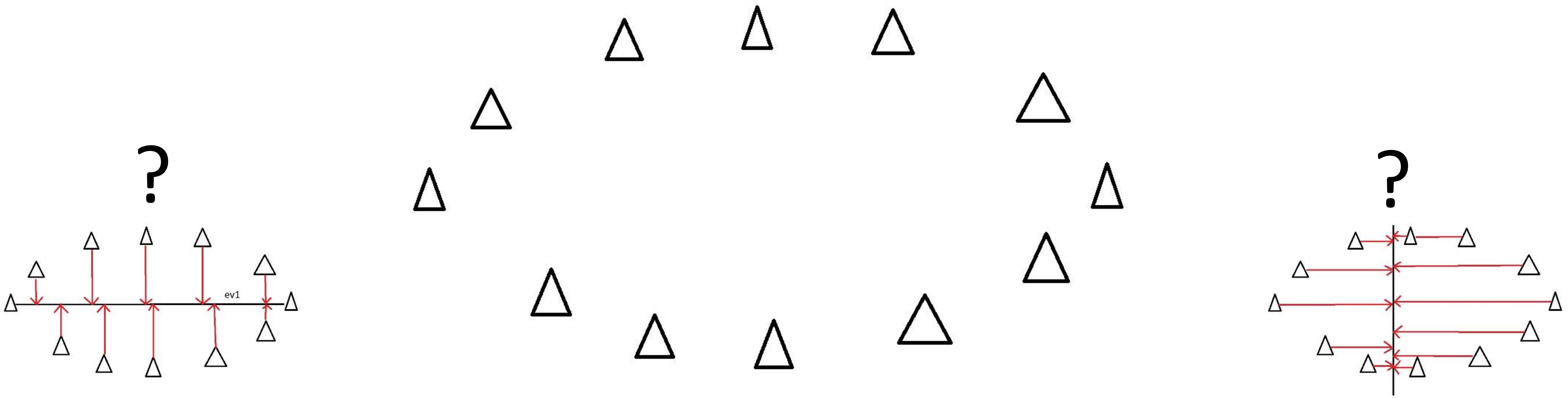
Directions with most variance

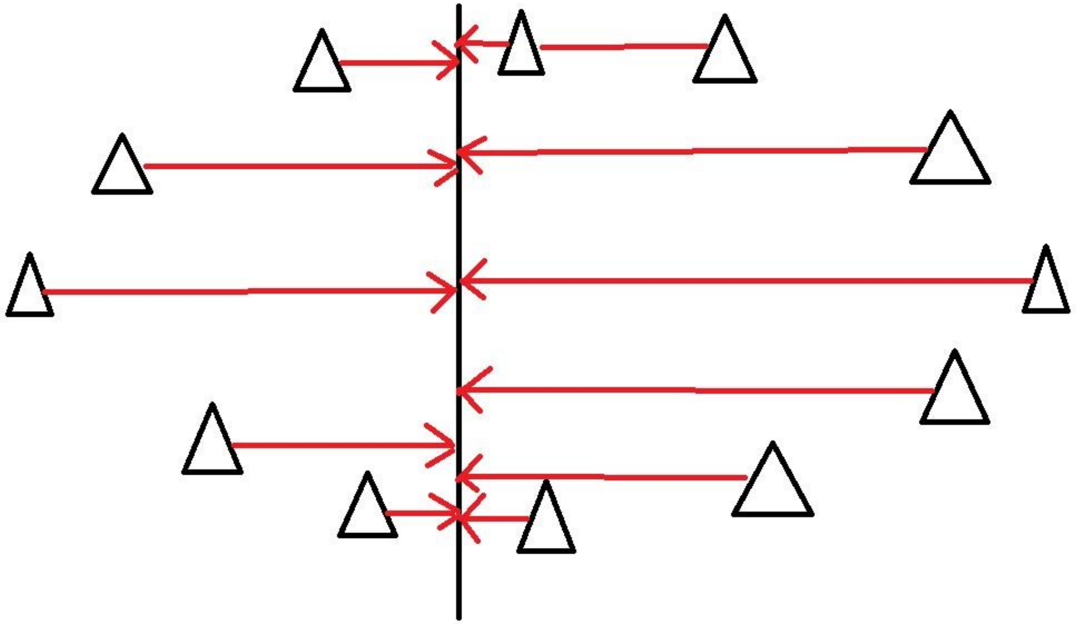
Assume that the triangles are data points.



Find the straight line where the data is most spread out when projected onto it.

Directions with most variance

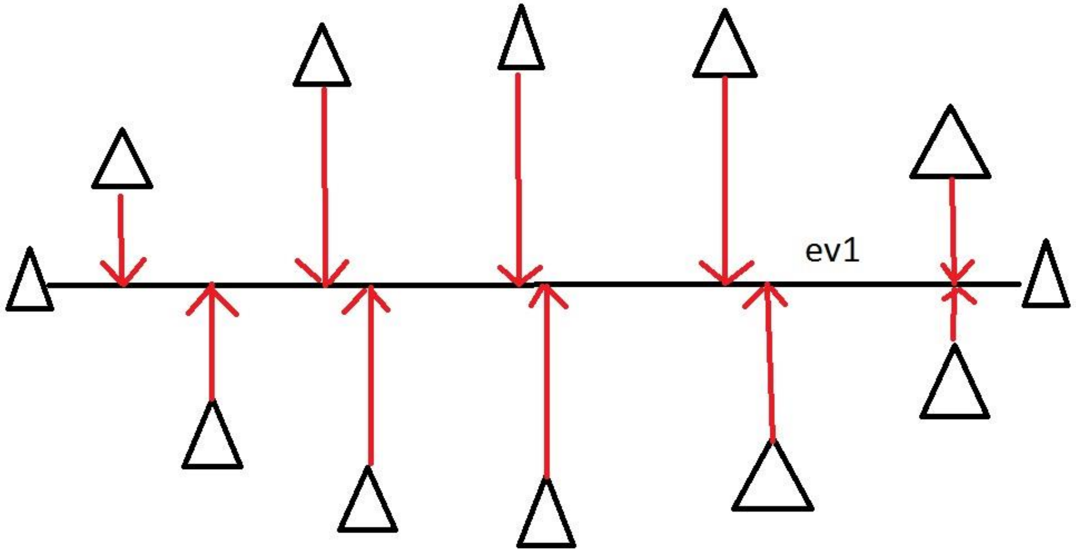
A vertical straight line with the points projected on to it will look like this.



The data is not very spread out here, therefore it does not have a large variance. It is probably not the principal component.

Directions with most variance

Now consider a horizontal line with lines from data points projected on this:



On this line the data is way more spread out and it has a large variance.

The horizontal line is therefore the principal component in this example.

PC | eigenvector and eigenvalue

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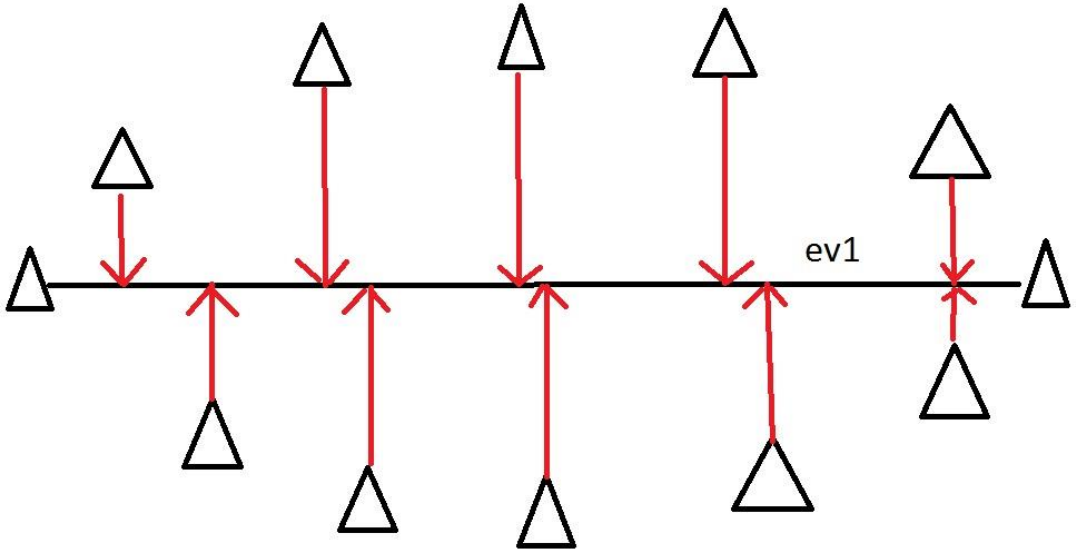

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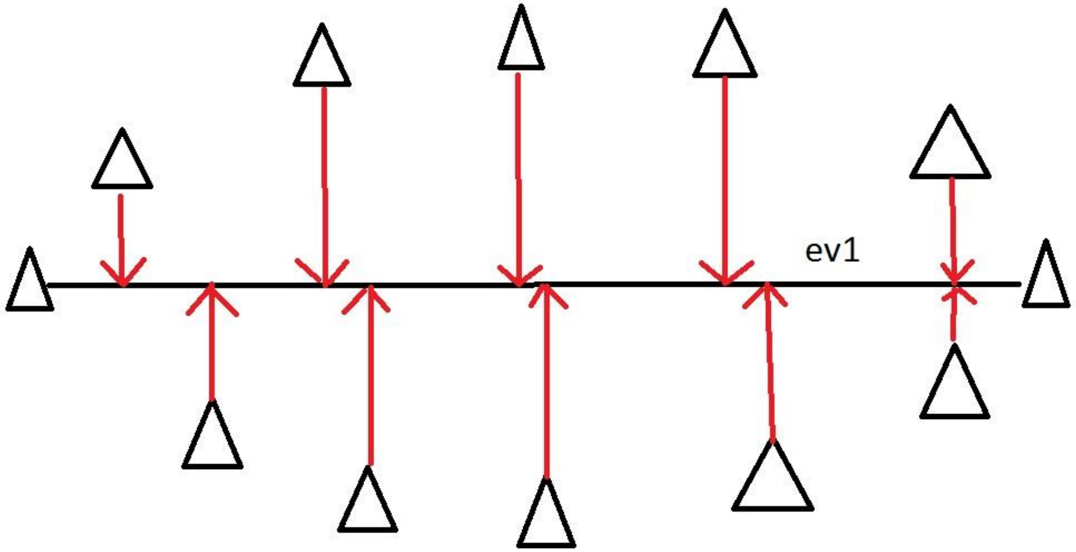
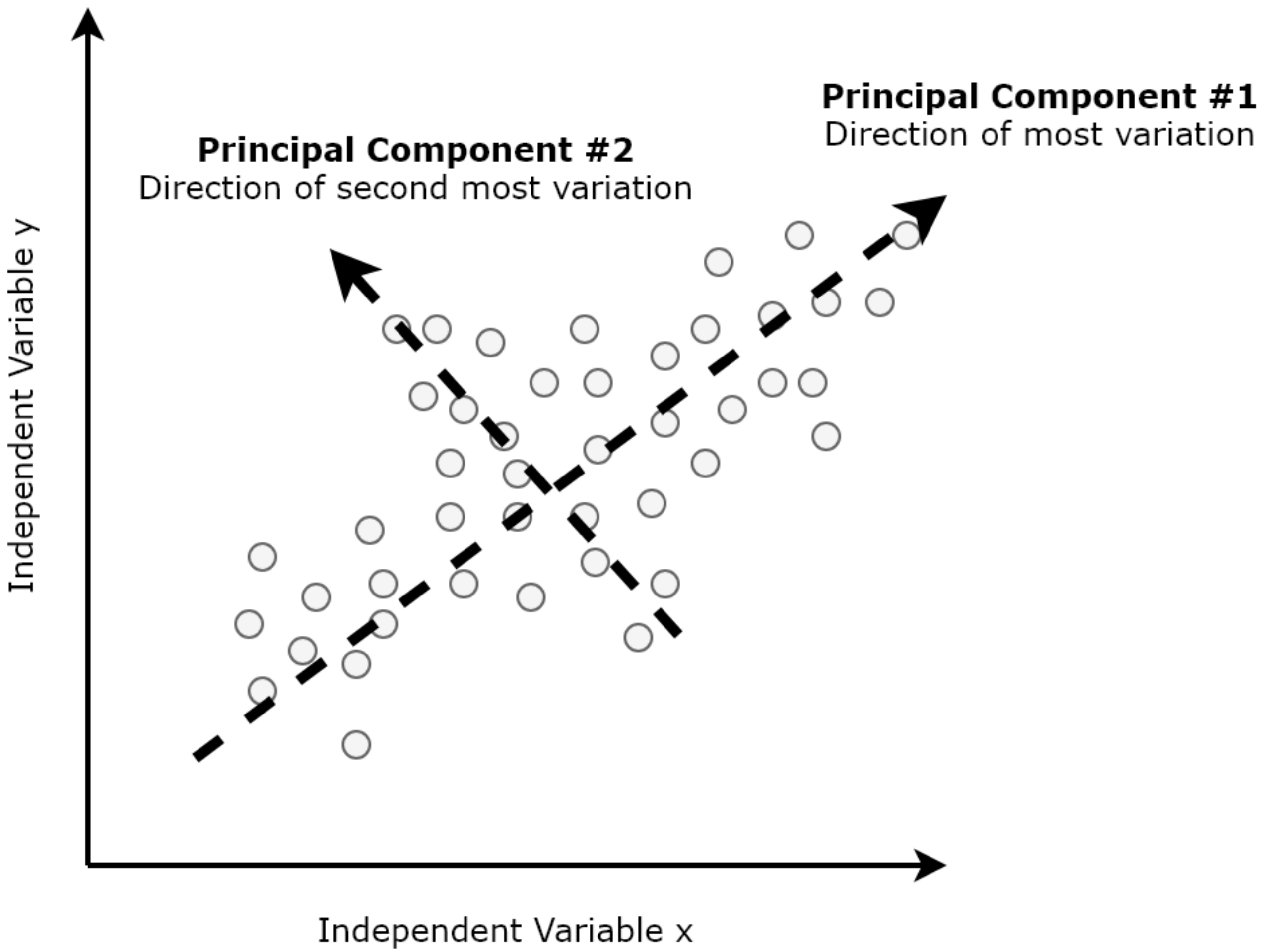


The direction of this line is called **eigenvector**.

An **eigenvalue** is a number telling us how spread out the data is on the line.

Eigenvector and eigenvalue

The Principal component directions are directions in the feature space along which the original data are high variable.



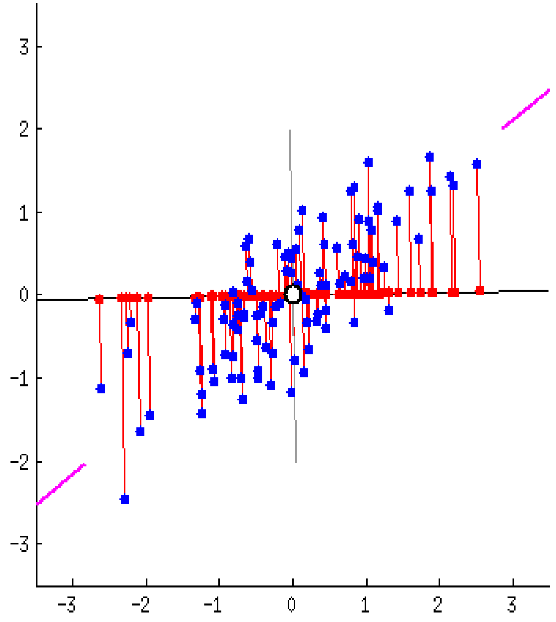
An **eigenvector** is a direction of the line

An **eigenvalue** is a number telling us how spread out the data is on the line

The eigenvector with the highest eigenvalue is therefore the principal component

PCA

- PCA allows us to **summarise** and to **visualise** the information in a data set containing individuals/observations/samples described by multiple inter-correlated quantitative variables.
- Each variable could be considered as a different dimension. If you have more than 3 variables in your data sets, it could be very difficult to visualize a multi-dimensional hyperspace.



PCA

PCA is used **to extract** the important information from a **multivariate** data table and to express this information as a set of few **new variables** called **PCs** (**principal components)**. These **new variables** correspond to **a linear combination of the originals**. The number of principal components is less than or equal to the number of **original variables**.

http://www.sthda.com/english/articles/31-principal-component-methods-in-r-practical-guide/112-pca-principal-component-analysis-essentials/

PCA

- A technique which is used to emphasise **variation** and **reveal strong patterns** in a dataset. It is often used to make data easy to **explore** and **visualise**.
- It's an **unsupervised learning method** and is similar to clustering.
- It could be considered as a **compression method**.
- Each **feature** could be considered as a different **dimension**. If you have more than 3 features in your dataset, it could be very difficult to visualise!
- Trade of between accuracy and **simplicity**

PCA analysis using *prcomp()* package

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# Standard deviation     324.1502 212.7478 73.87622 3.828e-14
# Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
# Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

```
PCA_Model_prcomp$x   # Showing the principle components
#                  PC1         PC2        PC3           PC4
# England   -144.99315    2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164   58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915  224.646925 -56.475555  7.770000e-13
```

PCA analysis using *prcomp()* package

```
PCA_Model_prcomp <- prcomp(t(Input_dataset), center = T, scale=F)
 # scale =T is appropriate for high-dimensional data
summary(PCA_Model_prcomp)
# Importance of components:
#                            PC1      PC2      PC3       PC4
# Standard deviation     324.1502 212.7478 73.87622 3.828e-14
# Proportion of Variance   0.6744   0.2905  0.03503 0.000e+00
# Cumulative Proportion    0.6744   0.9650  1.00000 1.000e+00
```

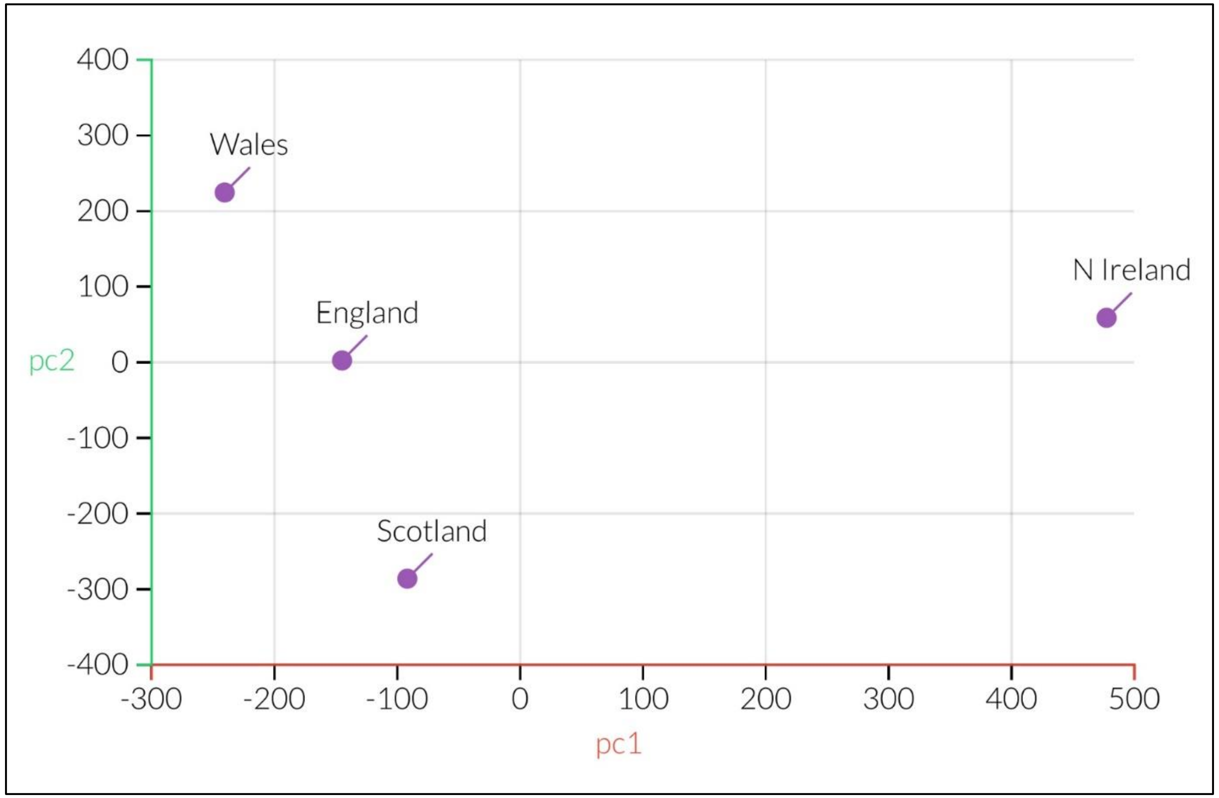
PCA_Model_prcomp$x # Showing the principle components

```
#                PC1        PC2        PC3           PC4
# England   -144.99315   2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164  58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915 224.646925 -56.475555  7.770000e-13
```

PCA visualisation of 17 food types …

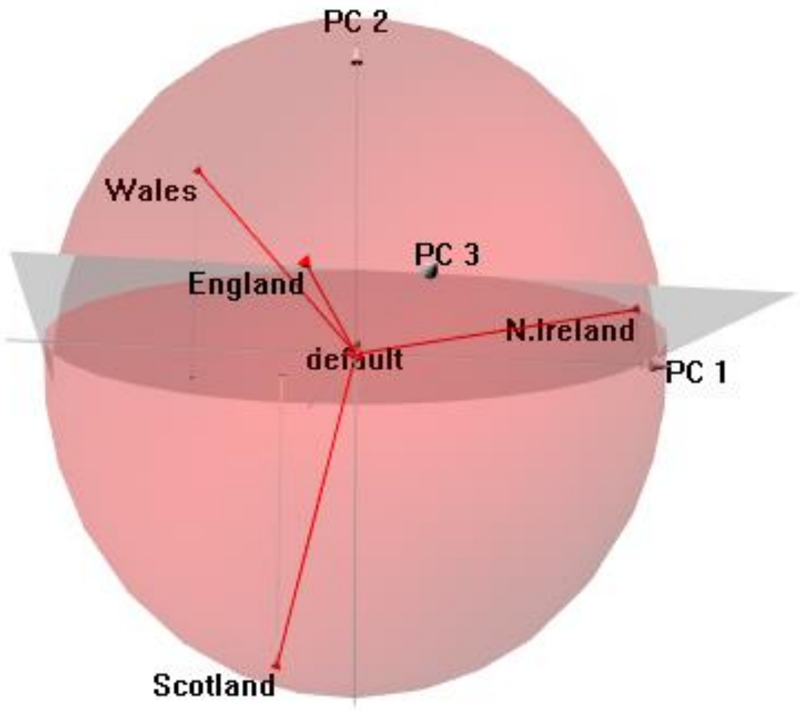
PCA_Model_prcomp$x # Showing the principle components

#	PC1	PC2	PC3	PC4
# England	**-144.99315**	**2.532999**	105.768945	-3.765391e-14
# N Ireland	**477.39164**	**58.901862**	-4.877895	1.667659e-13
# Scotland	**-91.86934**	**-286.081786**	-44.415495	-8.860586e-13
# Wales	**-240.52915**	**224.646925**	-56.475555	7.770000e-13



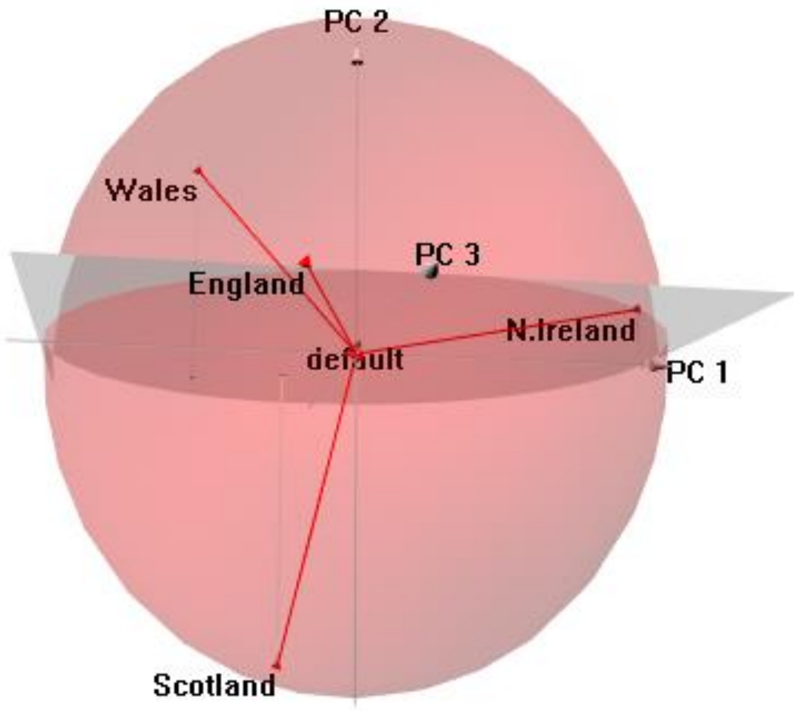
PCA visualisation using pca3d()

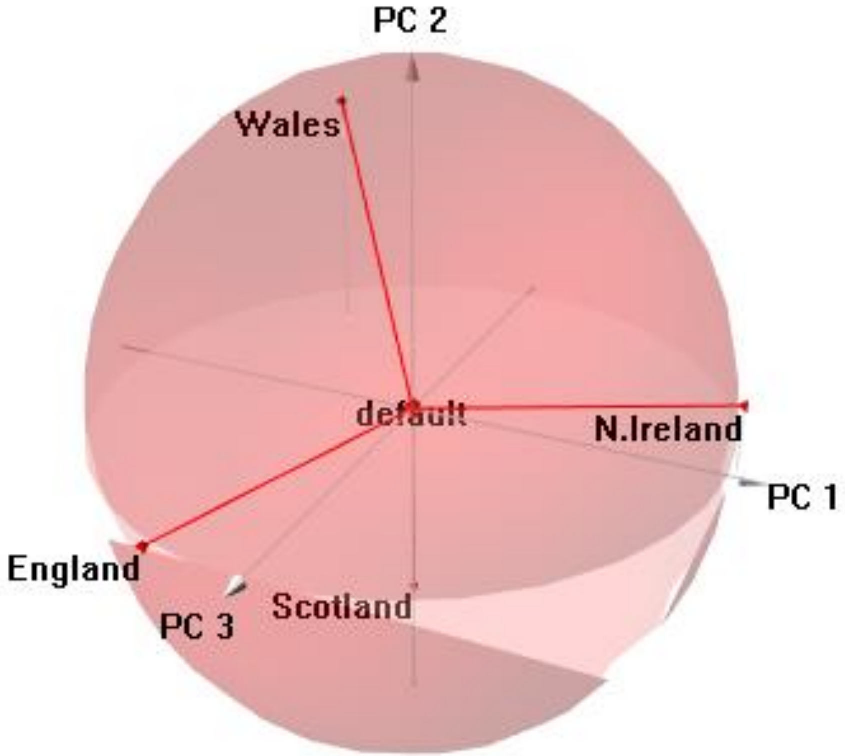
```
pca3d(PCA_Model_prcomp$x[,1:3],components = c(1,2,3), shape = 1,show.shapes = TRUE, show.ellipses = T,
ellipse.ci = 0.45, fancy = T)
#                PC1         PC2         PC3           PC4
# England   -144.99315    2.532999  105.768945  -3.765391e-14
# N Ireland  477.39164   58.901862   -4.877895   1.667659e-13
# Scotland   -91.86934 -286.081786  -44.415495  -8.860586e-13
# Wales     -240.52915  224.646925  -56.475555   7.770000e-13
```



PCA visualisation using pca3d()

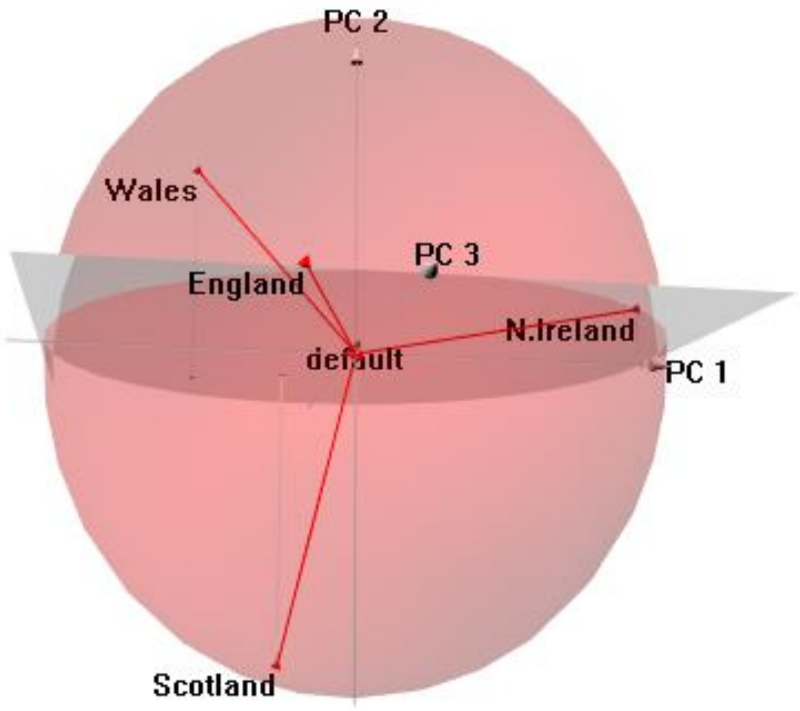
```
pca3d(PCA_Model_prcomp$x[,1:3],components = c(1,2,3), shape = 1,show.shapes = TRUE, show.ellipses = T, ellipse.ci = 0.45, fancy = T)
#                       PC1         PC2         PC3           PC4
# England    -144.99315    2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164   58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915  224.646925 -56.475555  7.770000e-13
```

