



IO17 | Large Scale Bioinformatics for Immuno-Oncology

**Deconvolution: exercise 3**

**Francesca Finotello, Federica Eduati, and Pedro L. Fernandes**

**GTPB | The Gulbenkian Training Programme in Bioinformatics**  
Instituto Gulbenkian de Ciência, Oeiras, Portugal | Sept 19th-22nd, 2017

## Deconvolution: Exercise 3 (Optional)

Implement an R function that takes as input a **matrix** of true cell fractions *cell.true* and a **matrix** of estimated cell fractions *cell.est* (format: samples on the rows, cell types on the columns).

The function must plot, for all cell types singularly and together, the **scatterplot** of the estimated versus the true cell fractions and report the Person's **correlation** and **RMSE**.

```
plotRes <- function (cell.true, cell.est) {  
  ...  
}
```

**Hint:** to consider all cell types together, you can transform a matrix into a vector with:

```
myvector <- as.vector(as.matrix(mymatrix))
```