

Fuchikoma: Revealing differentially expressed genes with non-linear dimensional reduction using single cell RNA-Seq data

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1 Introduction

2 Getting started

3 Setup

This vignette was built on:

```
> sessionInfo()
```

```
R version 3.2.2 (2015-08-14)
```

```
Platform: x86_64-apple-darwin13.4.0 (64-bit)
```

```
Running under: OS X 10.11.1 (El Capitan)
```

```
locale:
```

```
[1] ja_JP.UTF-8/ja_JP.UTF-8/ja_JP.UTF-8/C/ja_JP.UTF-8/ja_JP.UTF-8
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods
```

```
[7] base
```

```
loaded via a namespace (and not attached):
```

```
[1] tools_3.2.2
```

References

- [1] Tarazona, S. and Garcia-Alcalde, F. and Dopazo, J. and Ferrer, A. and Conesa, A. Genome Research *Differential expression in RNA-seq: A matter of depth*, 21(12): 2213-2223, 2011.