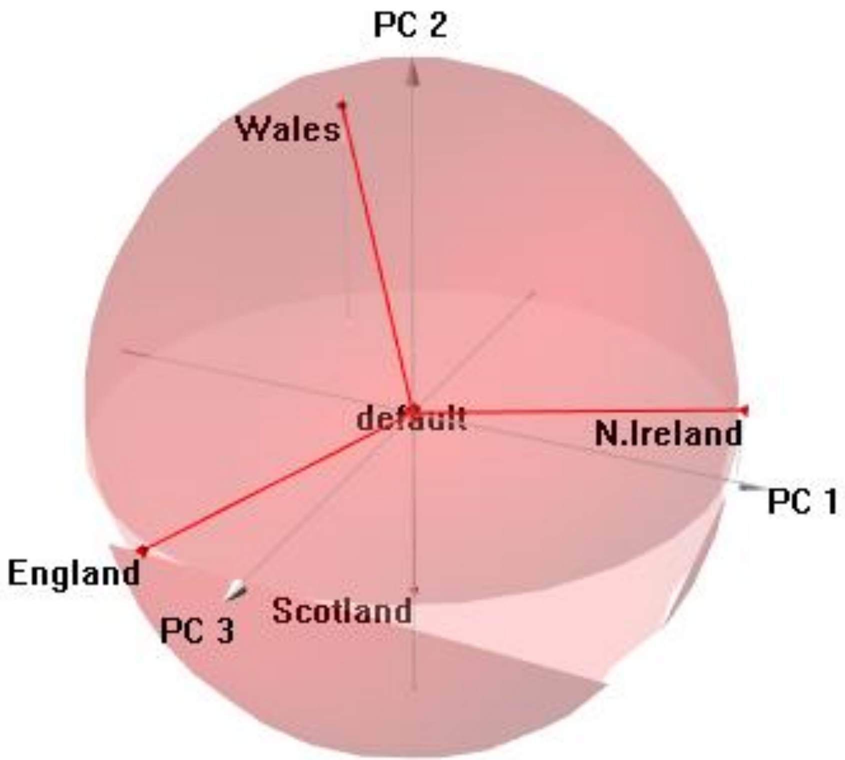


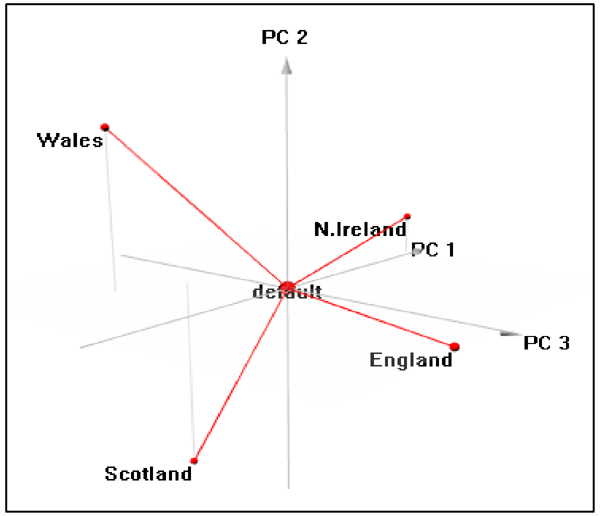


PCA visualisation using pca3d()

```
pca3d(PCA_Model_prcomp$x[,1:3],components = c(1,2,3), shape = 1,show.shapes = TRUE, show.ellipses = F,
ellipse.ci = 0.45, fancy = T)
#                  PC1        PC2        PC3          PC4
# England   -144.99315   2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164  58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915 224.646925 -56.475555  7.770000e-13
```

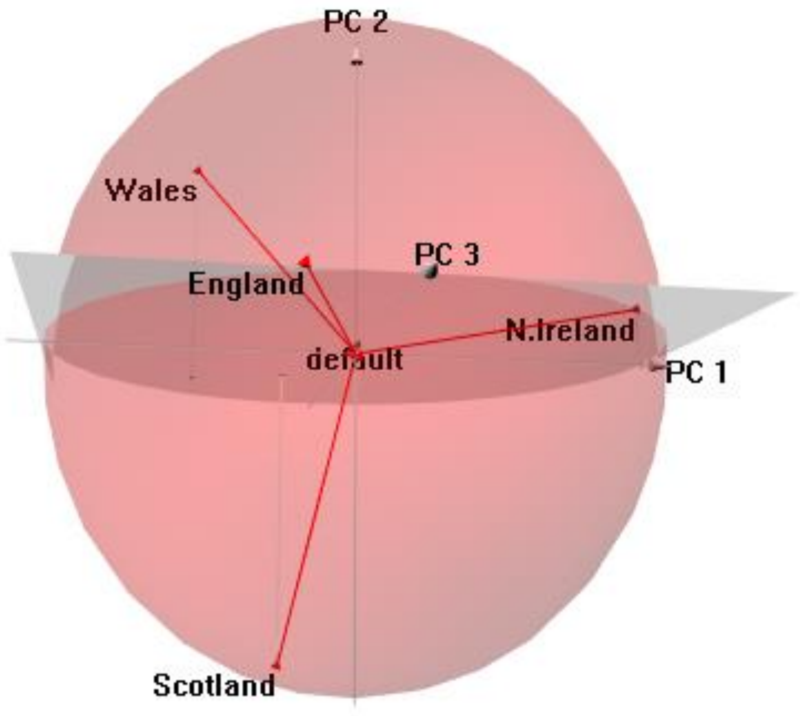


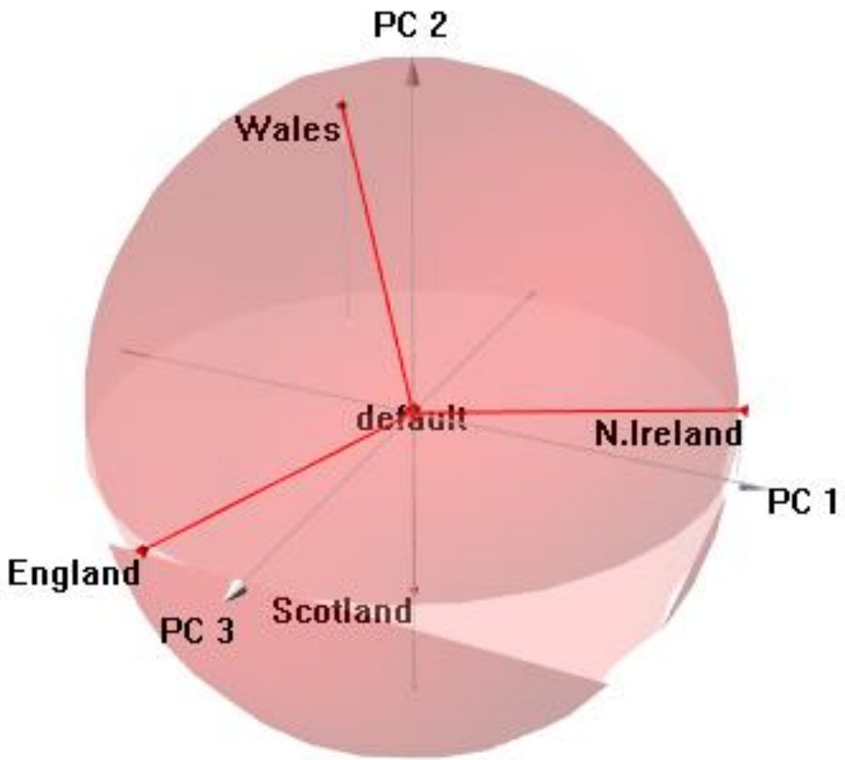


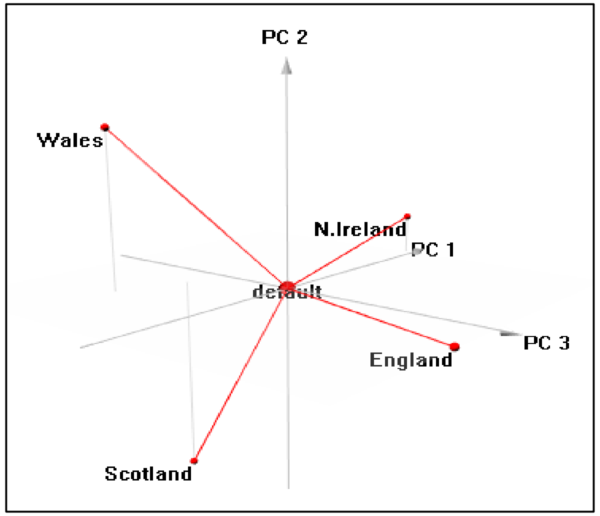


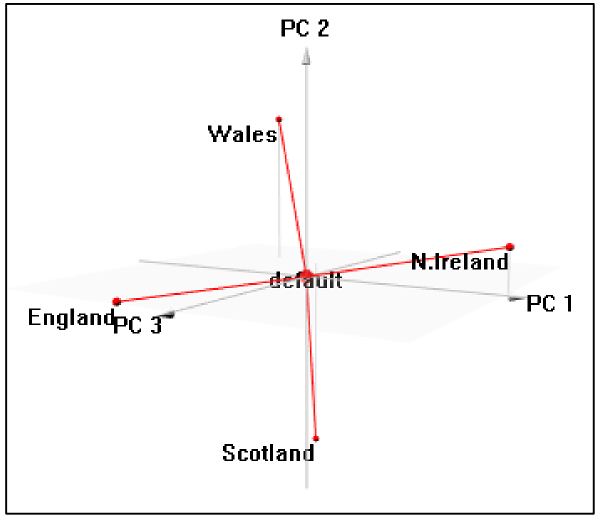
PCA visualisation using pca3d()

```
pca3d(PCA_Model_prcomp$x[,1:3],components = c(1,2,3), shape = 1,show.shapes = TRUE, show.ellipses = F,
ellipse.ci = 0.45, fancy = T)
#                  PC1         PC2        PC3           PC4
# England   -144.99315    2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164   58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915  224.646925 -56.475555  7.770000e-13
```



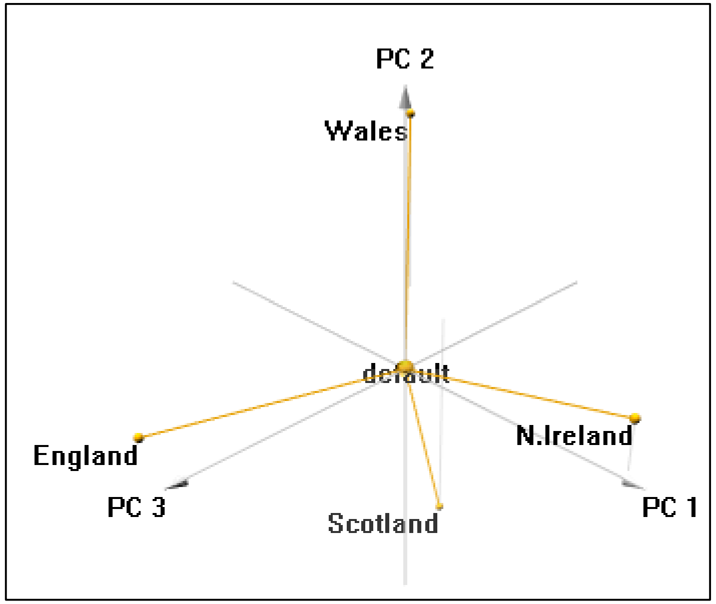


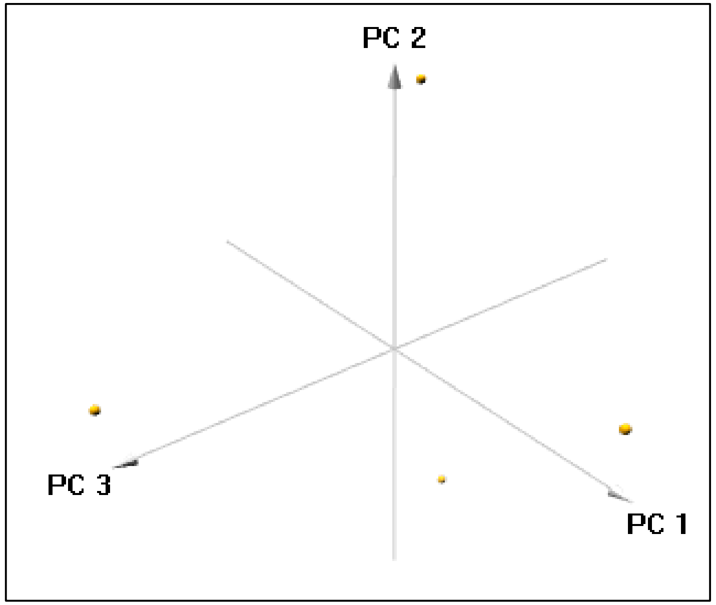




PCA visualisation using pca3d()

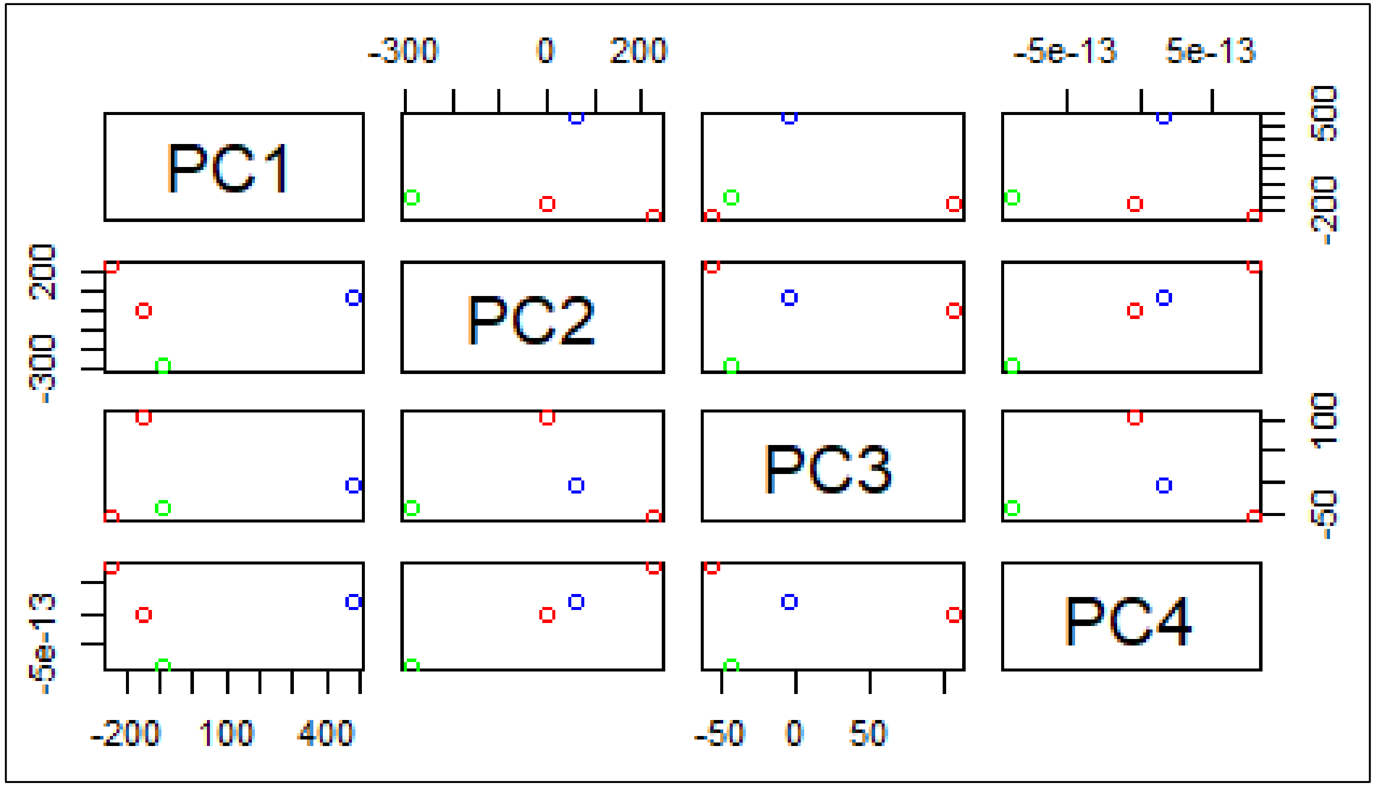
```
pca3d(PCA_Model_prcomp$x[,1:3],components = c(1,2,3), shape = 1,show.shapes = TRUE, show.ellipses = F,
ellipse.ci = 0.45, fancy = T)  # fancy = F for the second plot
#                  PC1        PC2        PC3          PC4
# England   -144.99315   2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164  58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915 224.646925 -56.475555  7.770000e-13
```



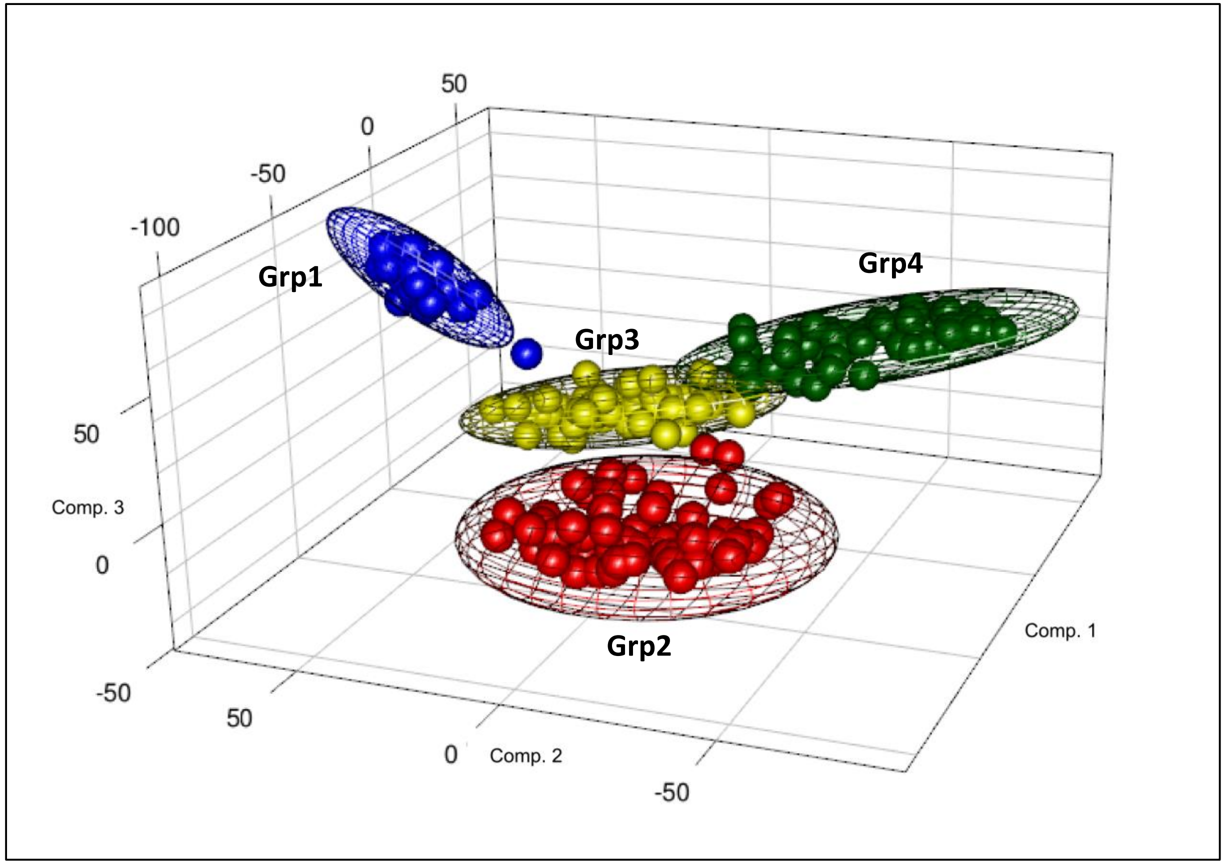


PCA visualisation – 2D using pairs()

```
pairs(PCA_Model_prcomp$x, col=c("red","blue","green"))
#                    PC1        PC2        PC3          PC4
# England   -144.99315   2.532999 105.768945 -3.765391e-14
# N Ireland  477.39164  58.901862  -4.877895  1.667659e-13
# Scotland   -91.86934 -286.081786 -44.415495 -8.860586e-13
# Wales     -240.52915 224.646925 -56.475555  7.770000e-13
```



PCA visualisation



PCA visualisation of groups identified using a consensus NMF clustering

220 samples with 17 features

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PCA analysis using FactoMineR() package

```
PCA_Model_Input_Dataset <- PCA(Input_dataset, scale.unit = TRUE, ncp = 17, graph = TRUE)
# Rows are individuals and columns are numeric variables, ncp: number of dimensions

print(PCA_Model_Input_Dataset)
```

PCA analysis using FactoMineR() package

```
PCA_Model_Input_Dataset <- PCA(Input_dataset, scale.unit = TRUE, ncp = 17, graph = TRUE)
# Rows are individuals and columns are numeric variables, ncp: number of dimensions

print(PCA_Model_Input_Dataset)
```

```
** Results for the Principal Component Analysis (PCA)
** The analysis was performed on 4 individuals, described  by 17
variables
* The results are available in the following objects:
    name description
1 "$eig" "eigenvalues"
2 "$var" "results for the variables“
3 "$var$coord" "coord. for the variables“
4 "$var$cor" "correlations variables - dimensions“
5 "$var$cos2" "cos2 for the variables“
```

Next page ...

PCA analysis using FactoMineR() package

```
PCA_Model_Input_Dataset <- PCA(Input_dataset, scale.unit = TRUE, ncp = 17, graph = TRUE)
# Rows are individuals and columns are numeric variables, ncp: number of dimensions

print(PCA_Model_Input_Dataset)
```

```
6 "$var$contrib" "contributions of the variables“
7 "$ind" "results for the individuals“
8 "$ind$coord" "coord. for the individuals"
9 "$ind$cos2" "cos2 for the individuals“
10 "$ind$contrib" "contributions of the individuals“
11 "$call" "summary statistics“
12 "$call$centre" "mean of the variables“
13 "$call$ecart.type" "standard error of the variables"
14 "$call$row.w" "weights for the individuals"
15 "$call$col.w" "weights for the variables"
```

Eigenvalues and percentage of variance

PCA_Model_Input_Dataset$eig

	eigenvalue	percentage of variance	cumulative percentage of variance
comp 1	11.615738	68.32787	68.32787
comp 2	4.228119	24.87129	93.19916
comp 3	1.156143	6.80084	100.00000

Contribution of features to PCs

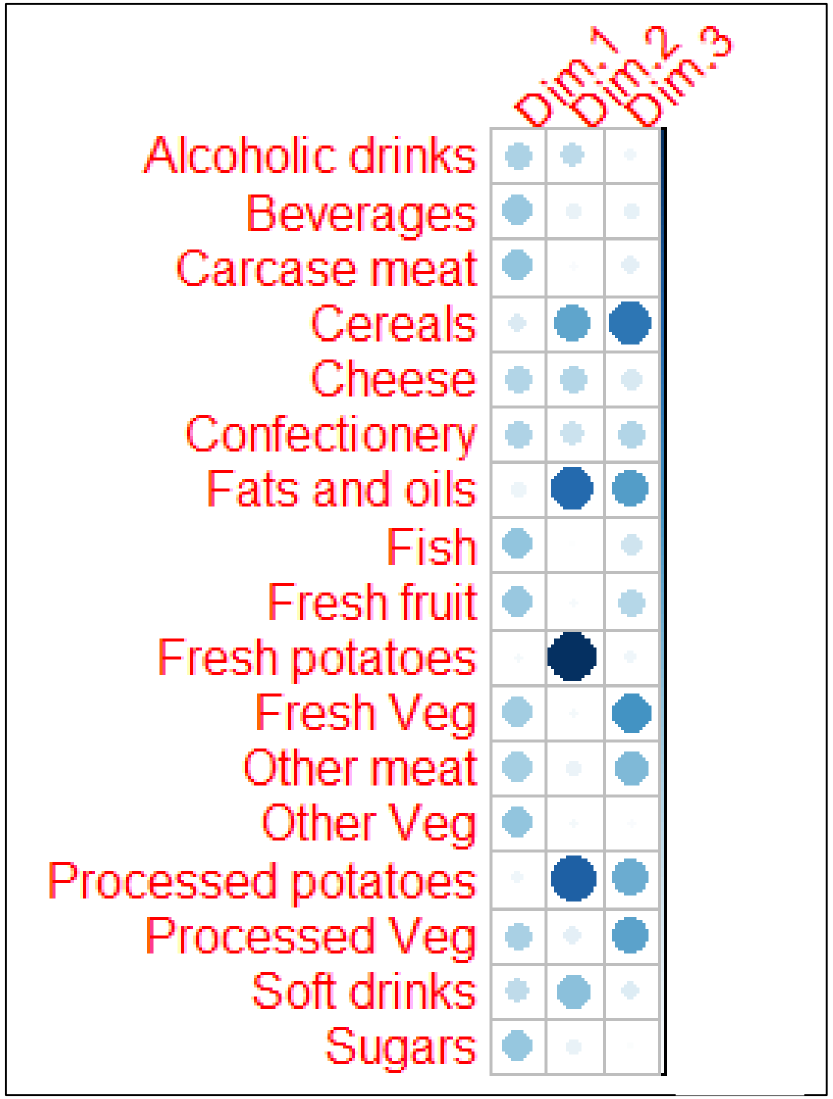
Question: how to assess the contribution of features to principal components

The larger the value of the contribution, the more the feature contributes to the component.

Variable (feature) contributions to PCs

```
corrplot(PCA_Model_Input_Dataset$var$contrib
, is.corr=F, method = "circle", addCoefasPercent
= T, mar = c(0, 0, 0, 0),number.font=1,
number.cex = 0.1, tl.offset = 0.2, tl.srt = 45,
cl.offset = 0.5,cl.align.text = "l")
```

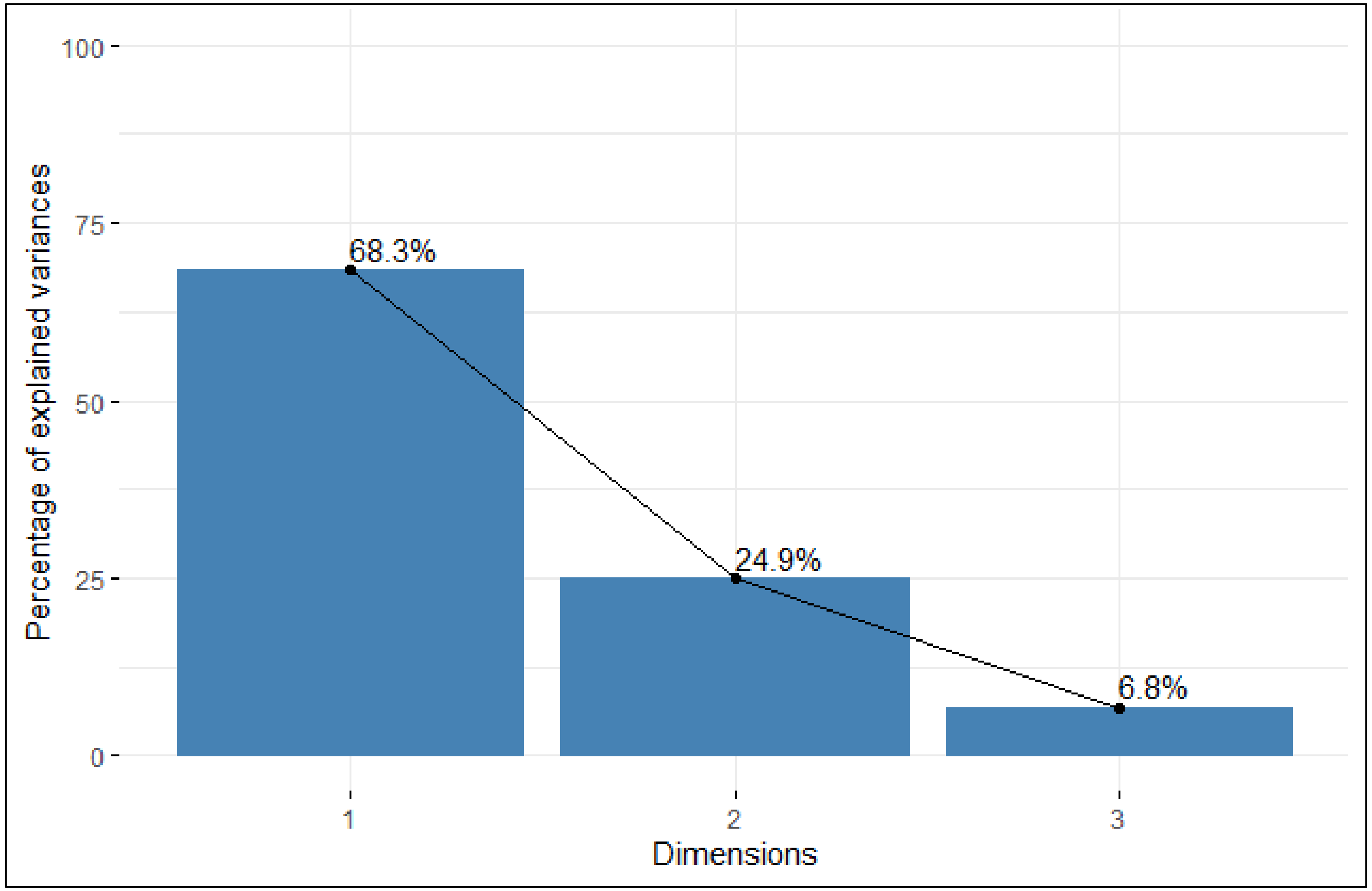
The larger the value of the contribution (bigger/darker), the more the feature contributes to the component.




```
library(corrplot)
```

PCA percentage of 3 principal components

Why 3 PCs?



fviz_eig(PCA_Model_Input_Dataset, addlabels = TRUE, ncp = 3, ylim = c(0, 100))

Consider 9126 samples with 440 features

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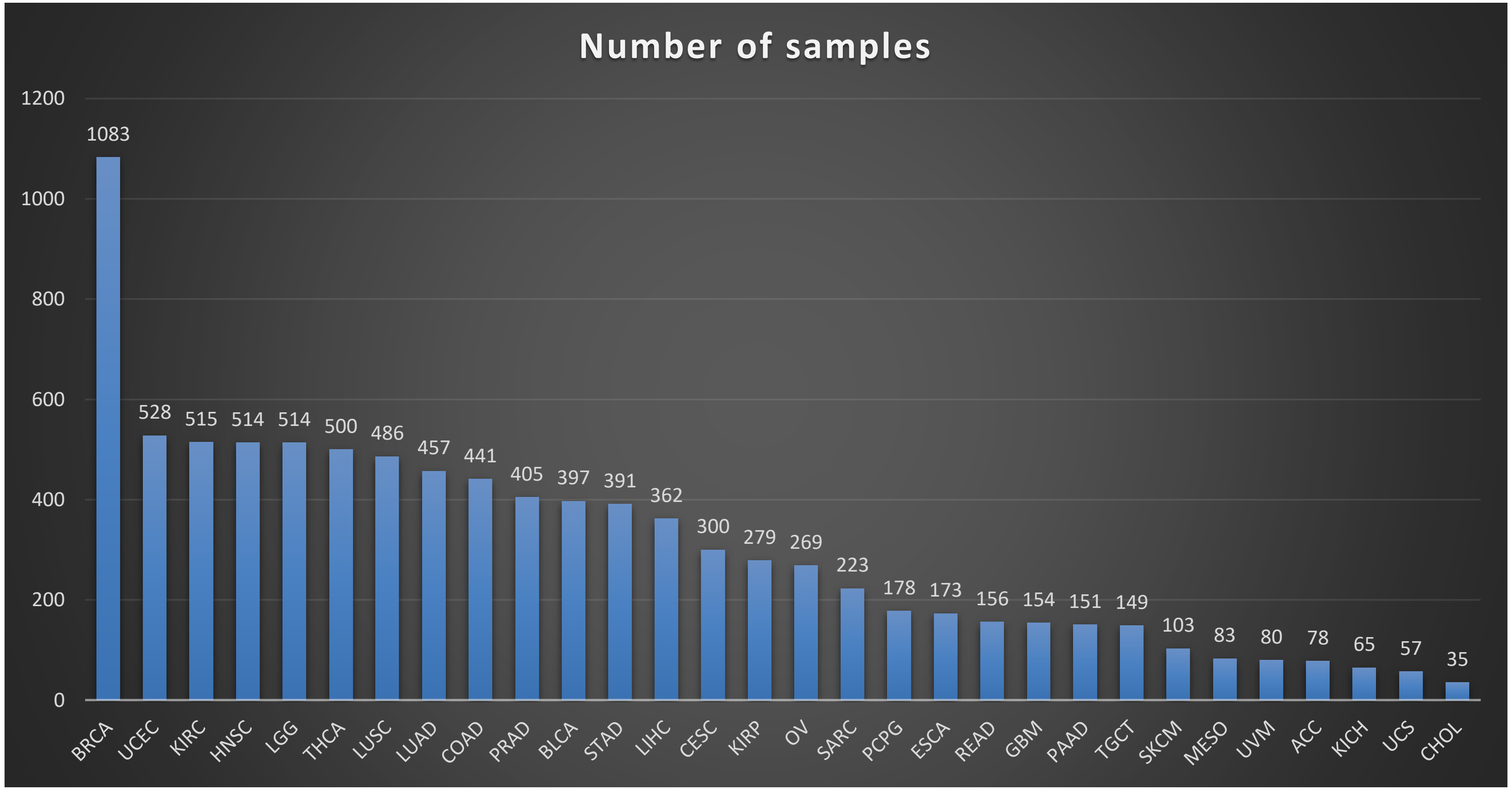
Sample distribution across cancers (n=9126)

BRCA: Breast Invasive Carcinoma
UCEC: Uterine Corpus Endometrial Carcinoma
KIRC: Kidney Renal Clear Cell Carcinoma
HNSC: Head and Neck Squamous Cell Carcinoma
LGG: Low Grade Glioma
THCA: Thyroid Carcinoma
LUSC: Lung Squamous Cell Carcinoma
LUAD: Lung Adenocarcinoma
COAD: Colon Adenocarcinoma
PRAD: Prostate Adenocarcinoma
BLCA: Bladder Urothelial Carcinoma
STAD: Stomach Adenocarcinoma
LIHC: Liver Hepatocellular Carcinoma
CESC: Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma
KIRP: Kidney Renal Papillary Cell Carcinoma
OV: Ovarian Cancer
SARC: Sarcoma
PCPG: Pheochromocytoma and Paraganglioma
ESCA: Esophageal (Oesophageal) Carcinoma
READ: Rectum Adenocarcinoma
GBM: Glioblastoma Multiforme
PAAD: Pancreatic Adenocarcinoma
TGCT: Testicular Germ Cell Tumours
SKCM: Skin Cutaneous Melanoma
MESO: Mesothelioma
UVM: Uveal Melanoma
ACC: Adrenocortical carcinoma
KICH: Kidney Chromophobe
UCS: Uterine Carcinosarcoma
CHOL: Cholangiocarcinoma

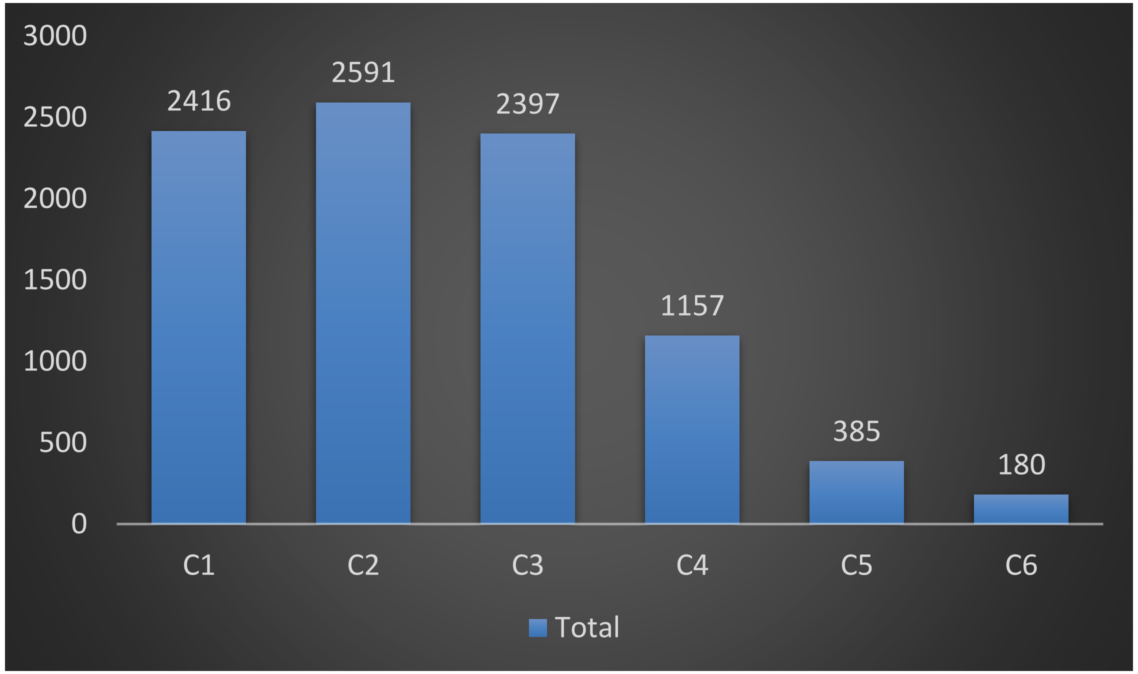


Samples from below cancers (hematologic) without any immune subtypes

DLBC: Diffuse Large B-cell Lymphoma
LAML: Acute Myeloid Leukemia
THYM: Thymoma

Sample distribution across immune subtype (n=9126)

Immune subtype	Number of samples in each immune subtype
C1	2416
C2	2591
C3	2397
C4	1157
C5	385
C6	180



Imbalance data across 5 classes

Penalising c5 and c6, imbalanced data/classifier

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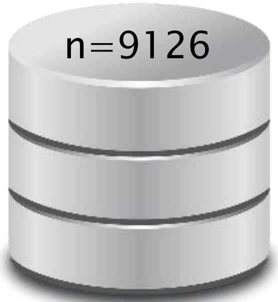
Consider 9126 samples with 440 features



RNA-seq (FPKM), **6 immune subgroups**
440 genes (5 signatures)

- MultipleImputationModelling()
- Dataset_Spilitter() including
- TCGA_Cancer_Immune_Subtypes()
- TCGA_Gene_Signature()
- Index_of_Sample_When_Spilit()

80%*

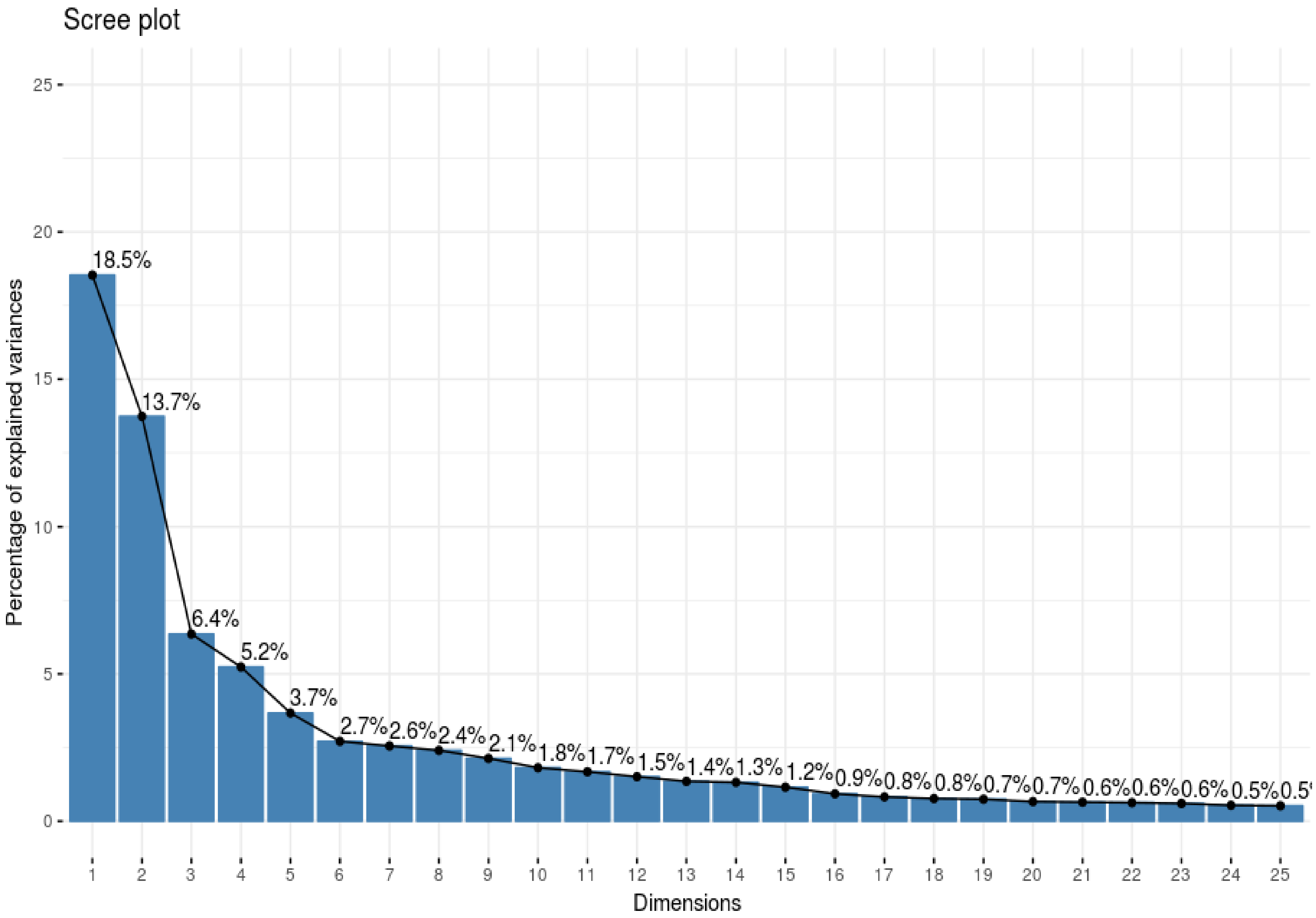
n=7302

Training/validation dataset

20%*

Test dataset (Unobserved data)

*80% - 20% of each class

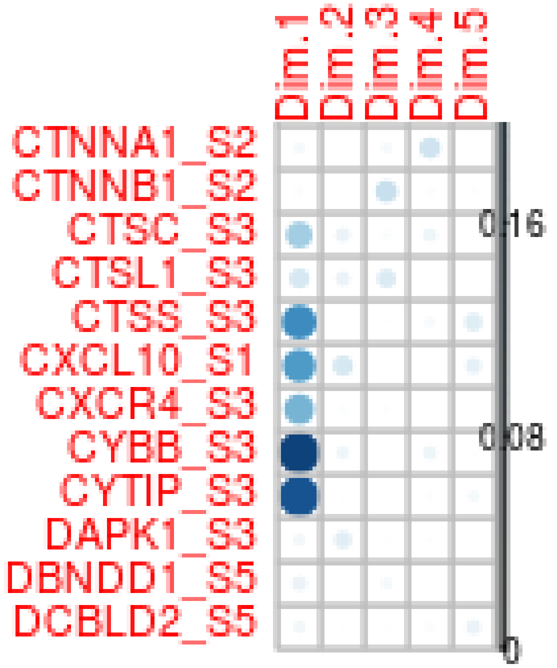


Variable (feature) contributions to PCs

n=7302 samples, 440 features (genes)

The larger the value of the contribution, the more the gene contributes to the component.

The most contributing features (genes) for each dimension



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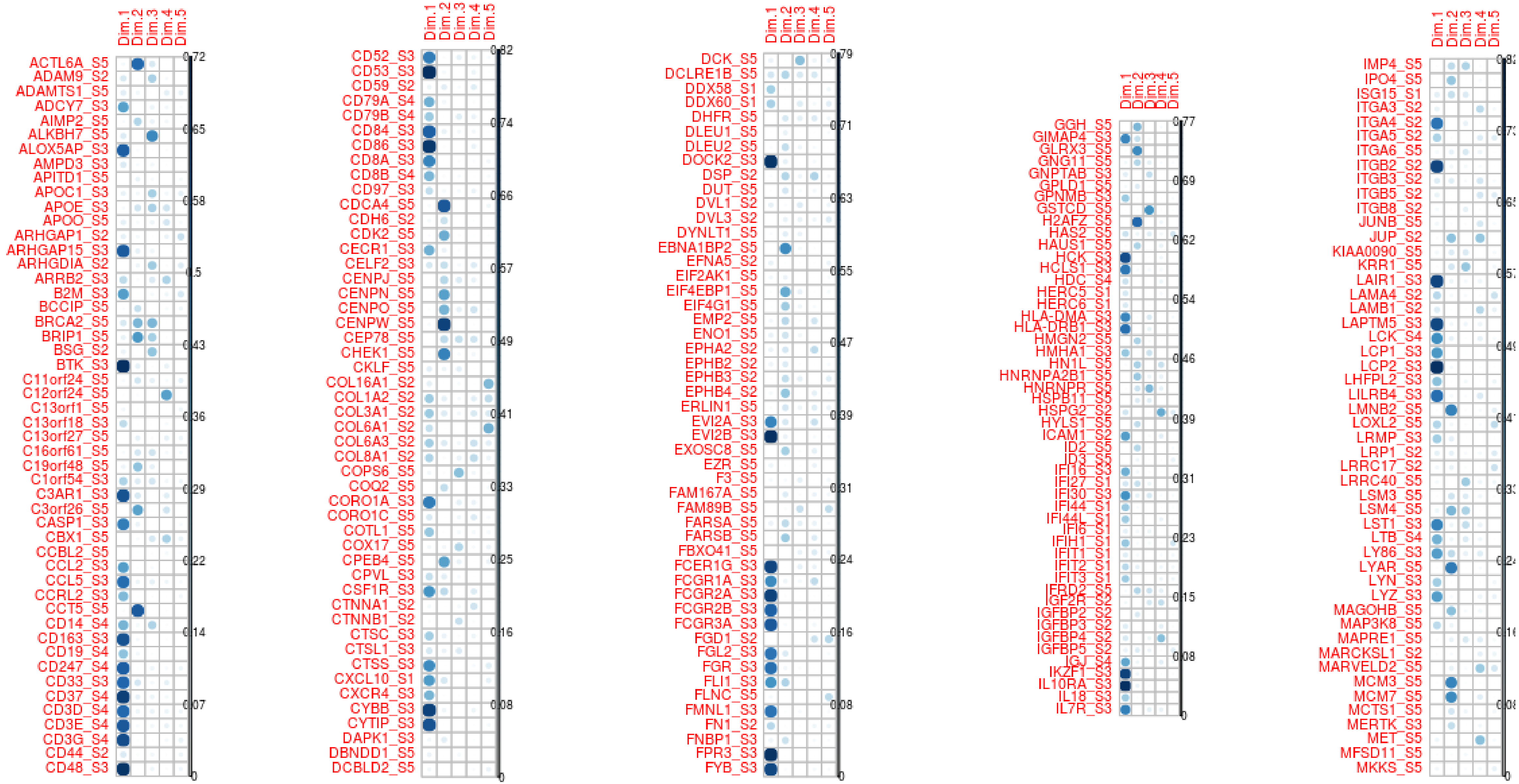
Variable (feature) contributions to PCs



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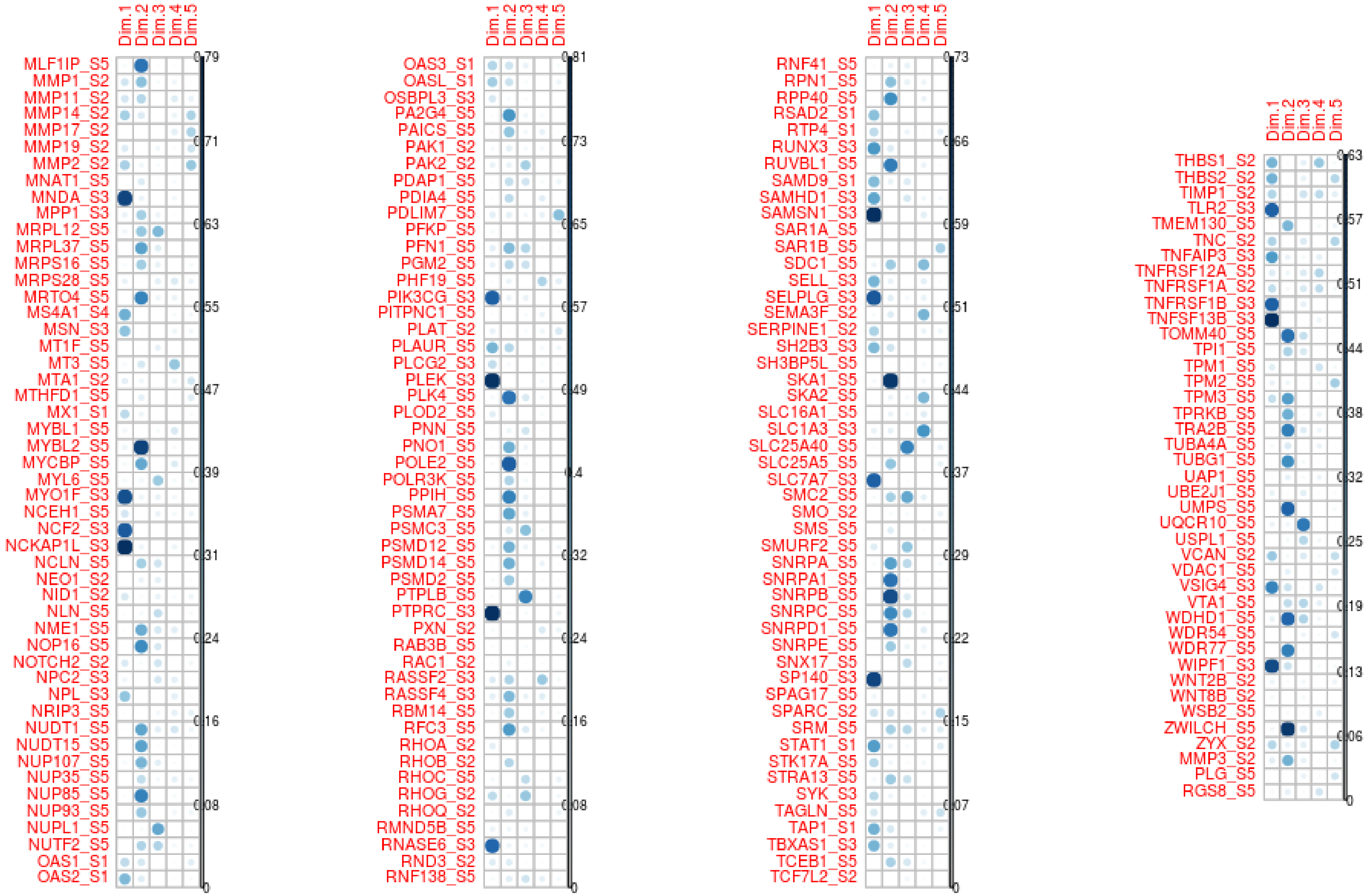
Variable (feature) contributions to PCs



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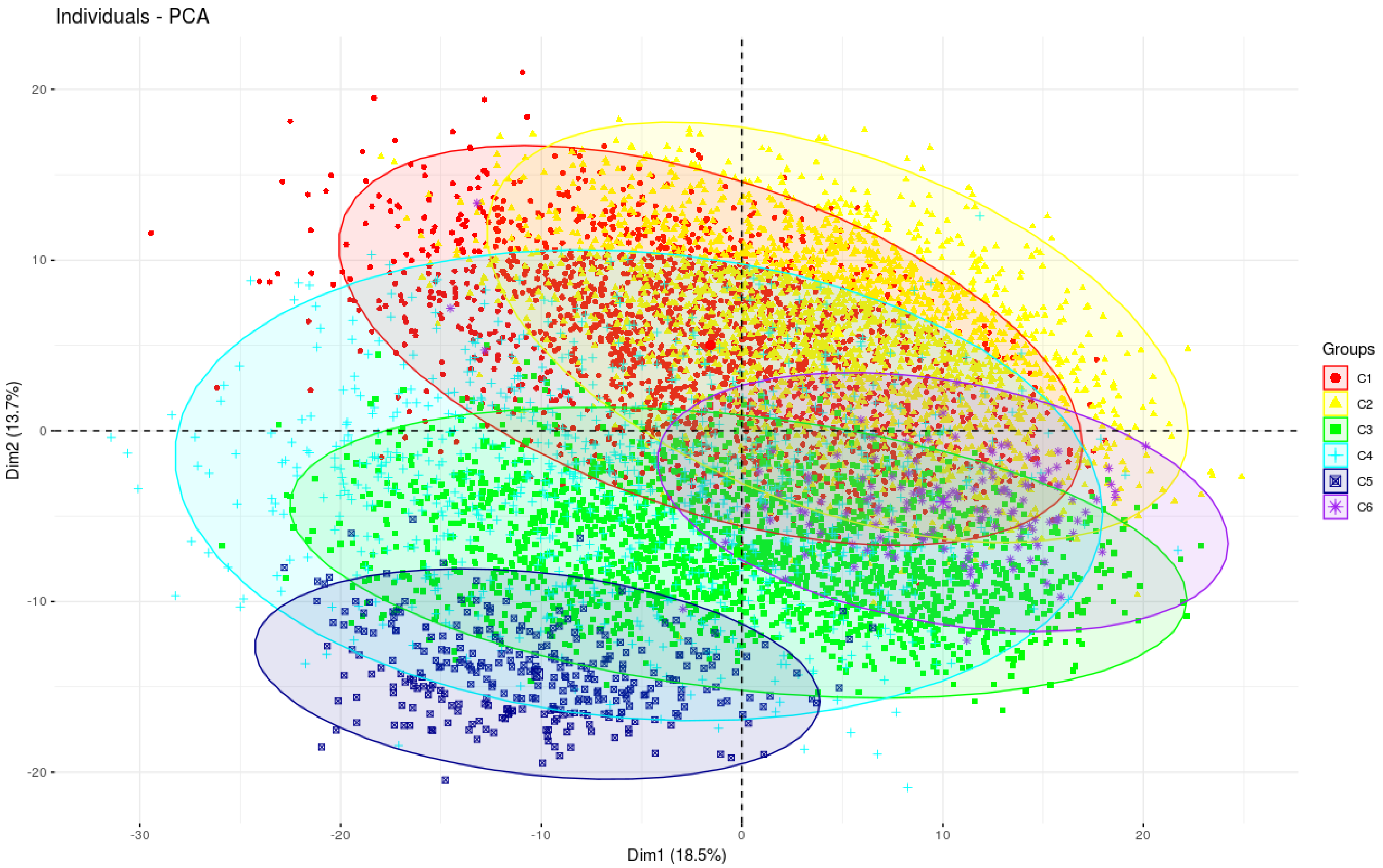
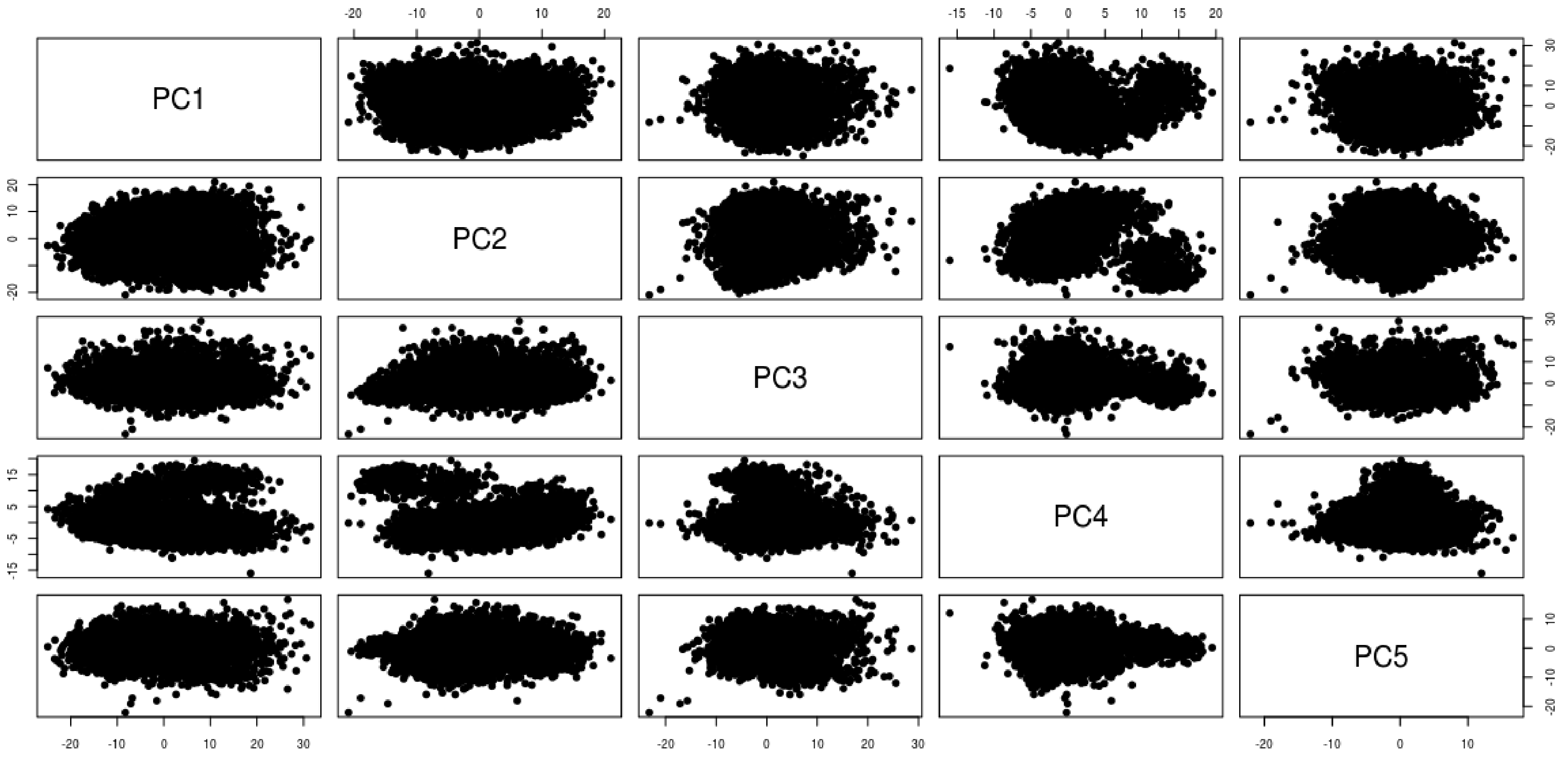
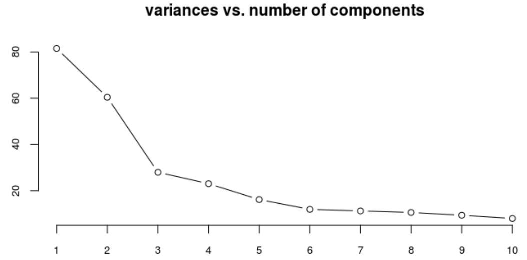
PCA visualisation – 2D



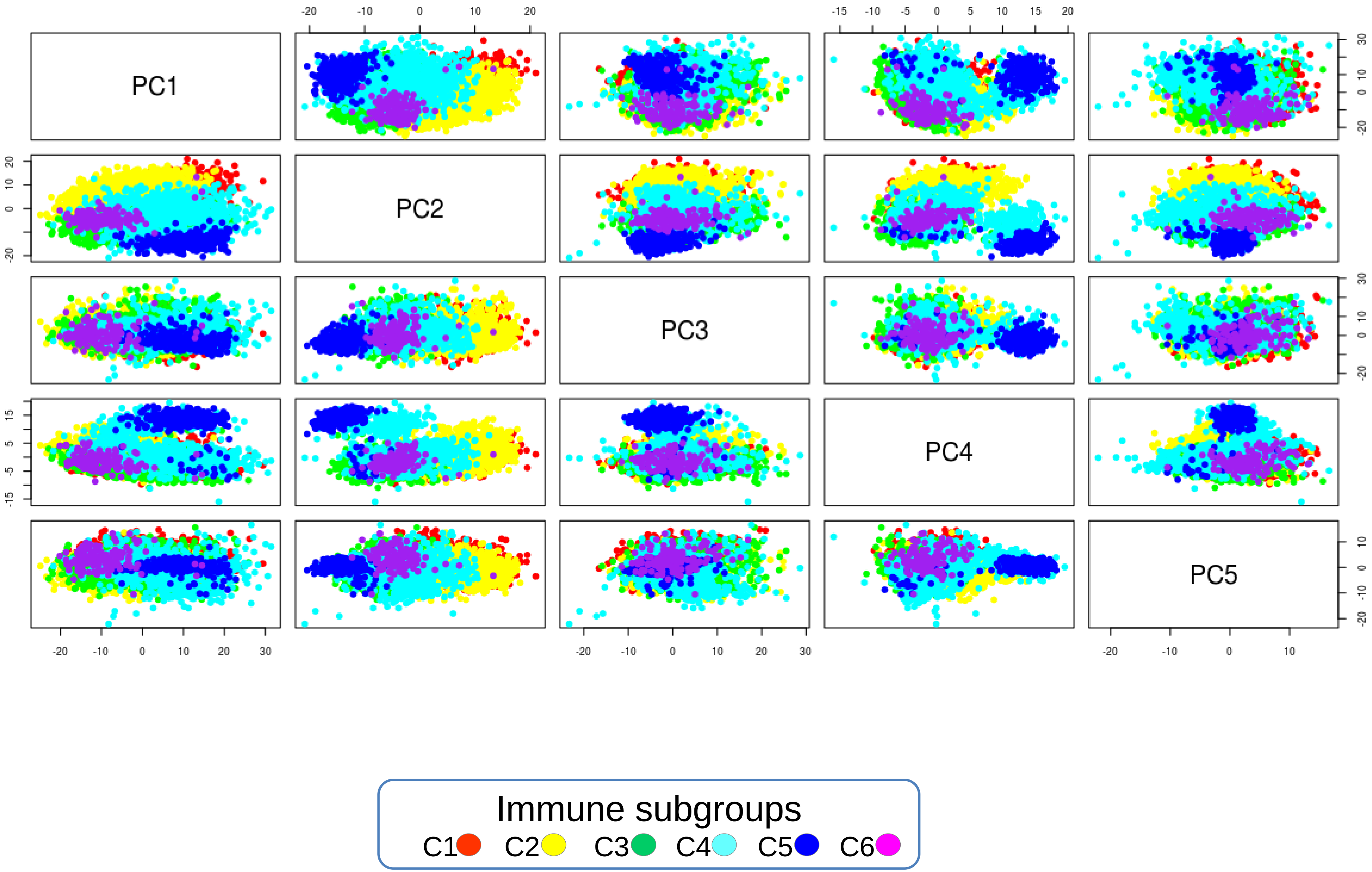
PCA visualisation – 2D





Immune subgroups
C1 C2 C3 C4 C5 C6

PCA visualisation – 2D



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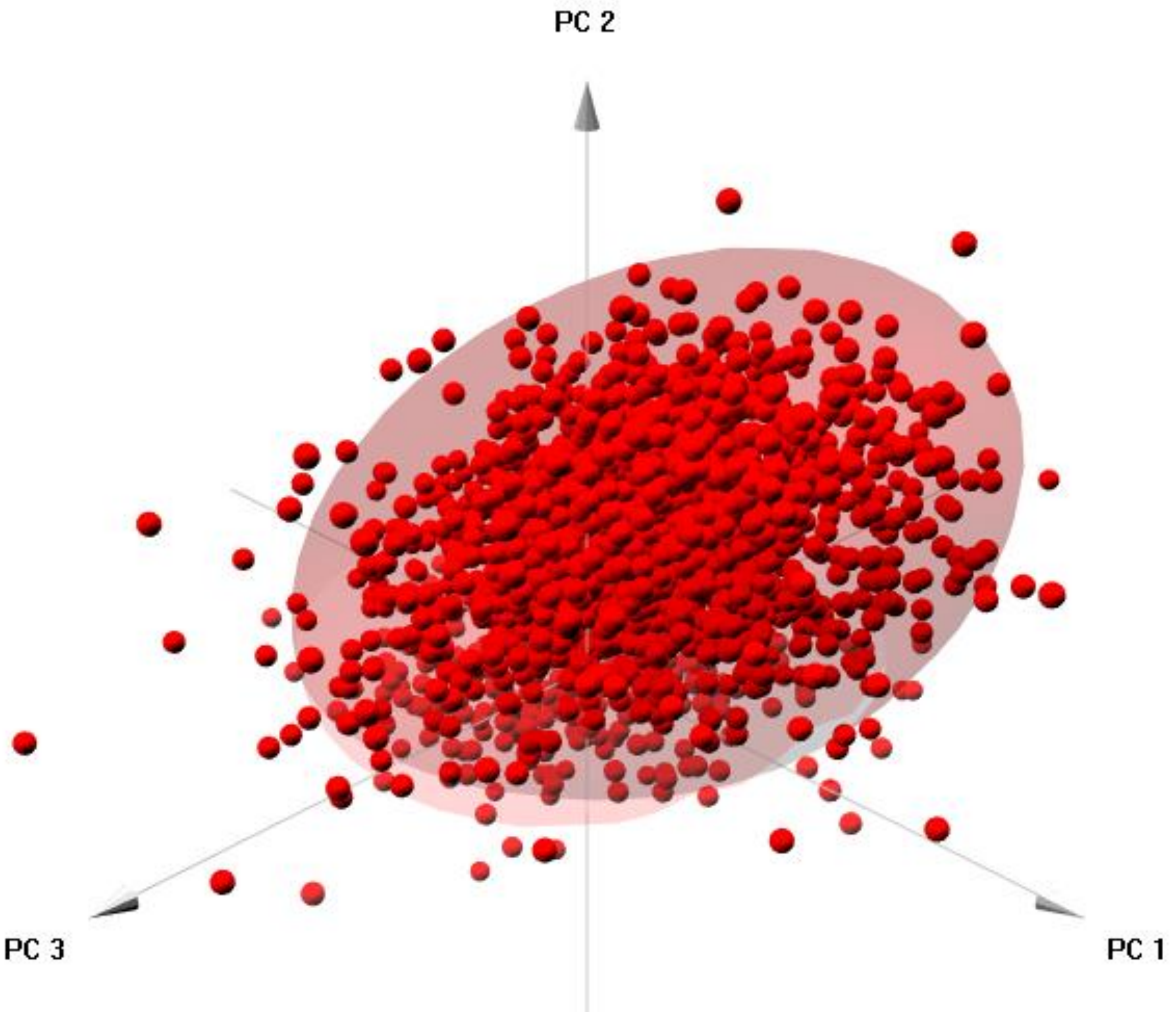
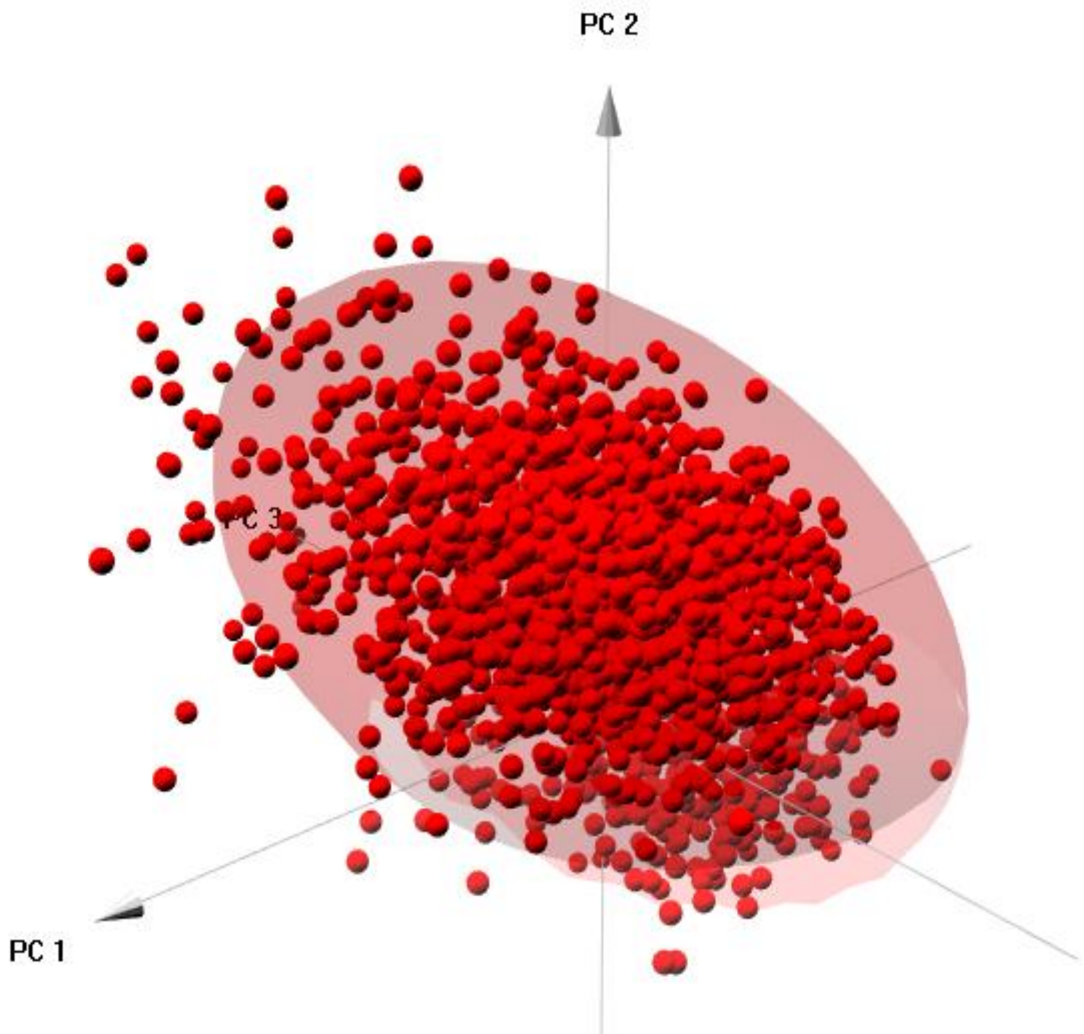
PCA visualisation of the C1 immune group (n=1933)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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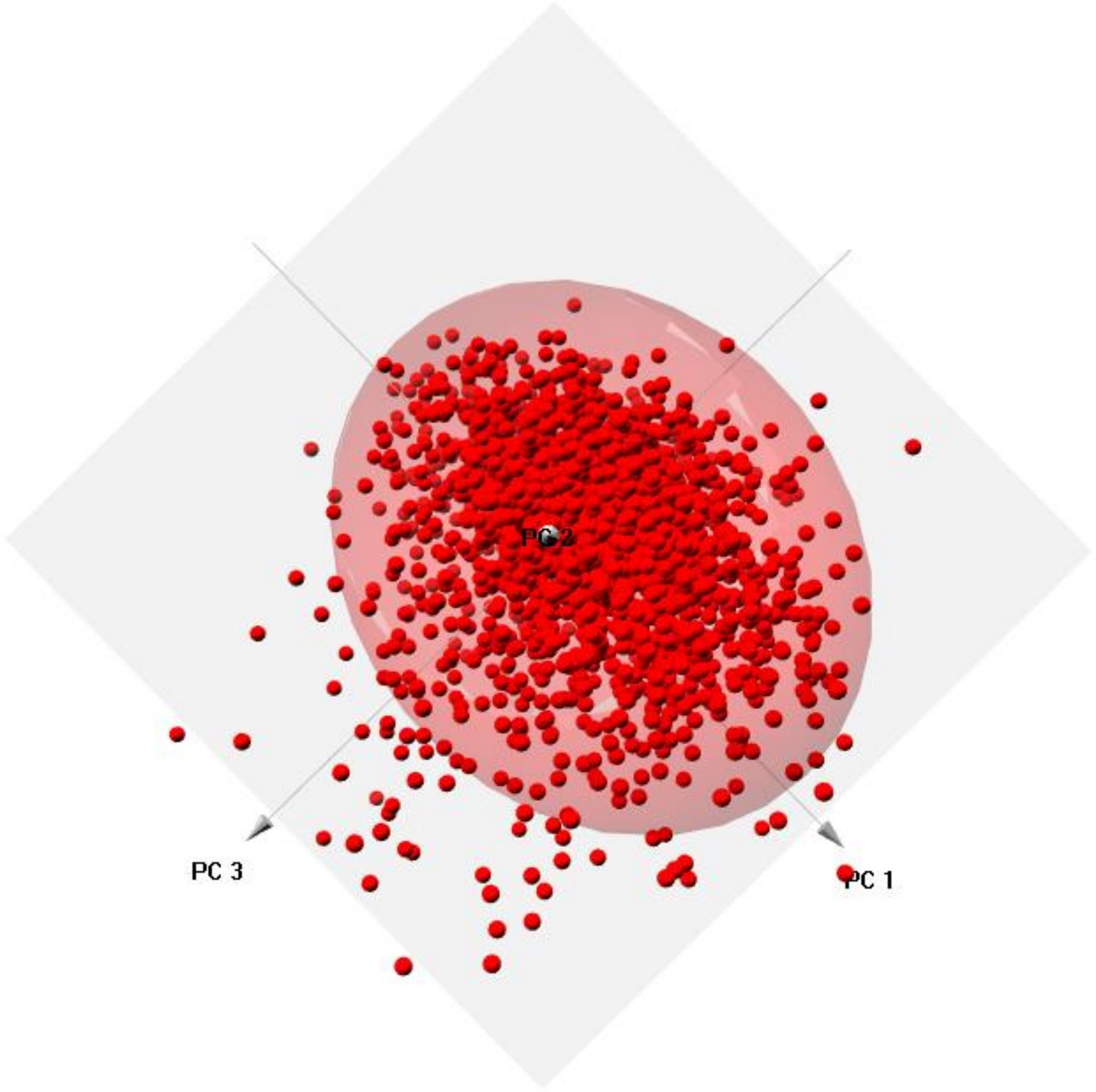
PCA visualisation of the C1 immune group (n=1933)

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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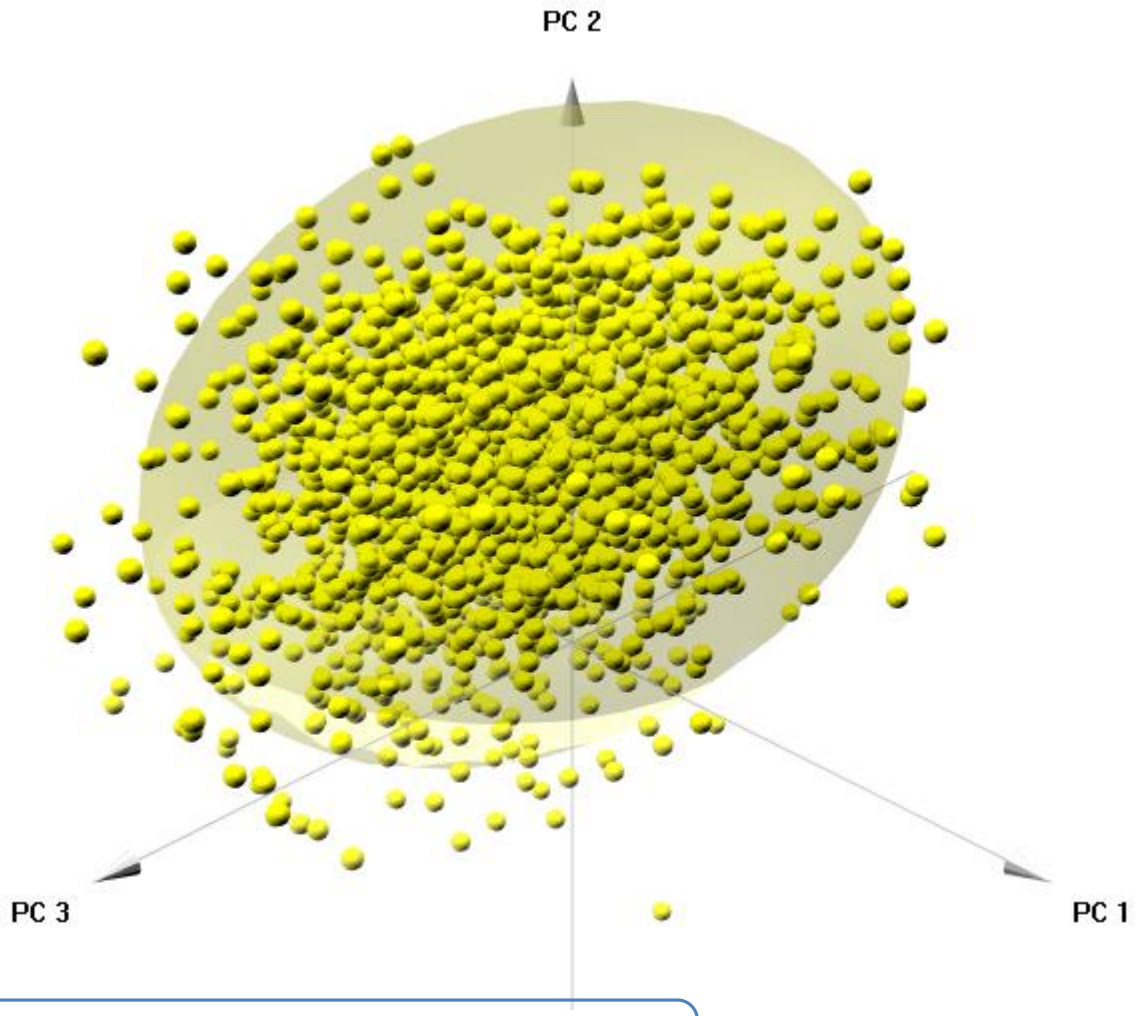
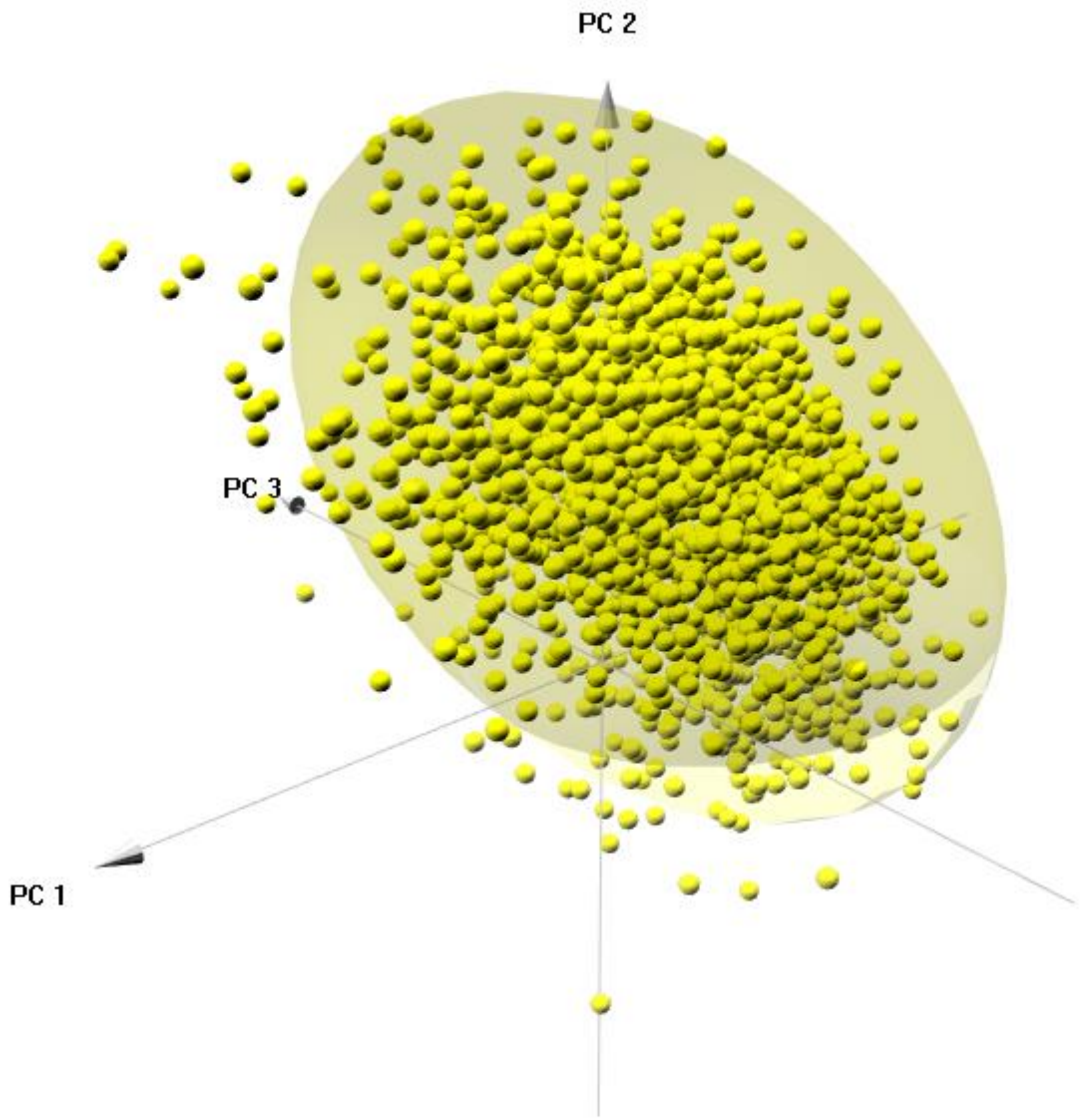
PCA visualisation of the C2 immune group (n=2073)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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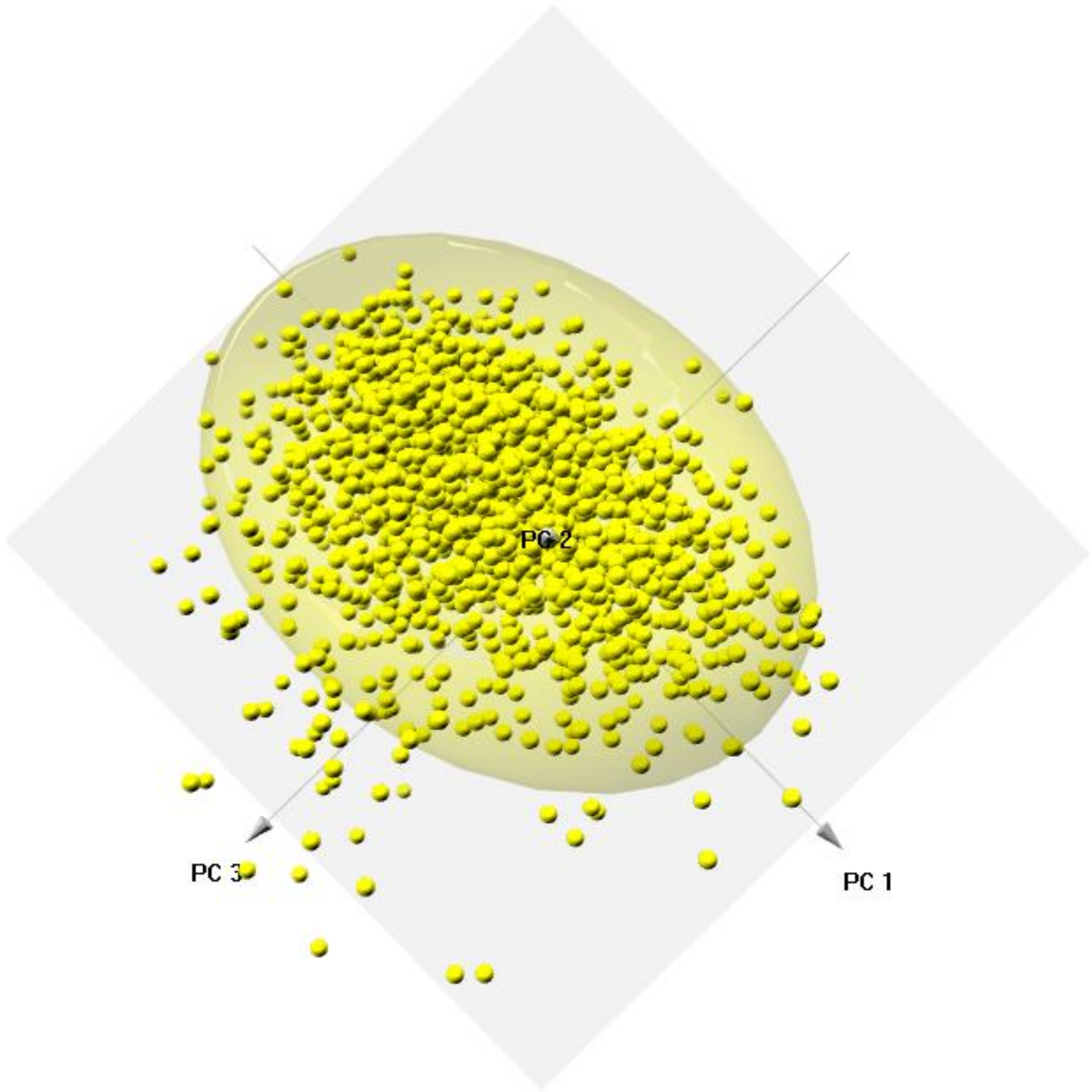
PCA visualisation of the C2 immune group (n=2073)
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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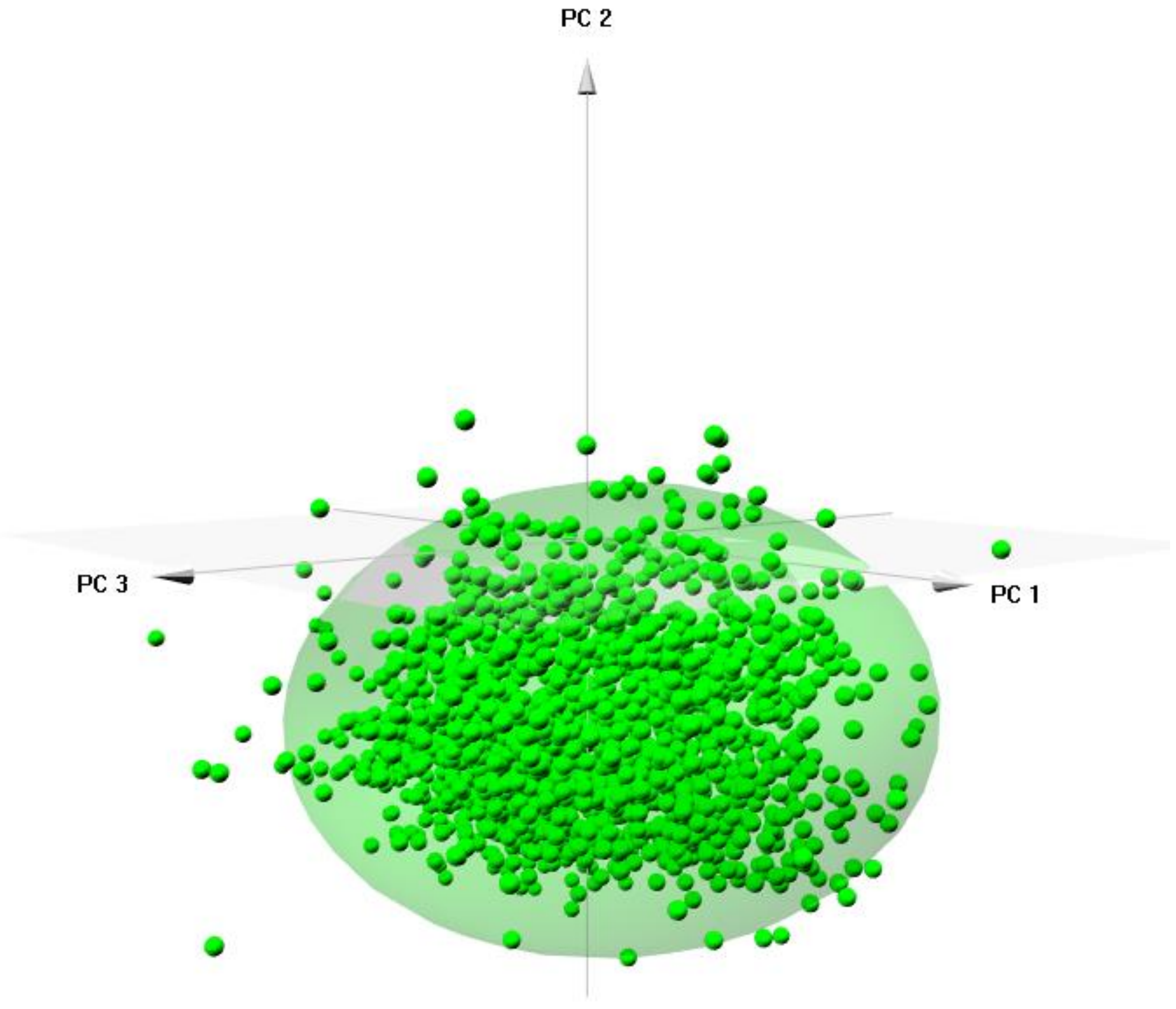
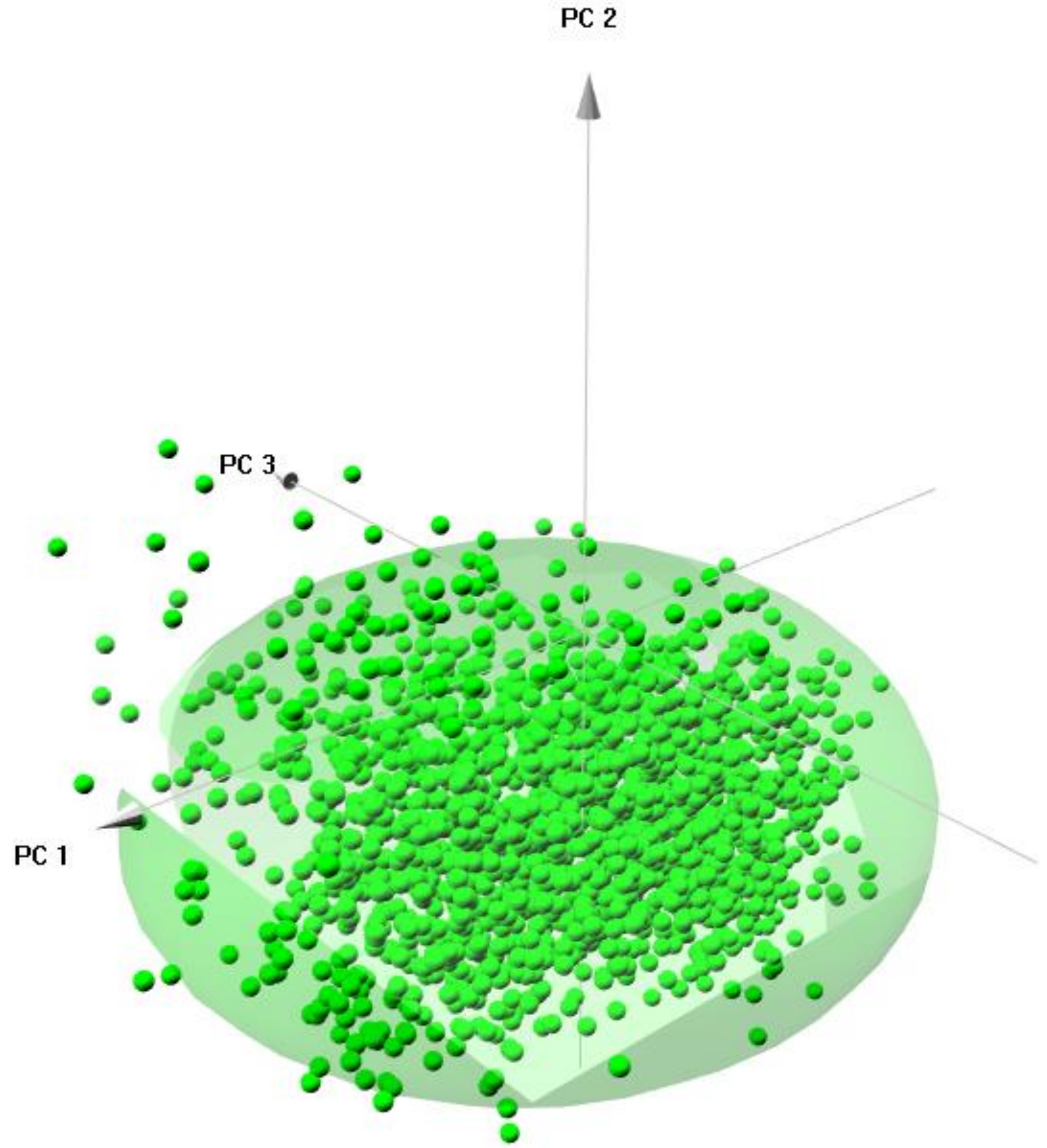
PCA visualisation of the C3 immune group (n=1918)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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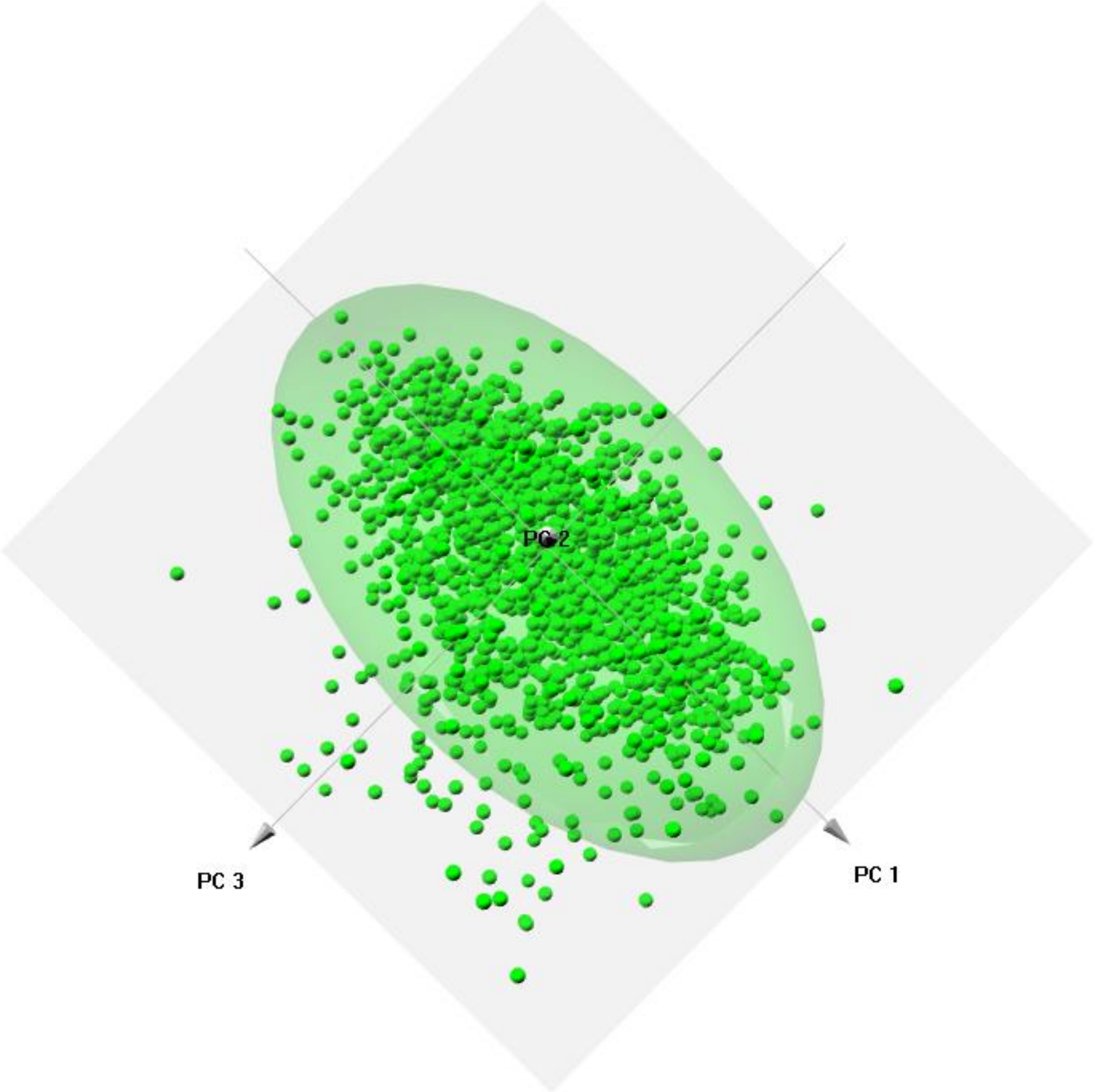
PCA visualisation of the C3 immune group (n=1918)

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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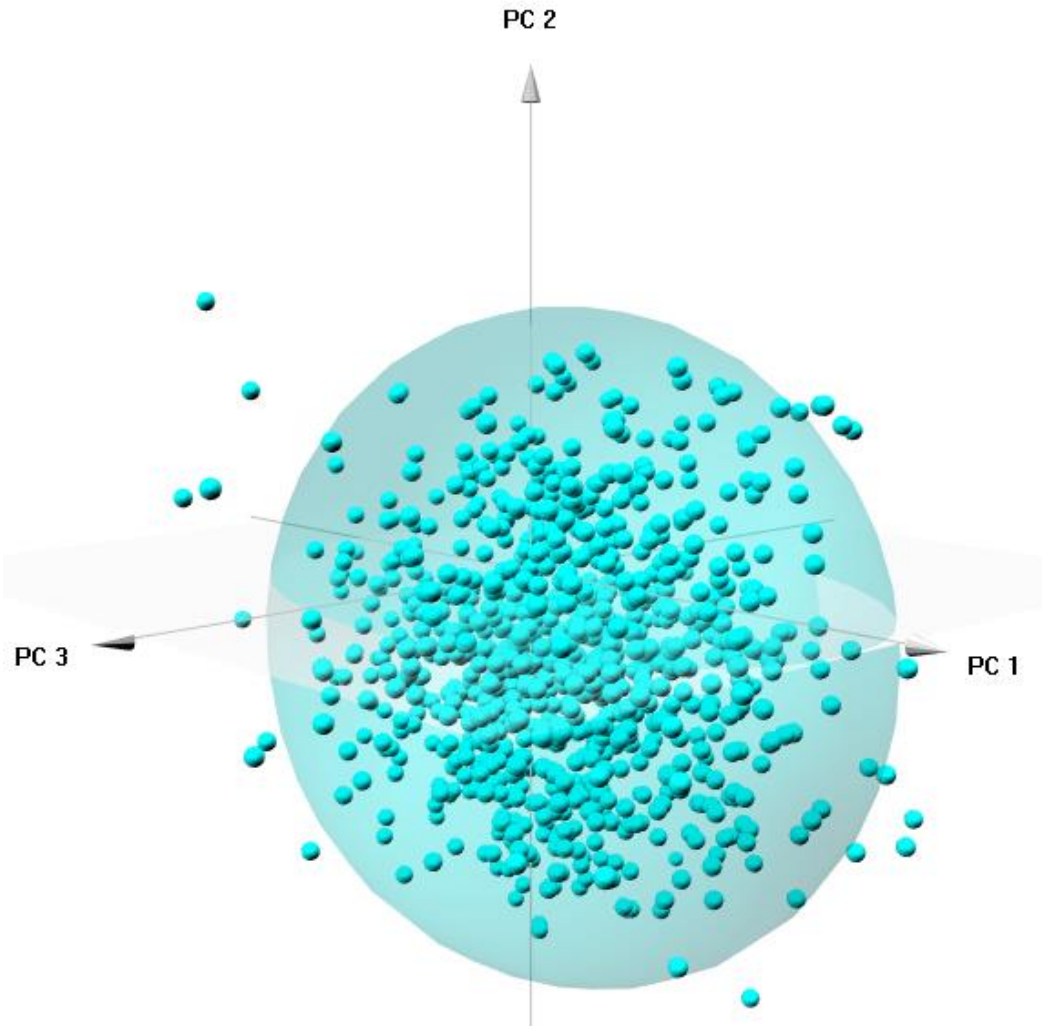
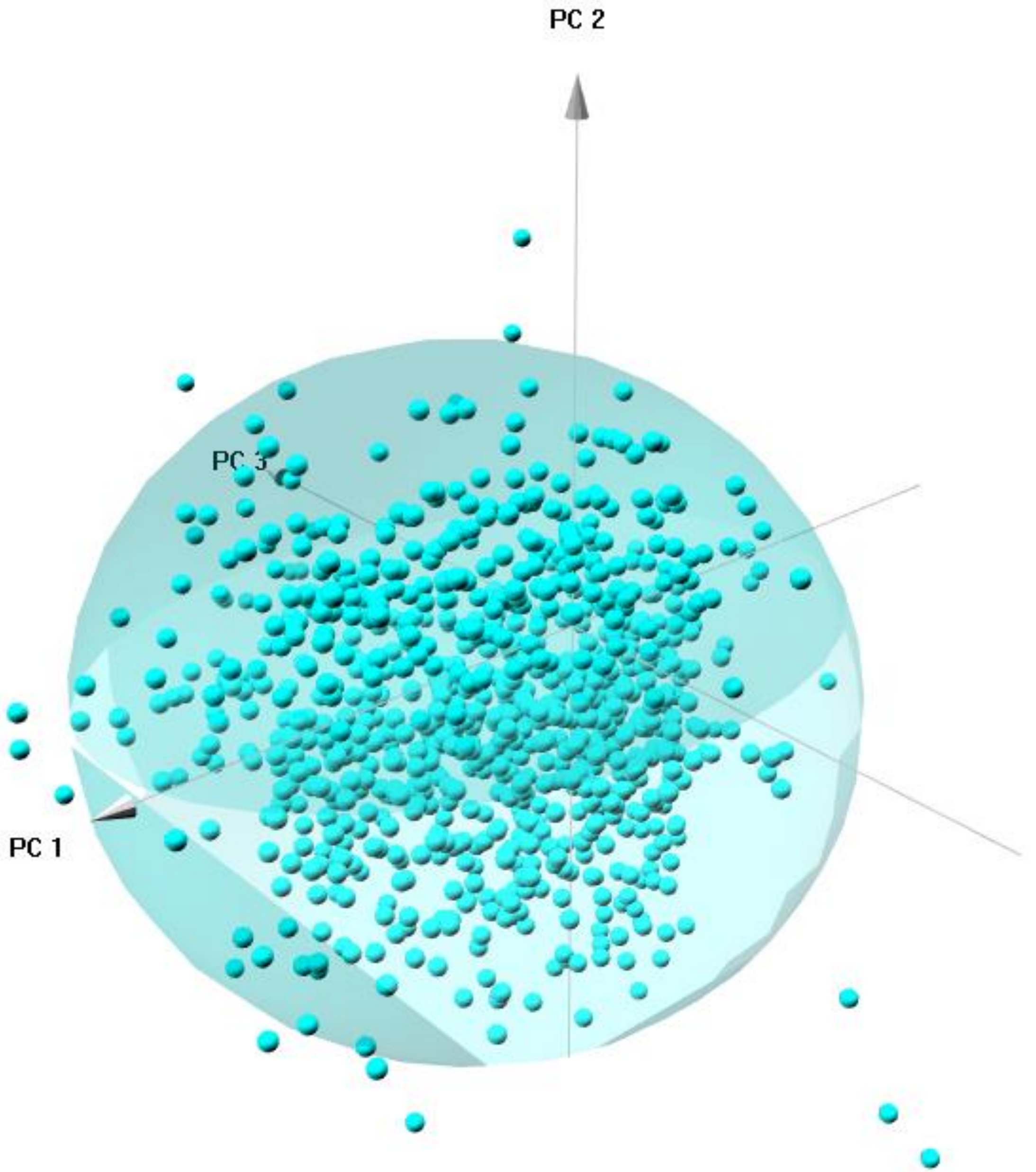
PCA visualisation of the C4 immune group (n=926)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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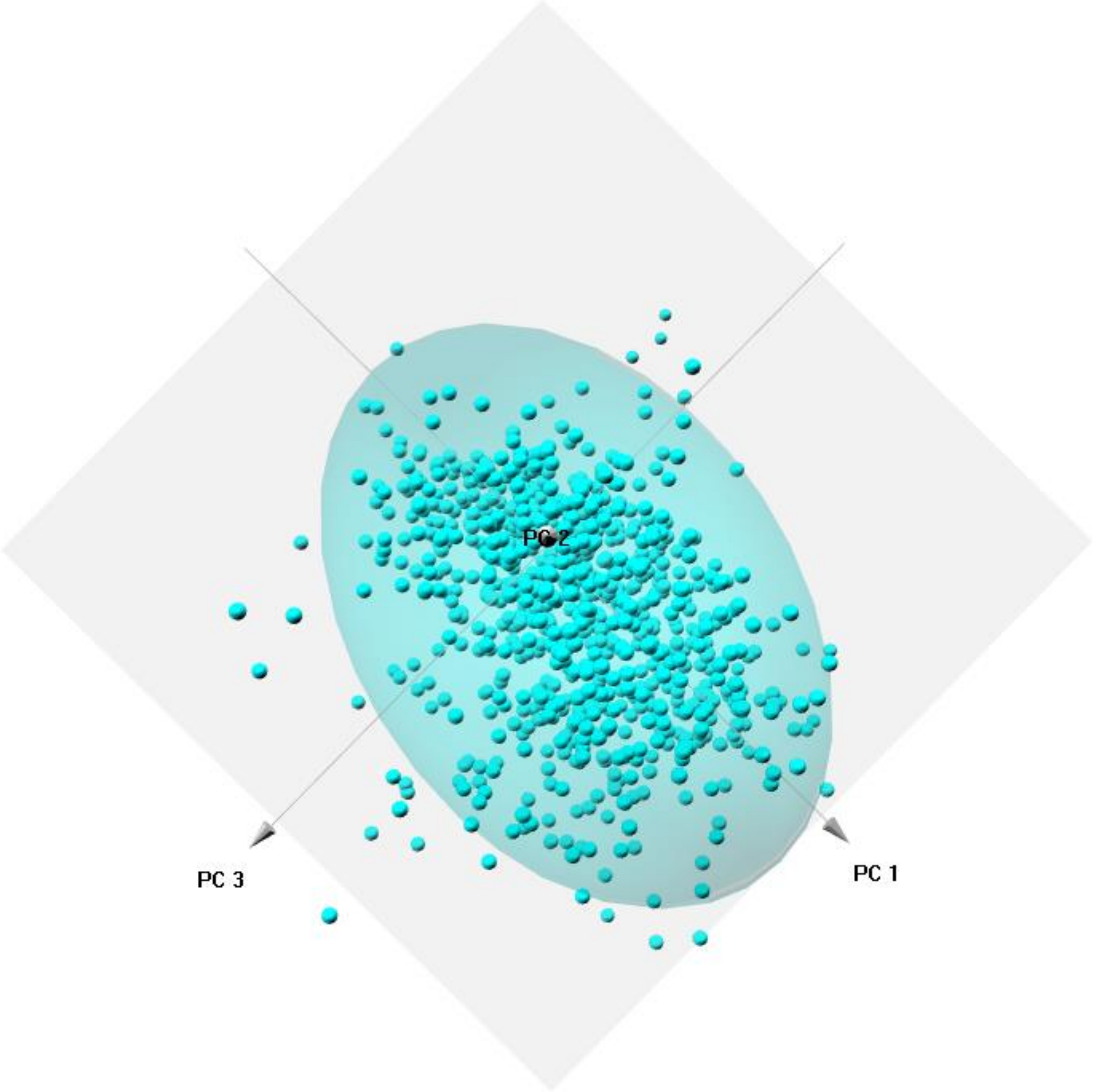
PCA visualisation of the C4 immune group (n=926)

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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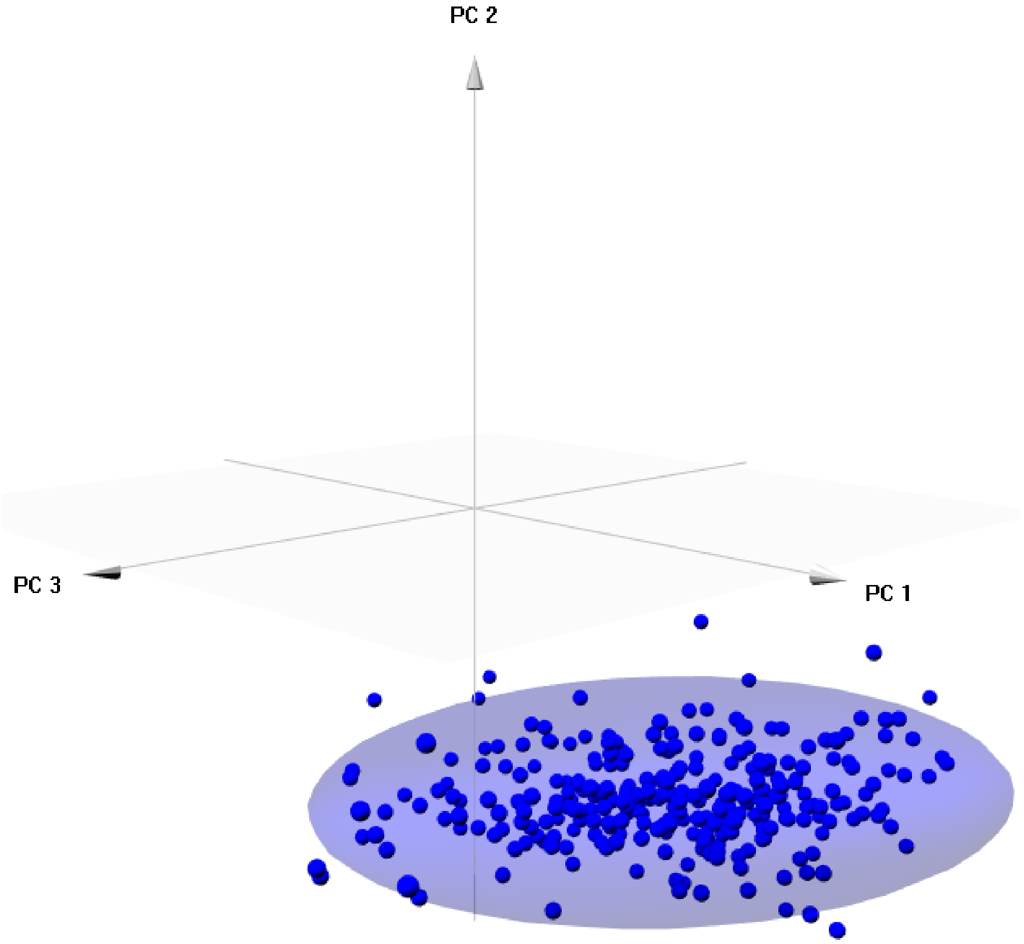
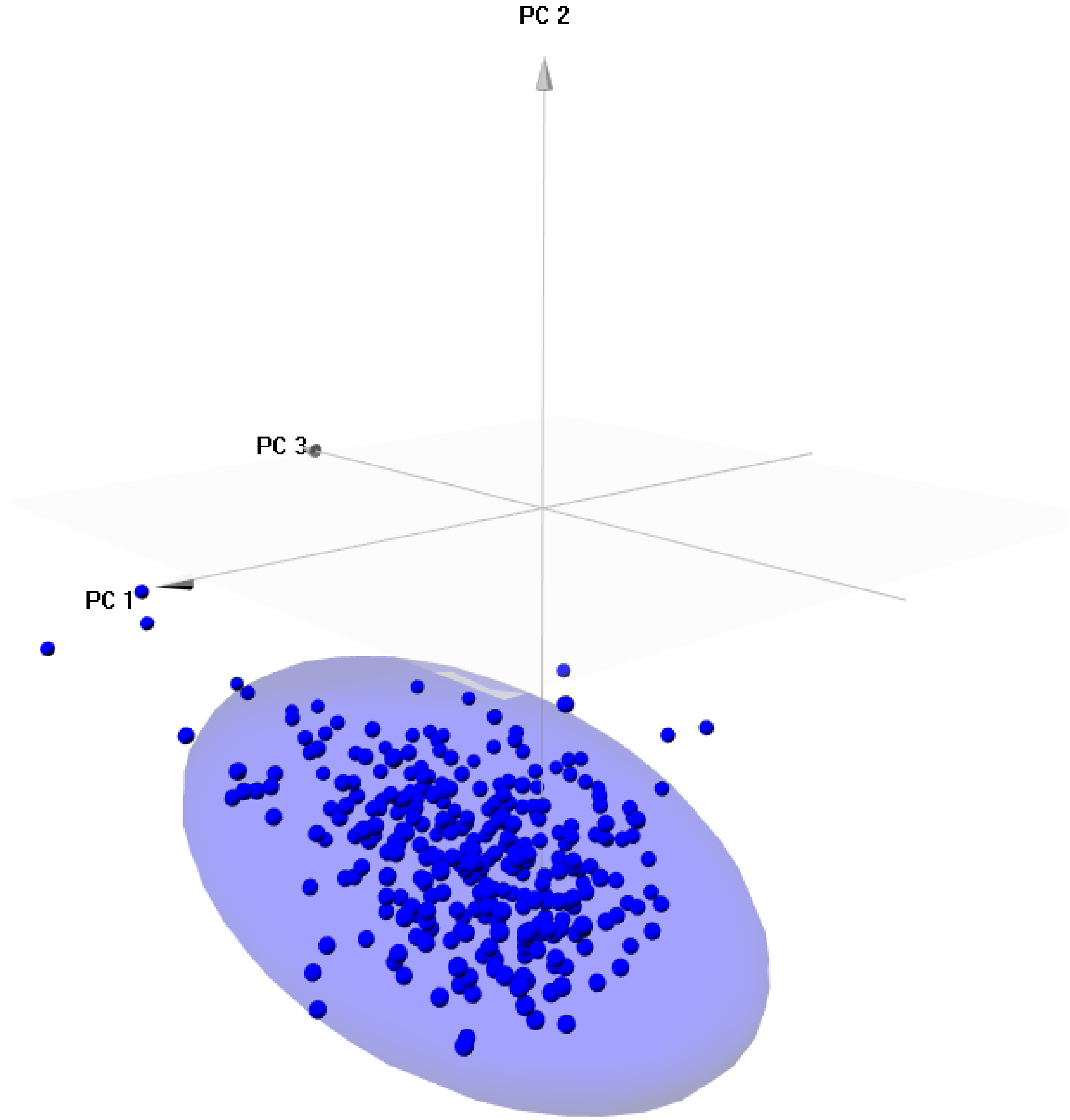
PCA visualisation of the C5 immune group (n=308)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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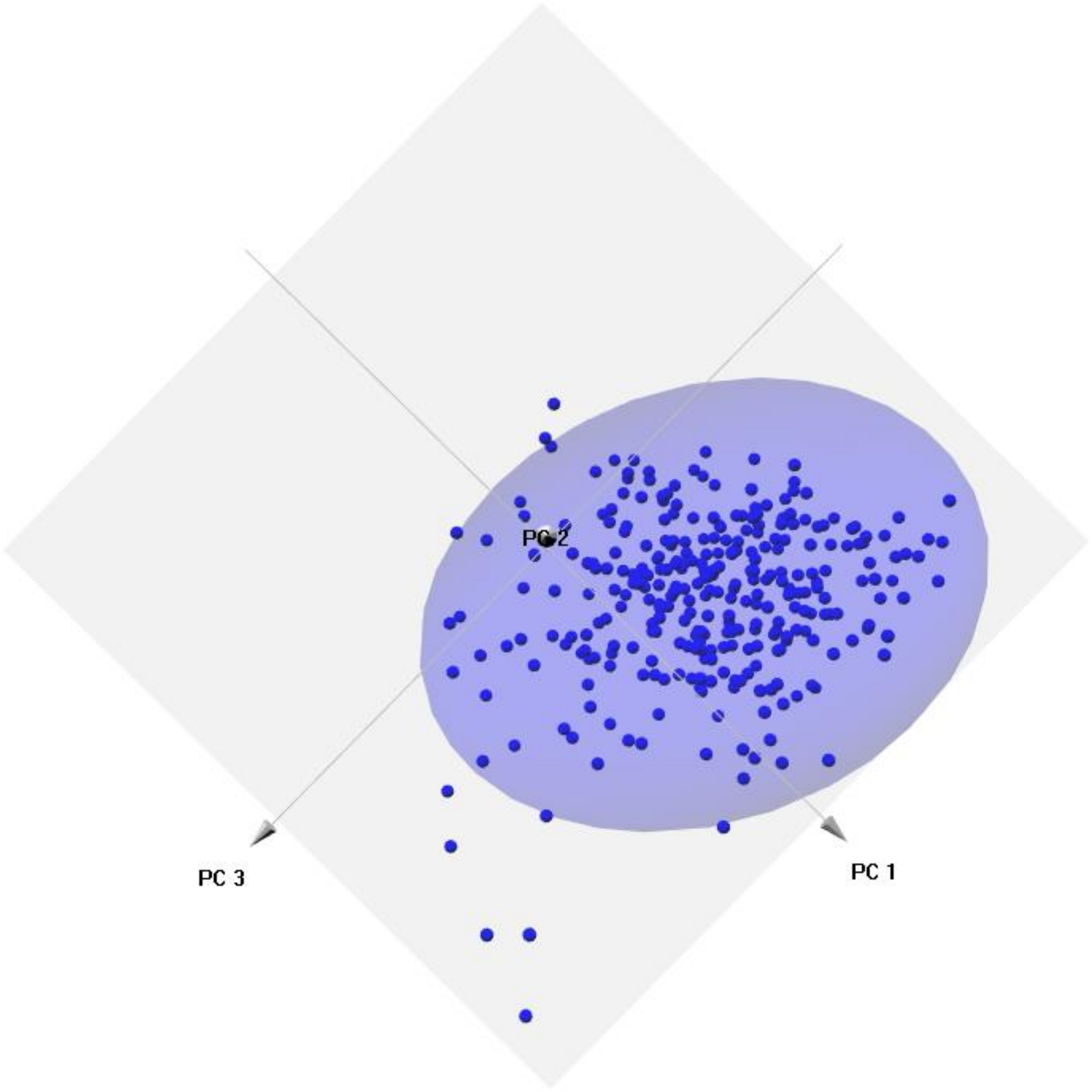
PCA visualisation of the C5 immune group (n=308)

(PC1, PC2 & PC3)



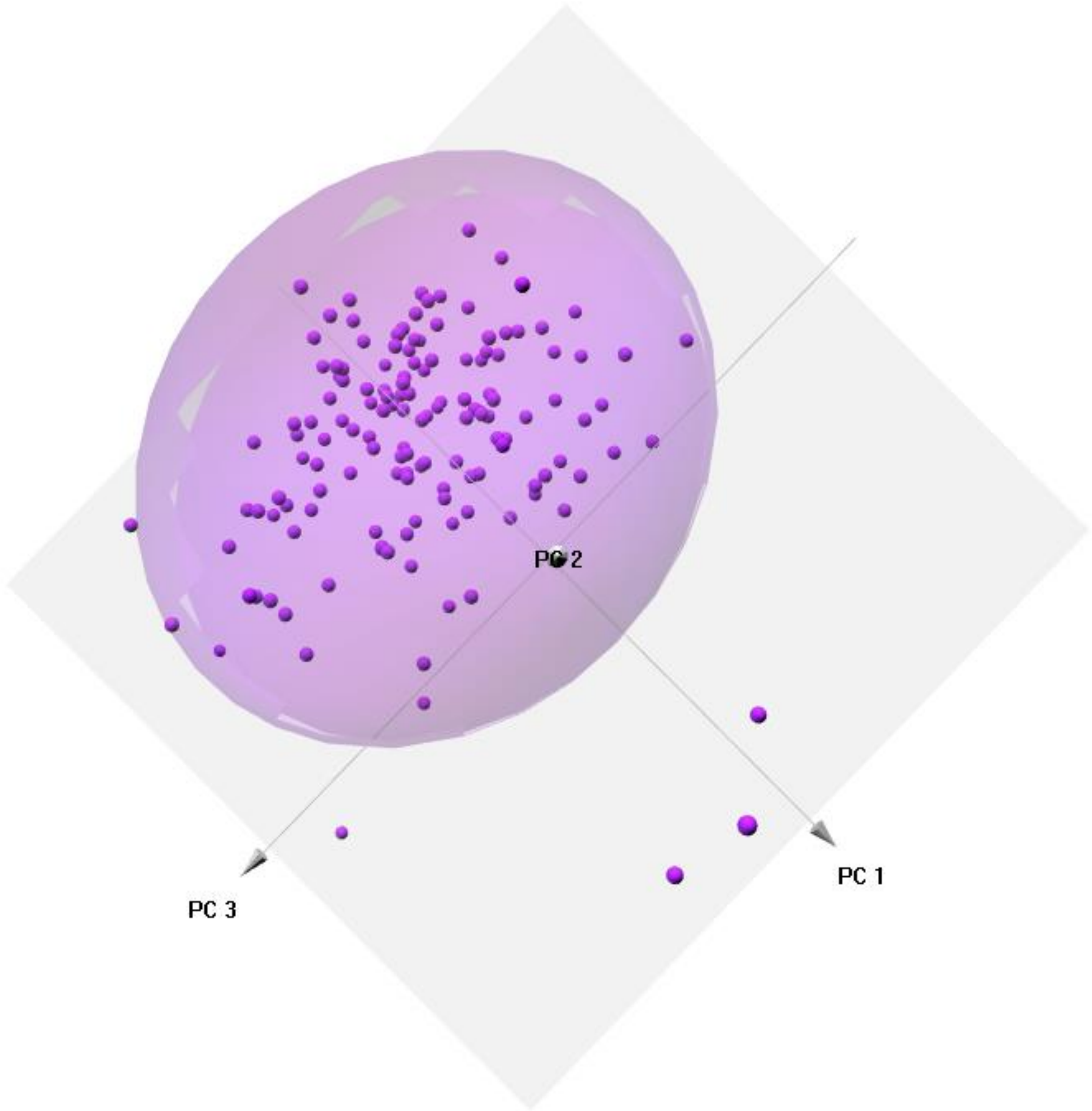
Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the “Immune Landscape of Cancer” paper

PCA visualisation of the C6 immune group (n=144)

(PC1, PC2 & PC3)

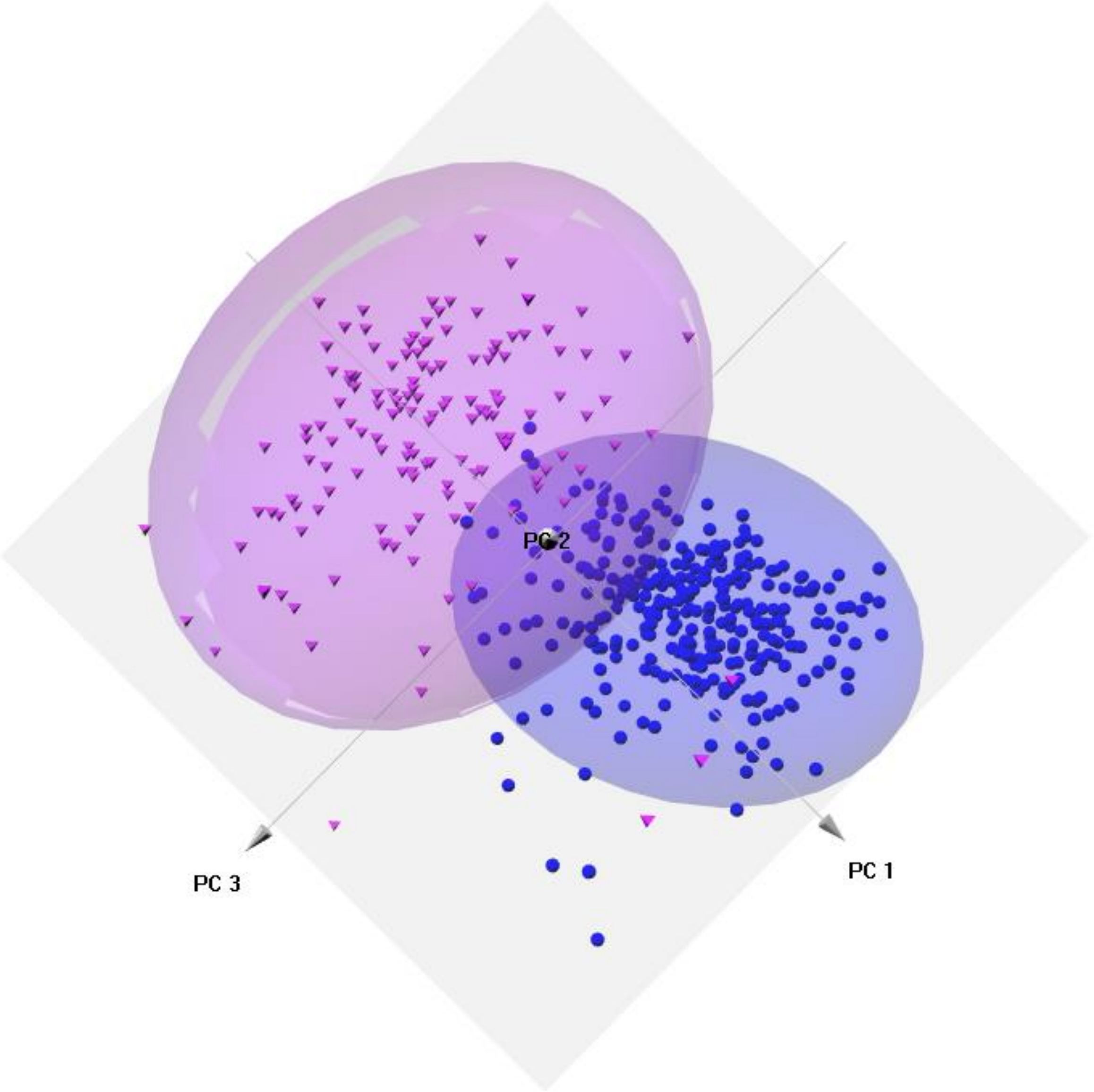


Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

PCA visualisation of the C5 & C6 immune groups
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the “Immune Landscape of Cancer” paper

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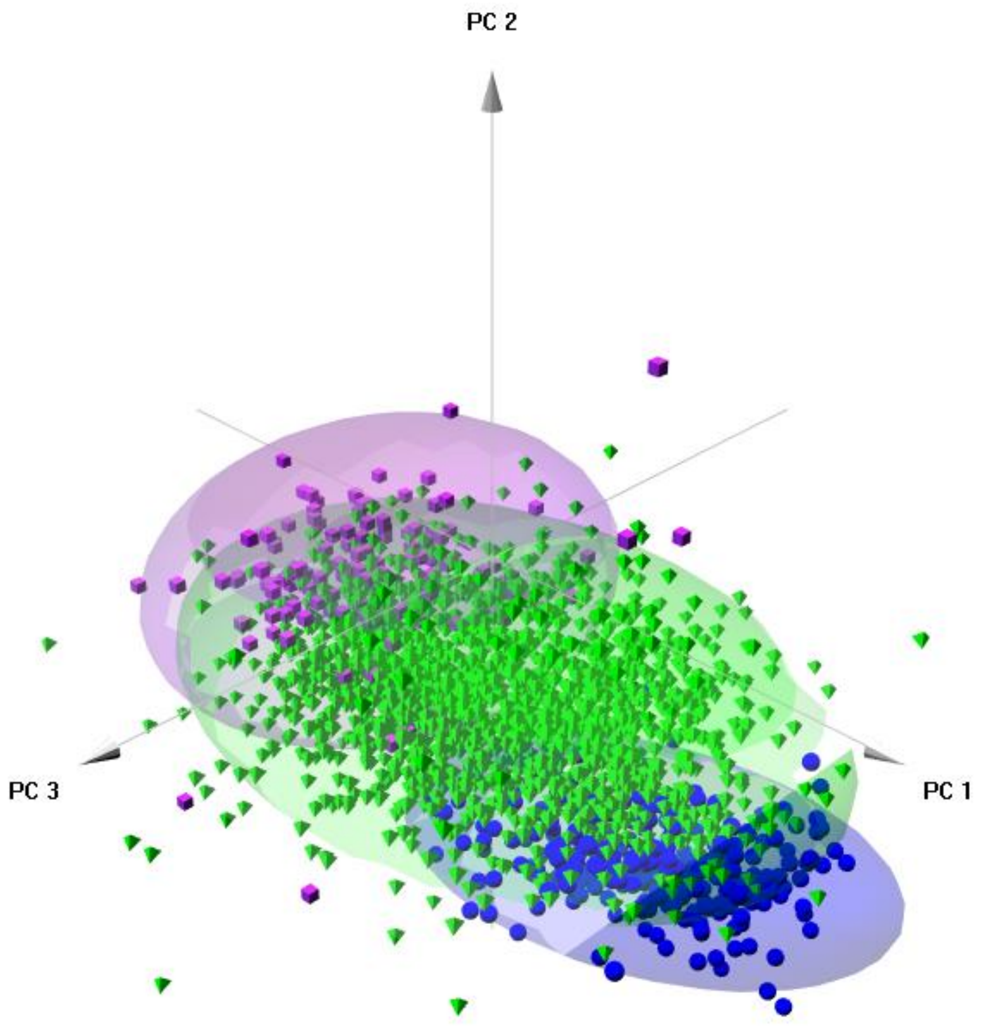
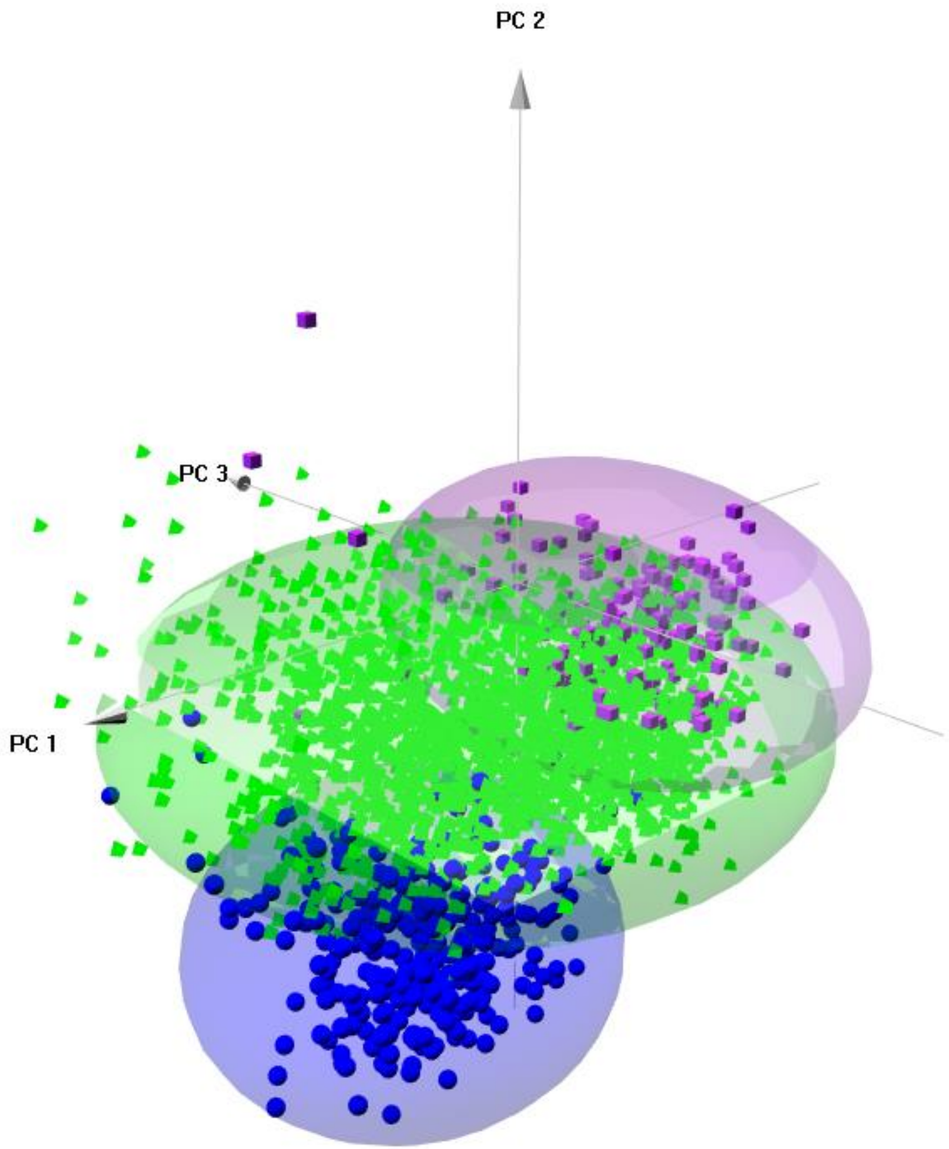
PCA visualisation of the C3, C5 & C6 immune groups
(PC1, PC2 & PC3)



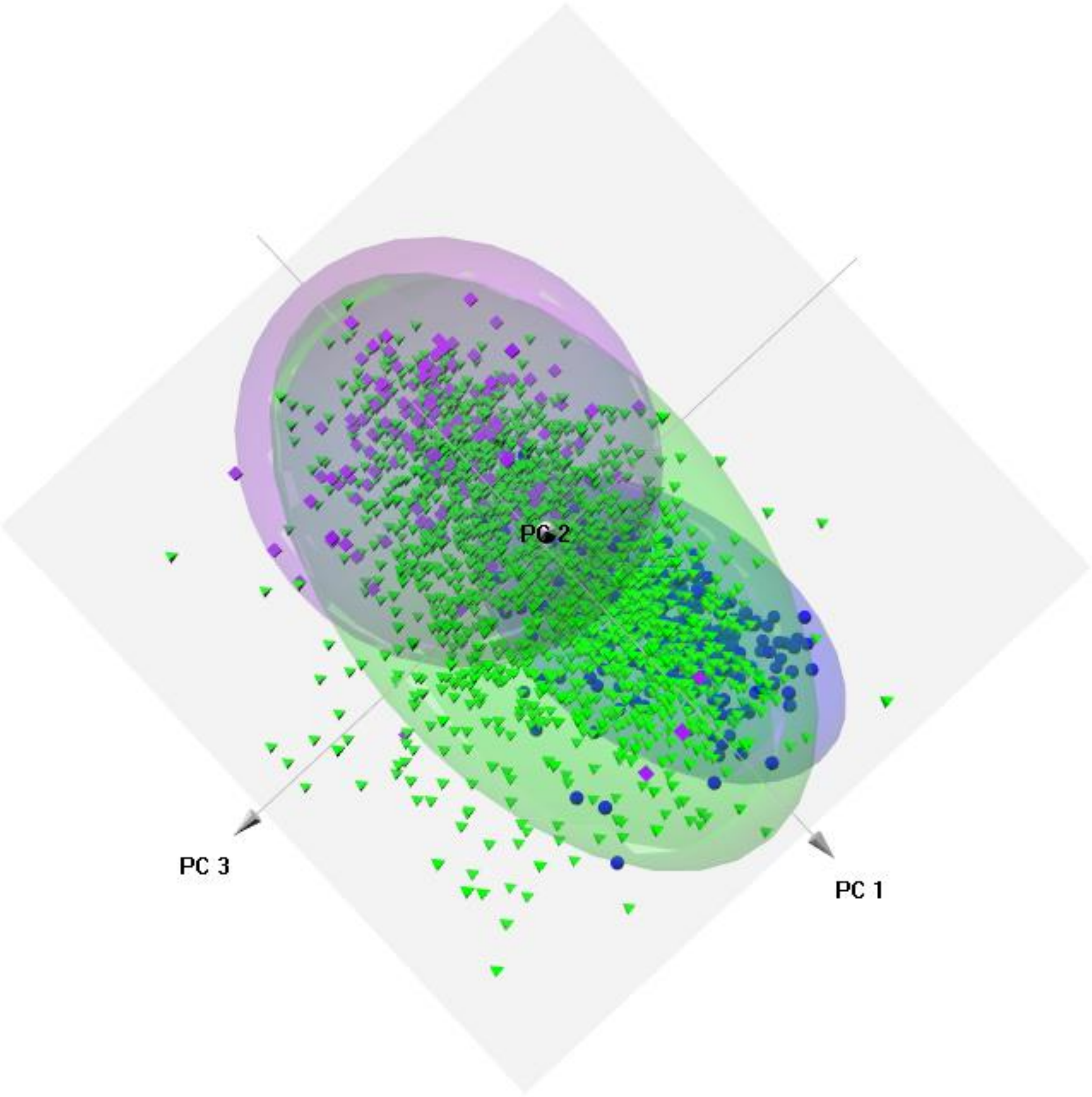


Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

PCA visualisation of the C3, C5 & C6 immune groups
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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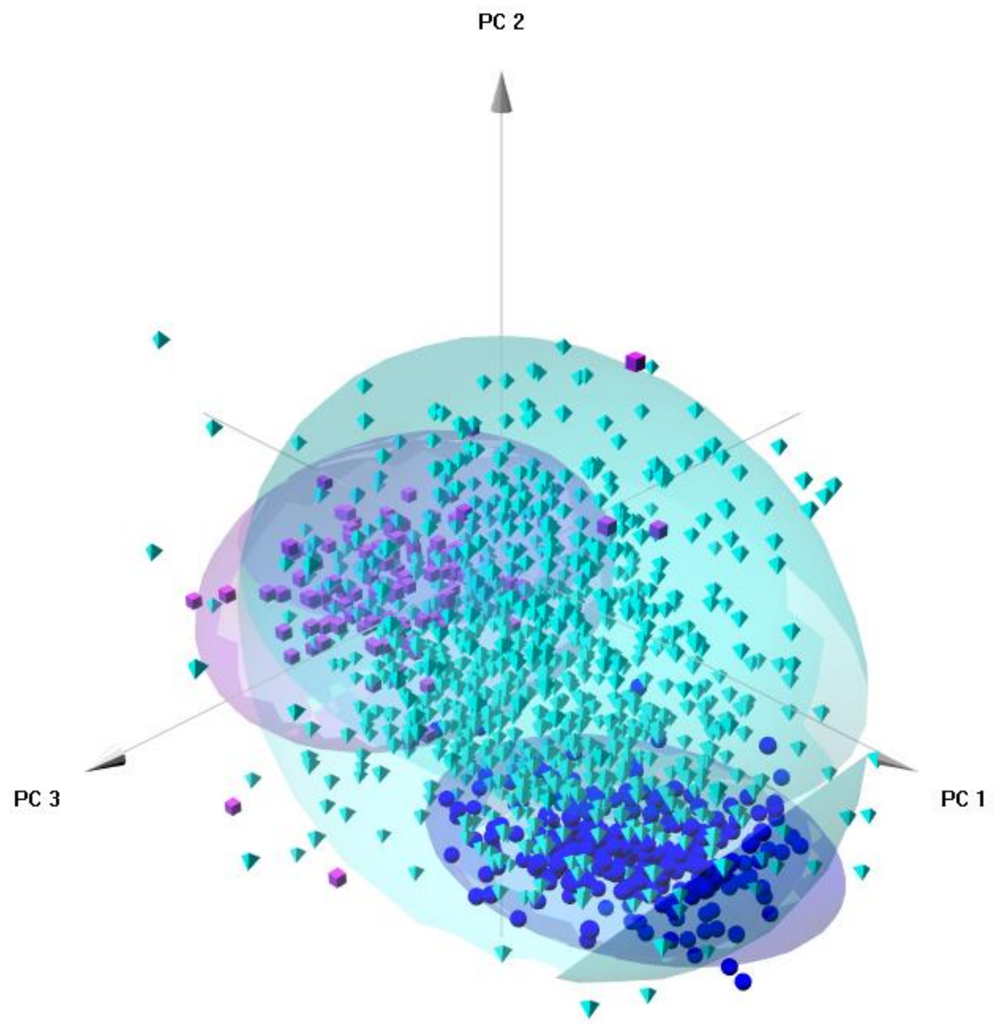
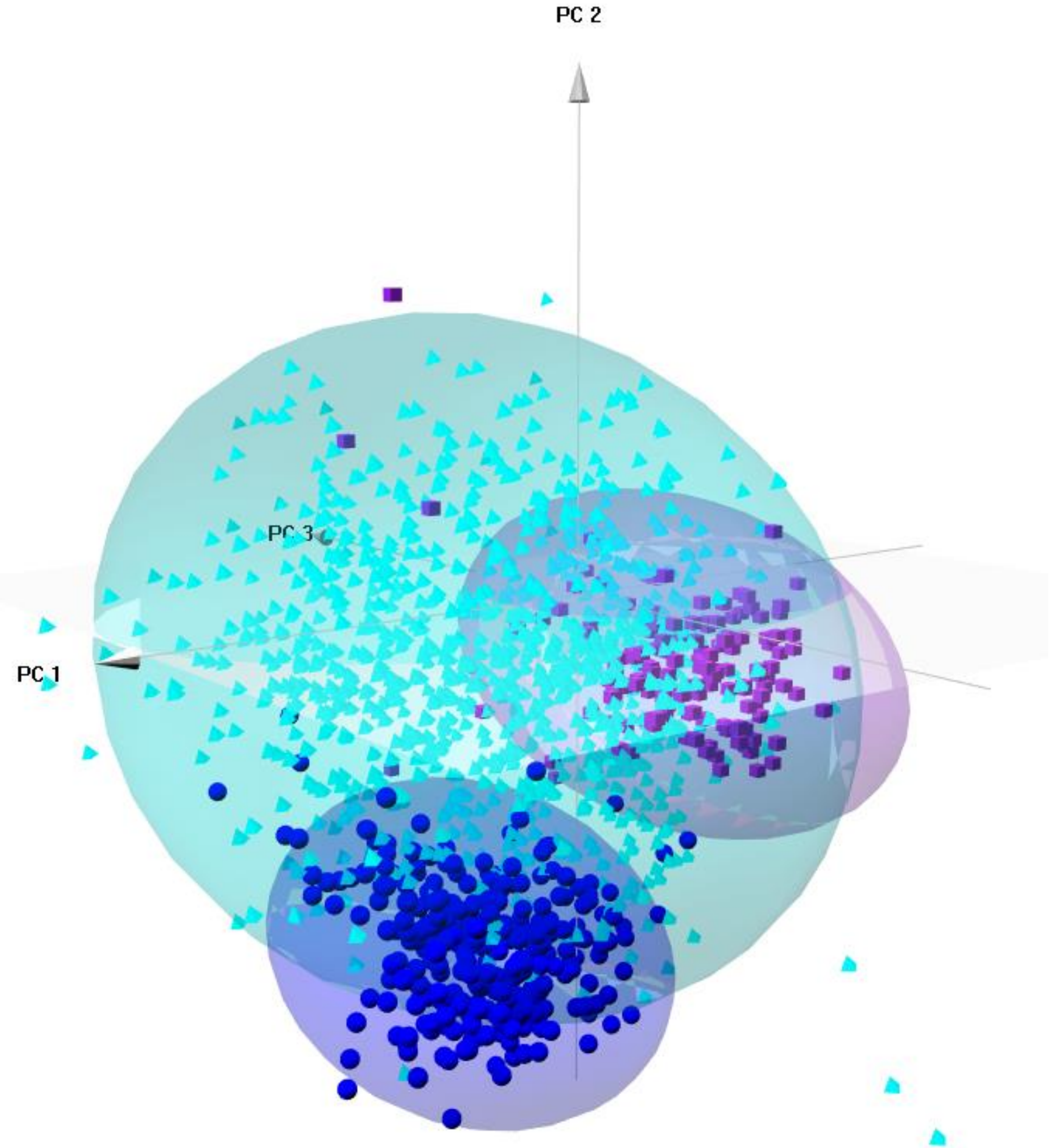
PCA visualisation of the C4, C5 & C6 immune groups
(PC1, PC2 & PC3)



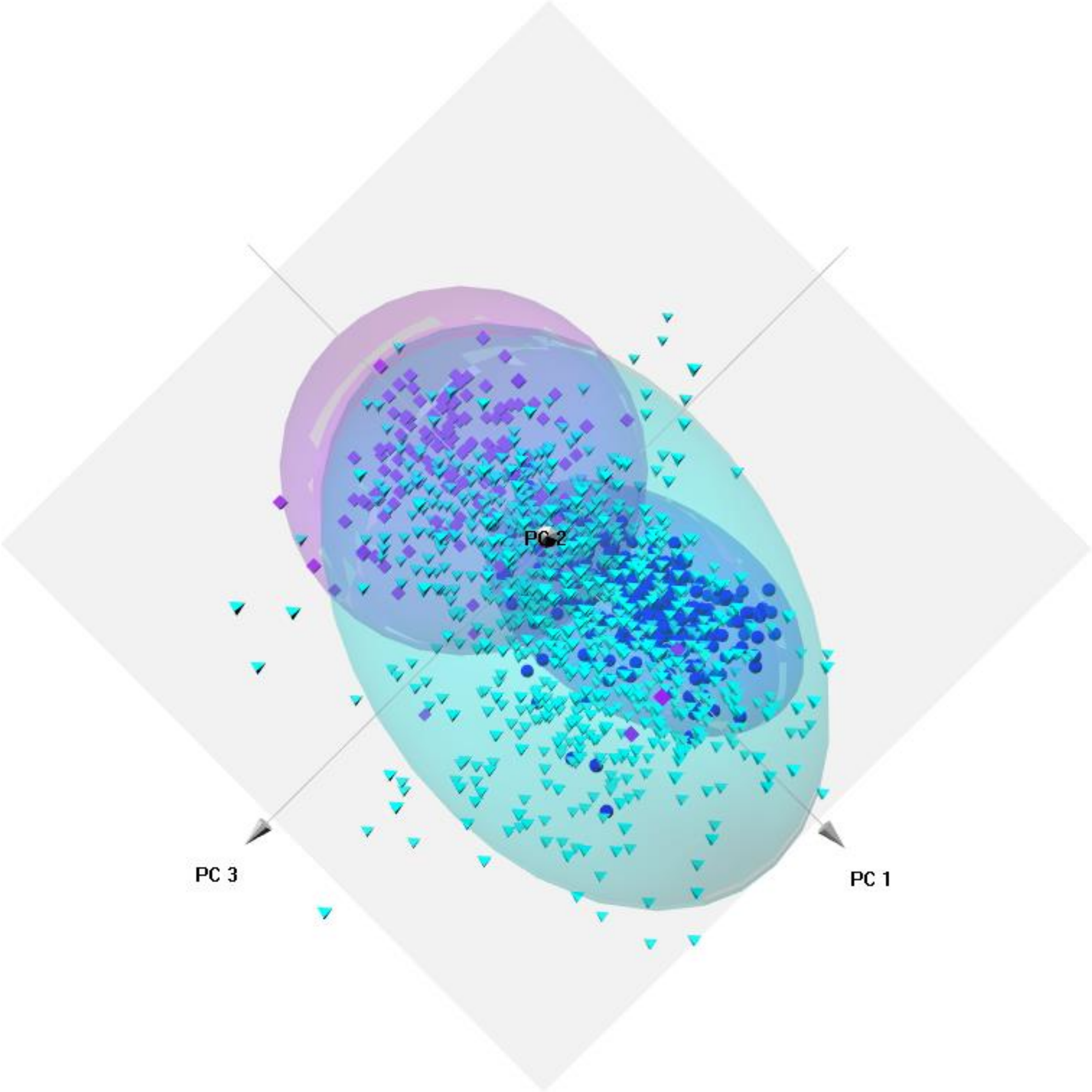


Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the “Immune Landscape of Cancer” paper

PCA visualisation of the C4, C5 & C6 immune groups

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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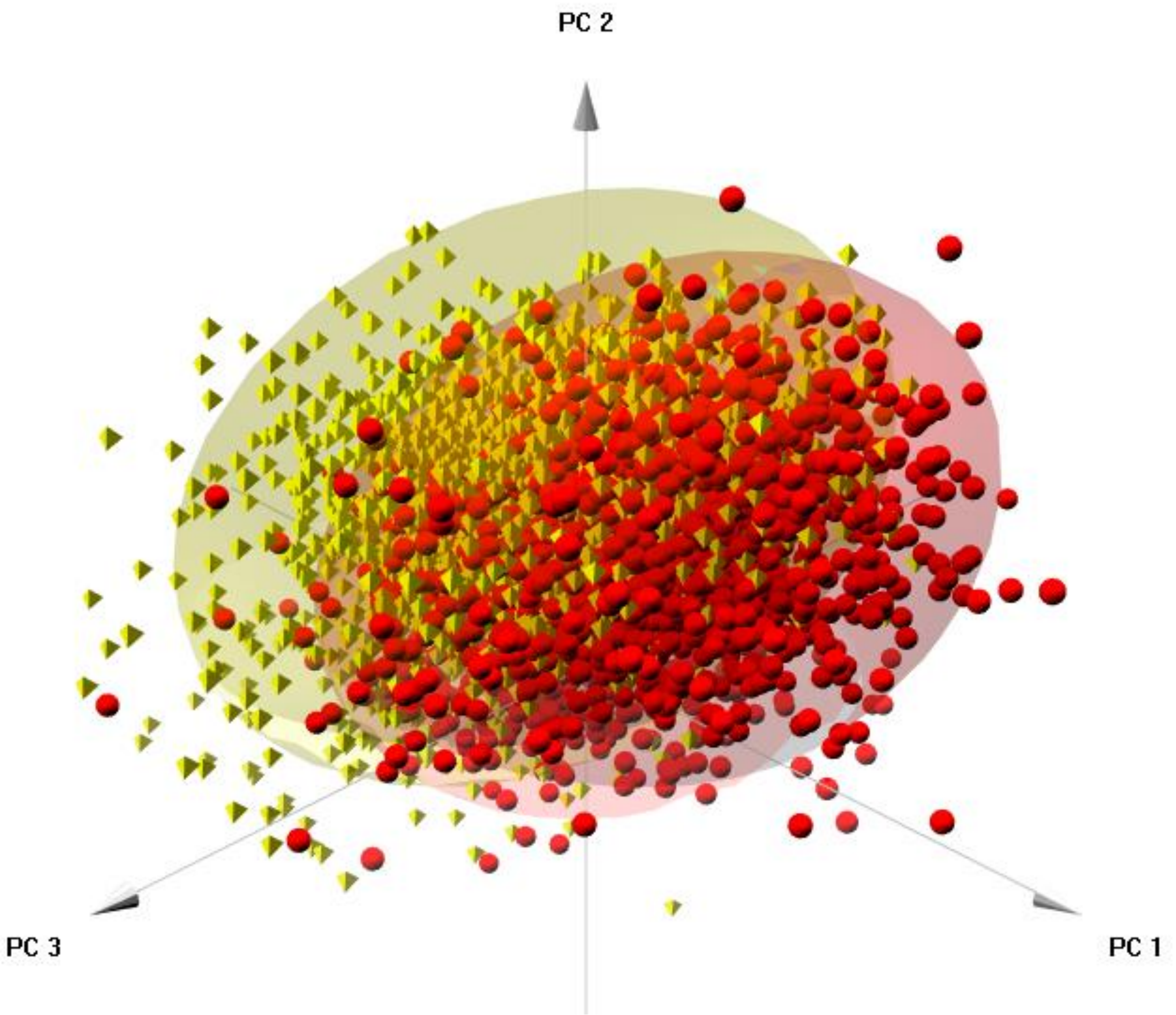
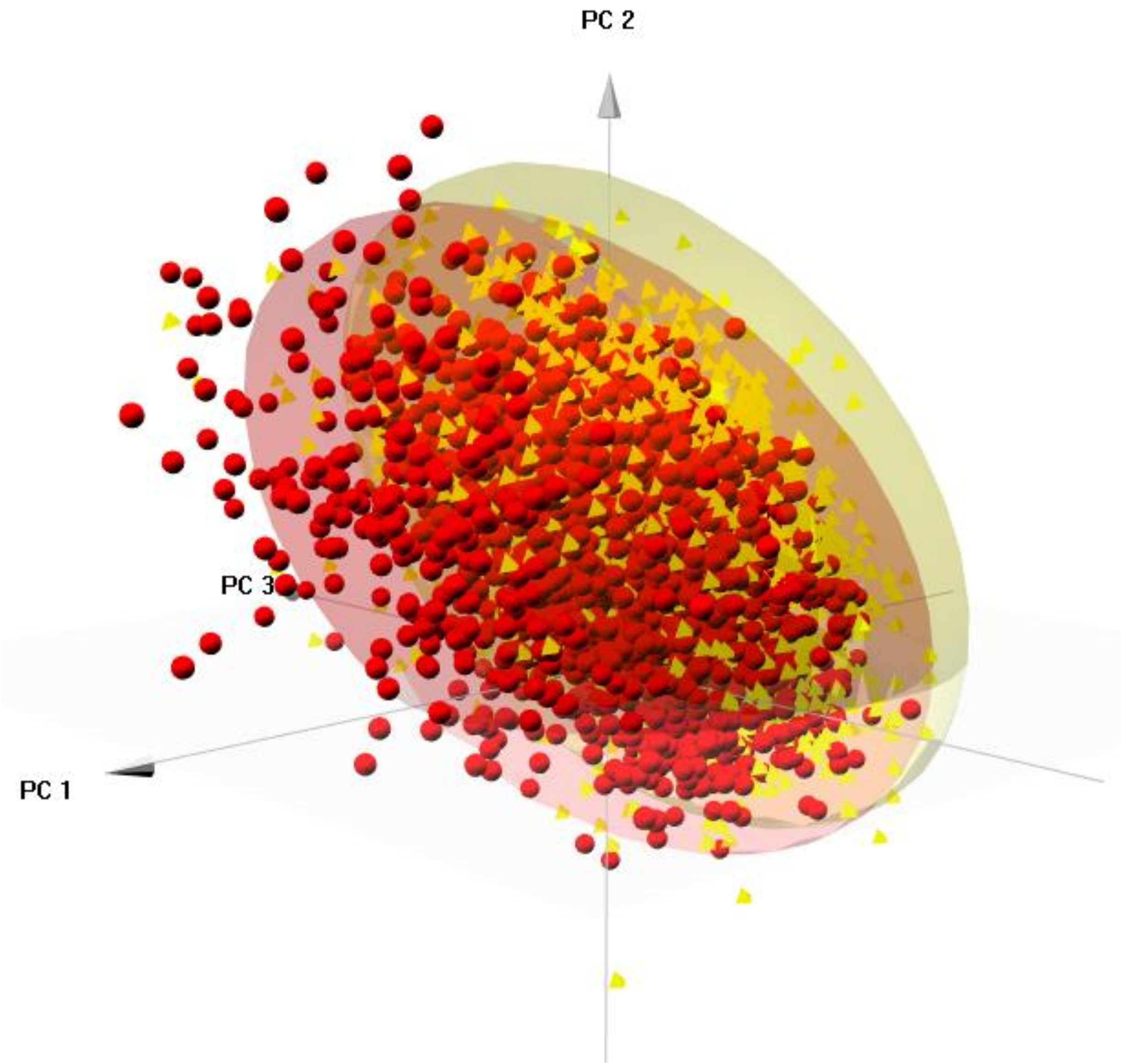
PCA visualisation of the C1 & C2 immune groups
(PC1, PC2 & PC3)



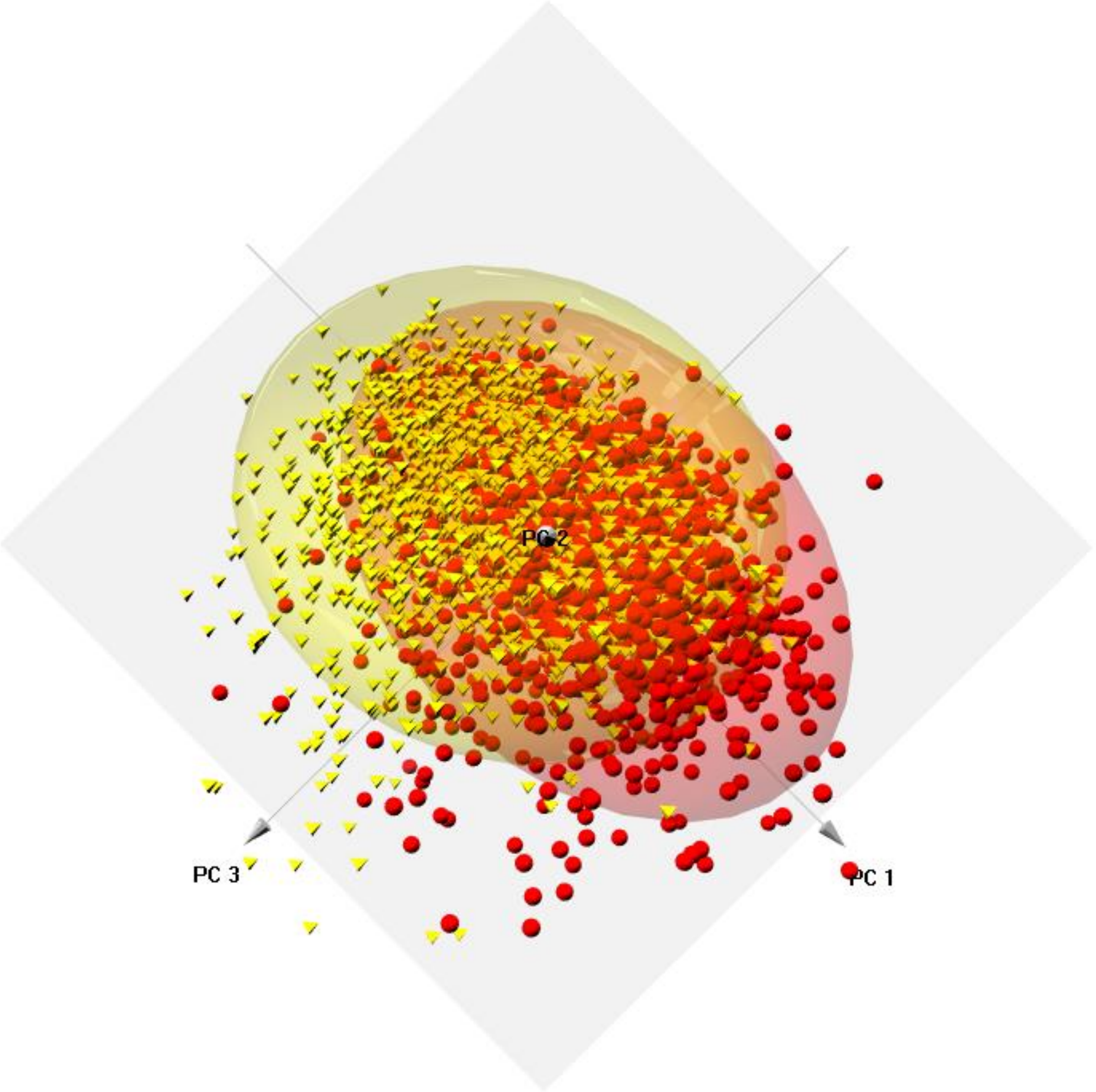


Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

PCA visualisation of the C5 & C6 immune groups
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the “Immune Landscape of Cancer” paper

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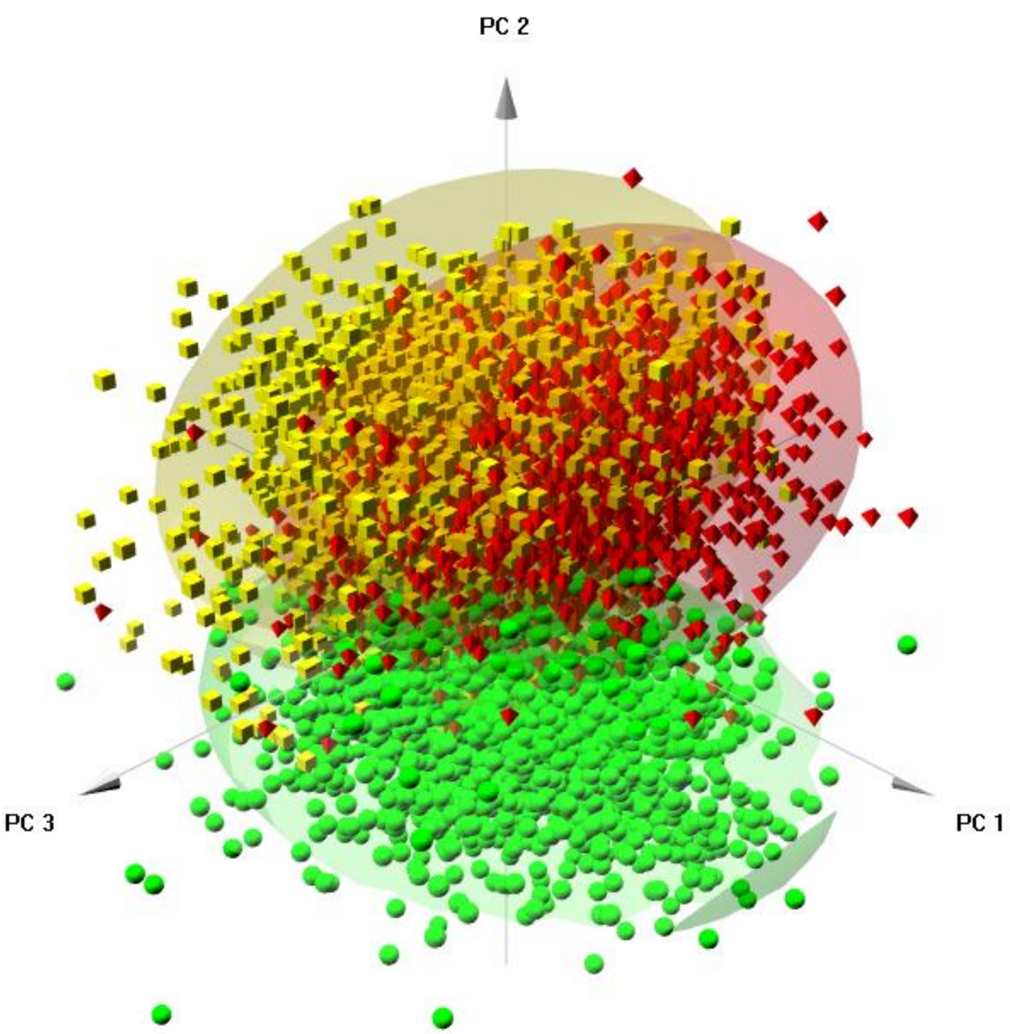
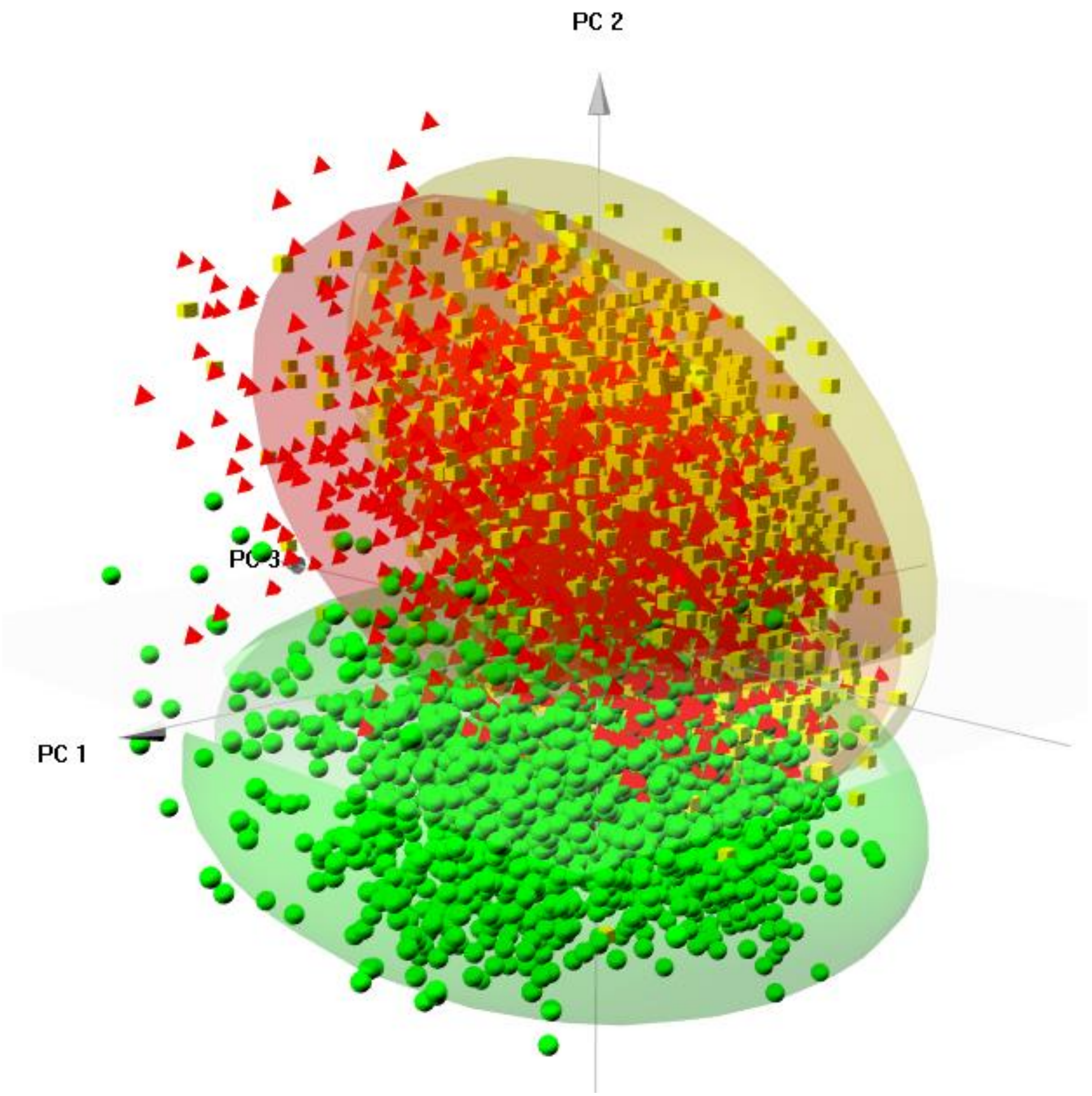
PCA visualisation of the C1, C2 & C3 immune groups

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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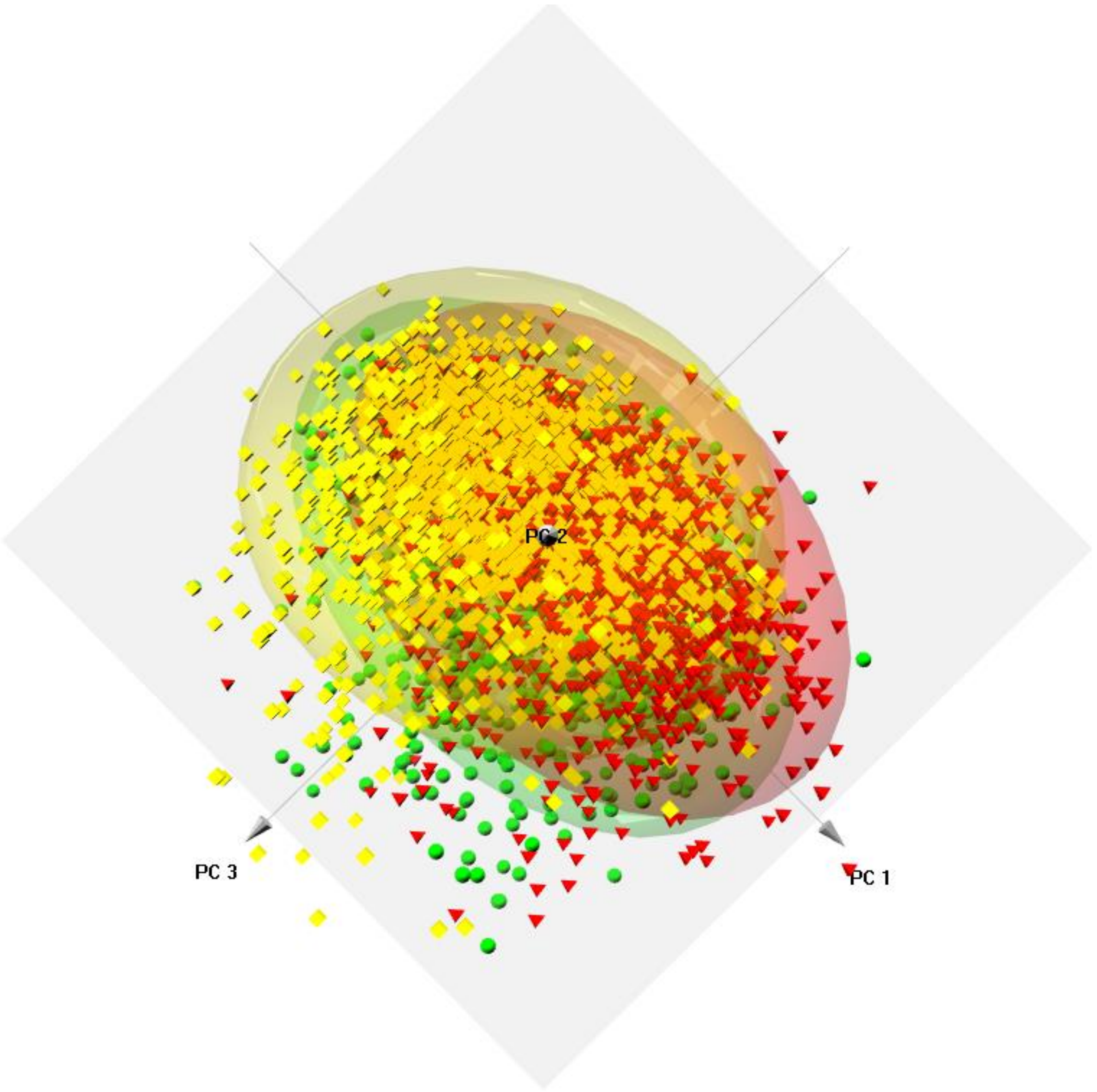
PCA visualisation of the C1, C2 & C3 immune groups

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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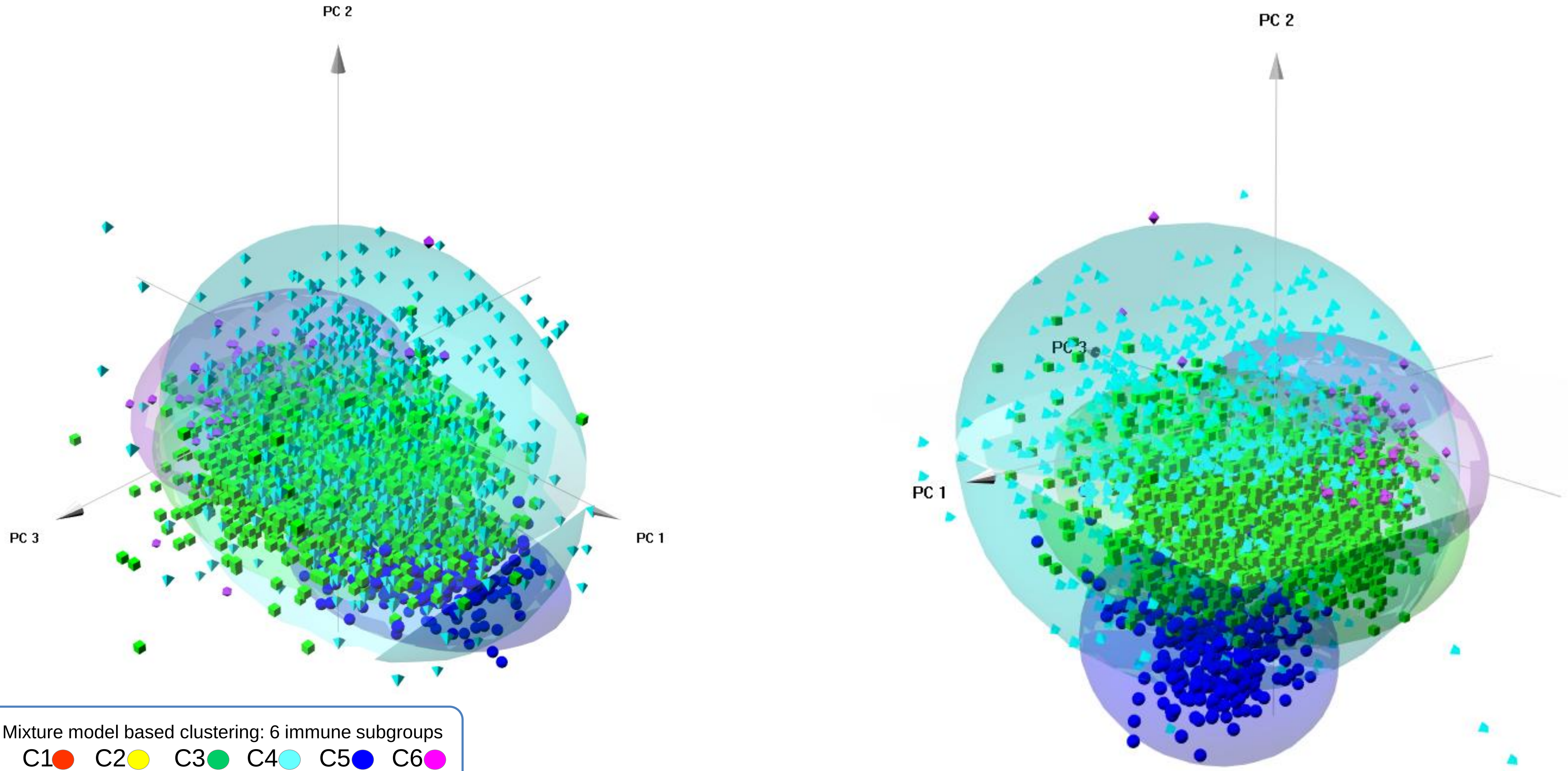
PCA visualisation of the C3, C4, C5 & C6 immune groups
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups
C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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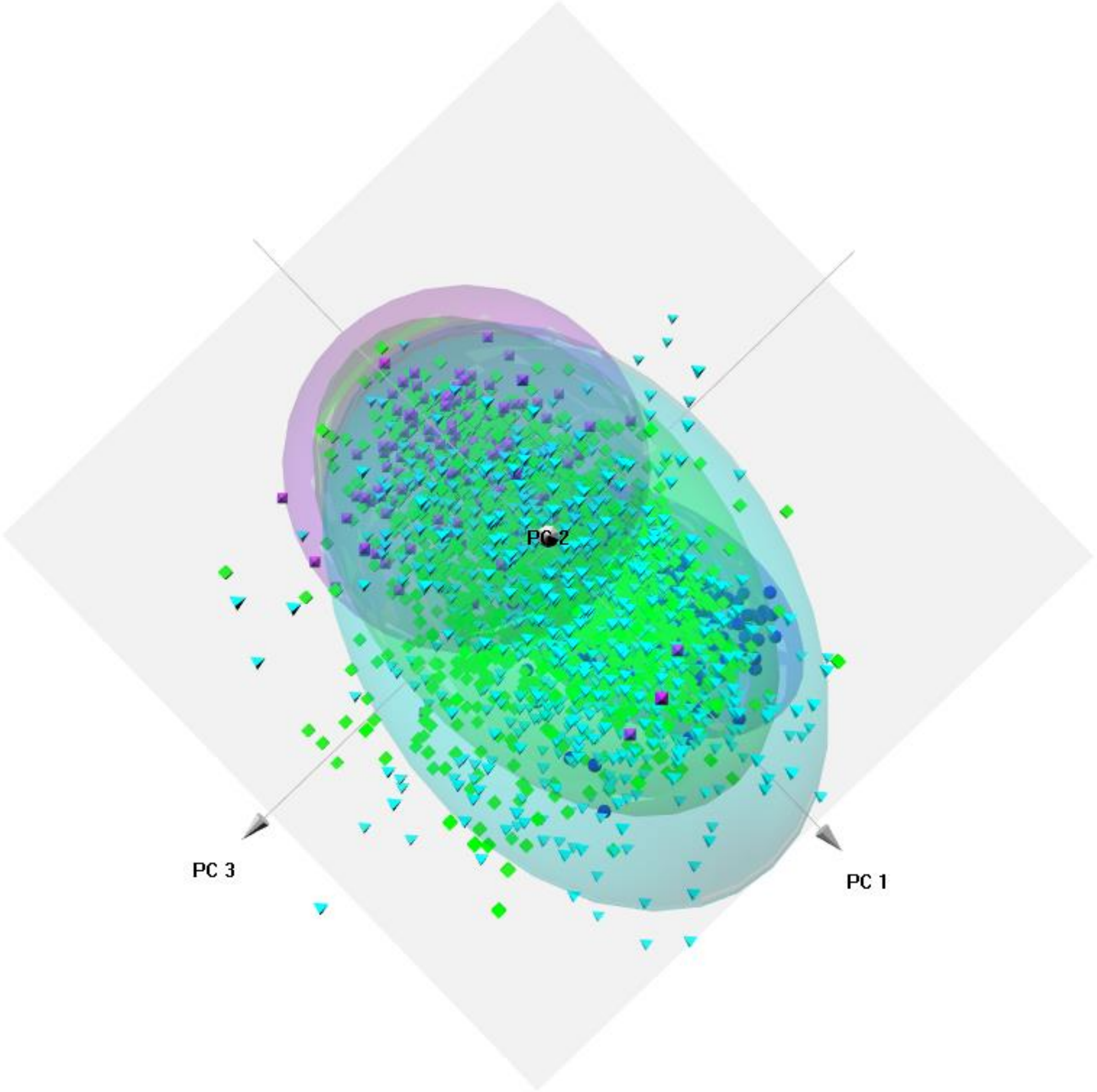
PCA visualisation of the C3, C4, C5 & C6 immune groups
(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

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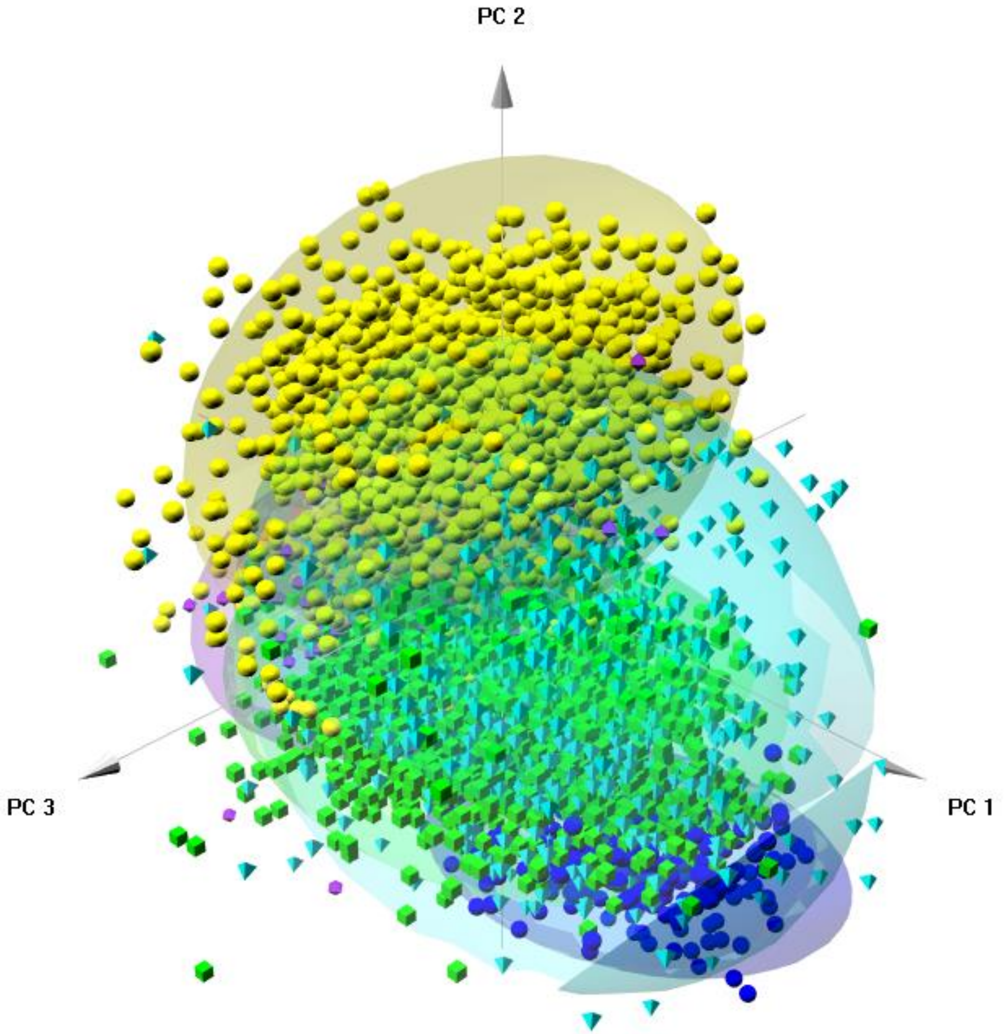
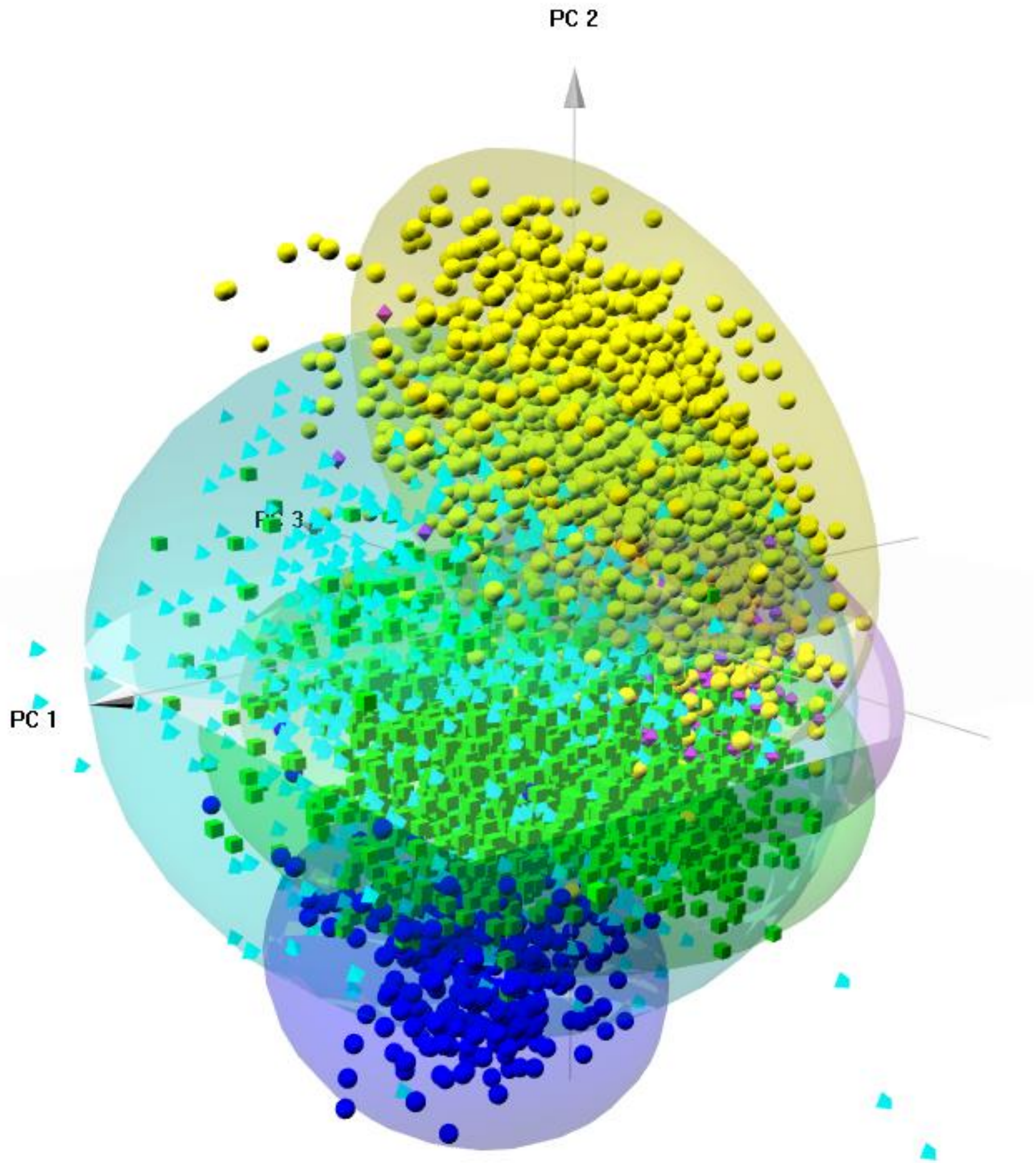
PCA visualisation of the C2, C3, C4, C5 & C6 immune groups

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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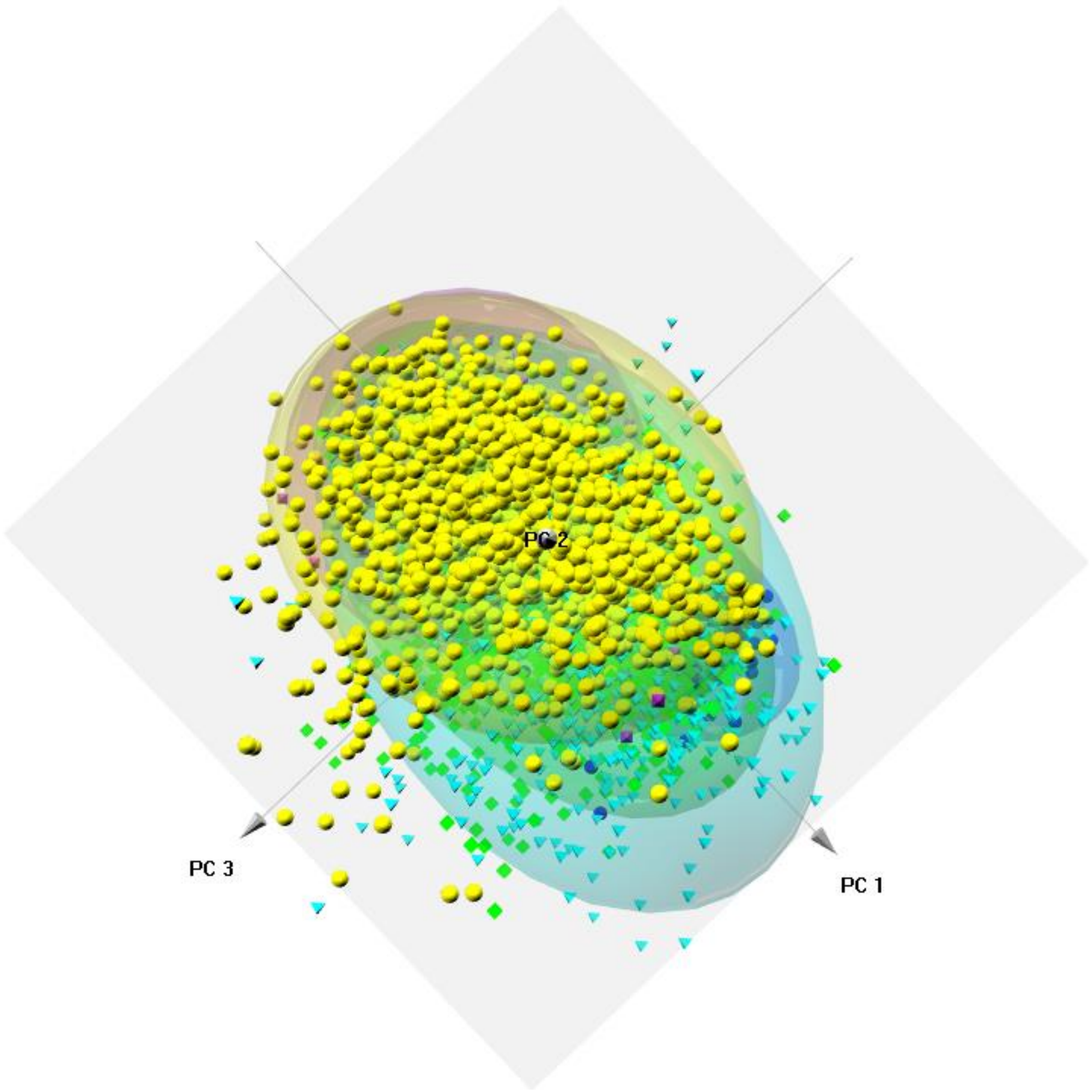
PCA visualisation of the C2, C3, C4, C5 & C6 immune groups

(PC1, PC2 & PC3)



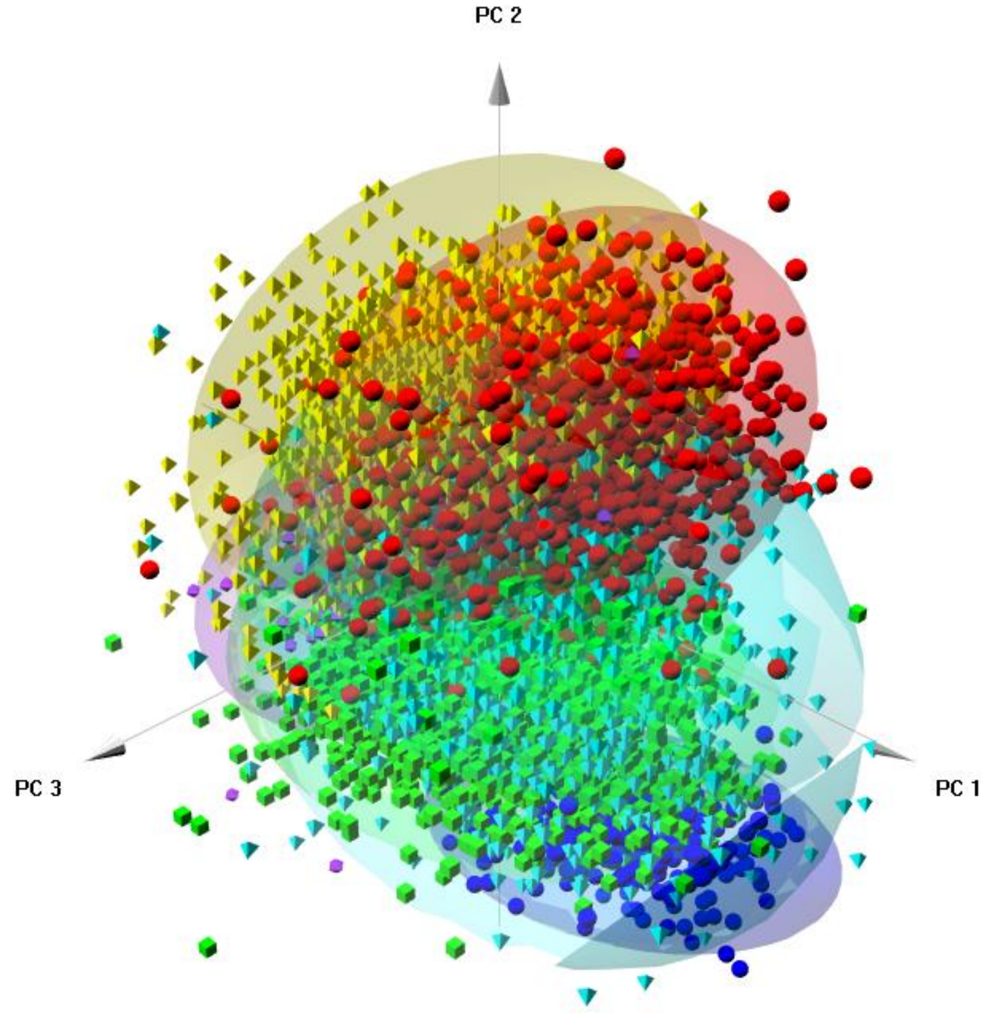
Mixture model based clustering: 6 immune subgroups

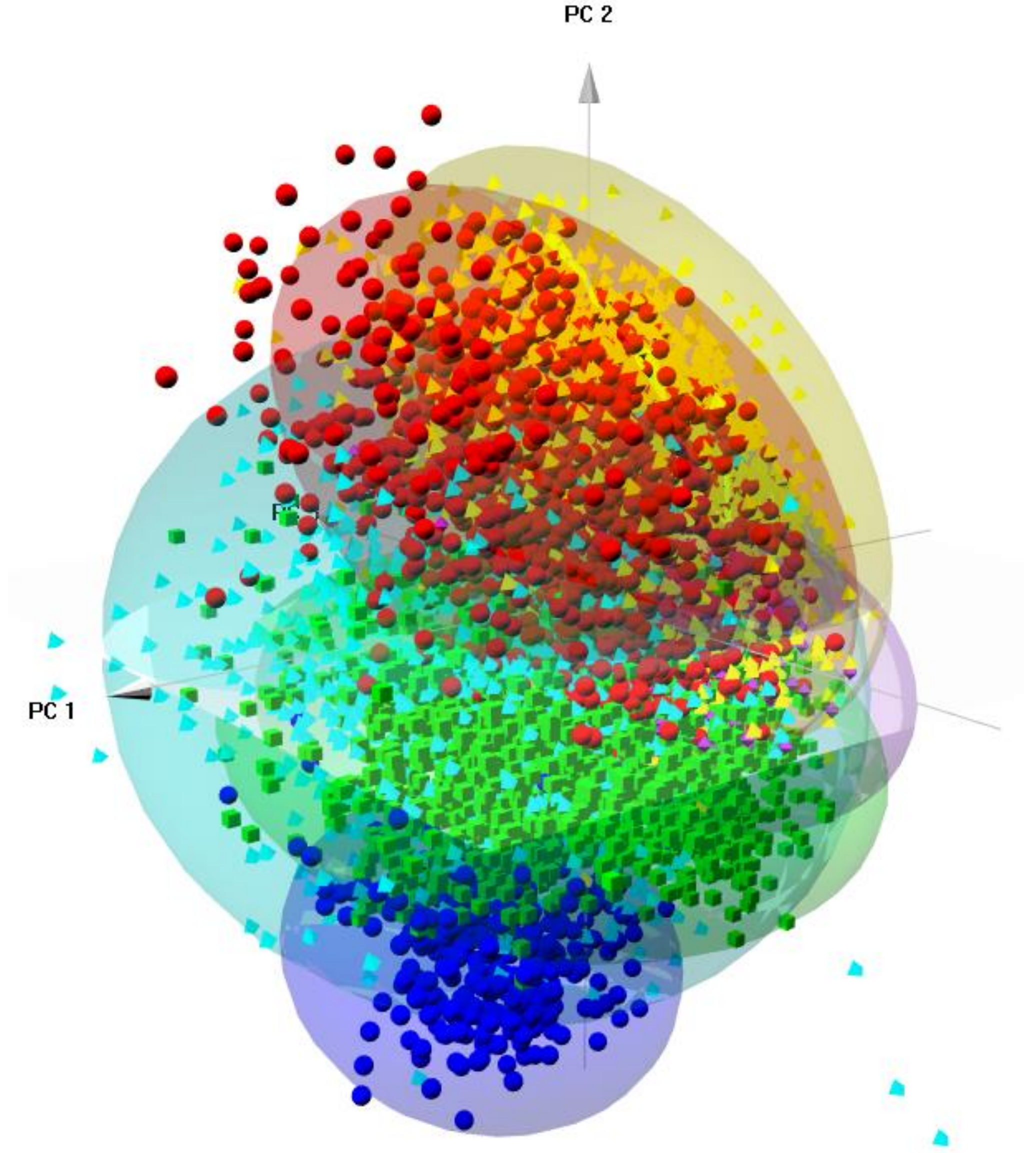
C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

PCA visualisation of the C1, C2, C3, C4, C5 & C6 immune groups (n=7302)

(PC1, PC2 & PC3)





Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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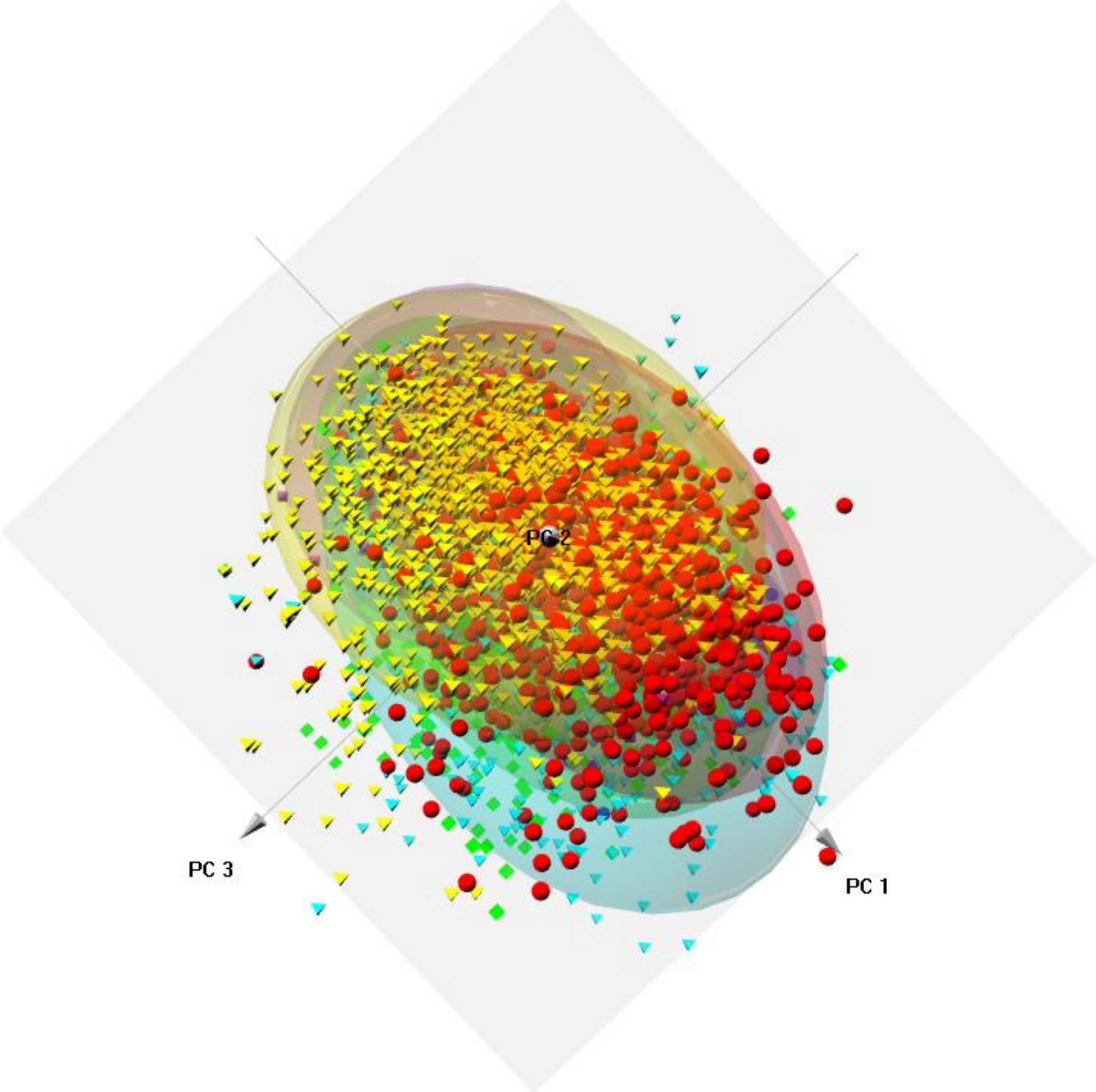
PCA visualisation of the C1, C2, C3, C4, C5 & C6 immune groups (n=7302)

(PC1, PC2 & PC3)



Mixture model based clustering: 6 immune subgroups

C1 C2 C3 C4 C5 C6

Based on the "Immune Landscape of Cancer" paper

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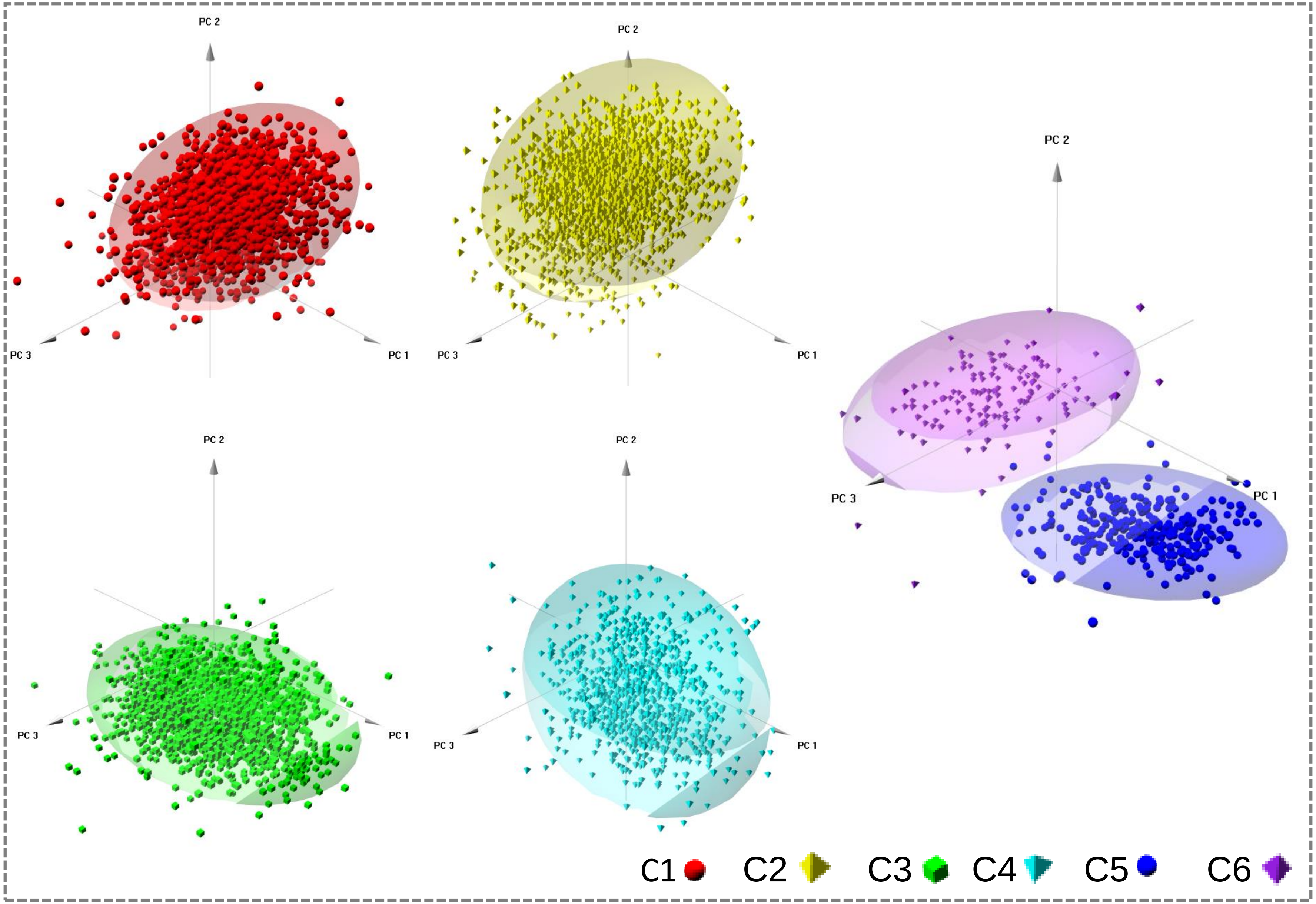
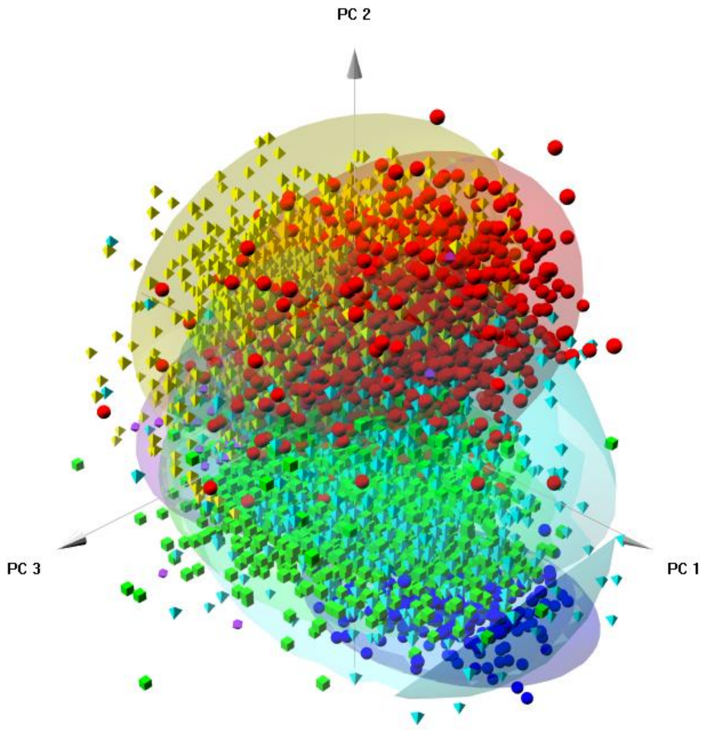
PCA visualisation of samples – 3D (n=7302)





Any Questions?