HPAanalyze at CRUG Hacktoberfest

Anh Tran

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The Why of this package

- The Human Protein Atlas (HPA) maps human proteins via multiple technologies.
- Beautiful web portal, but certain aspects of data retrieval and analysis left something to be desired.

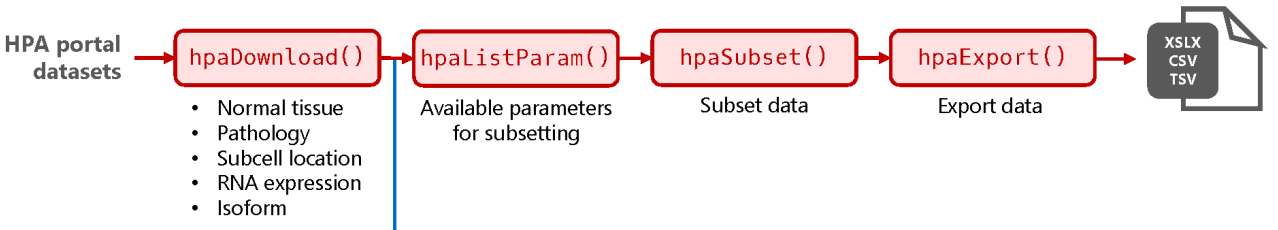
The real Why of this package

- I had just learned R (in 2017).
- My PhD mentor was overly excited to see some EDA I did with HPA data and suggested that I wrote a software package.

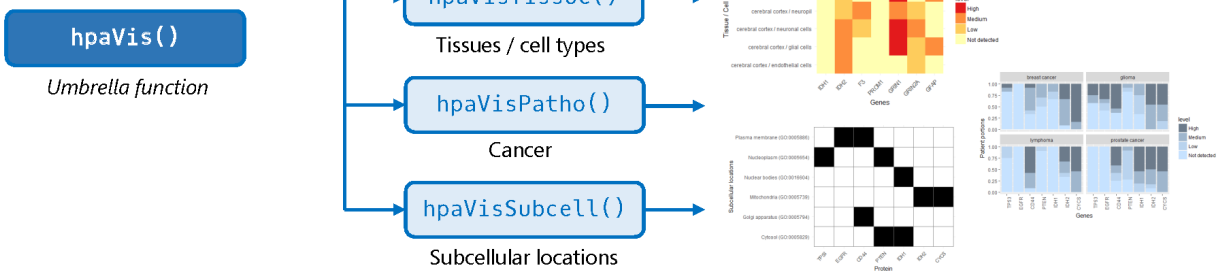
The real Why of this package

- I had just learned R (in 2017).
- My PhD mentor was overly excited to see some EDA I did with HPA data and suggested that I wrote a software package.
- … she meant an iPhone app.
- I wrote this package to learn how R worked.

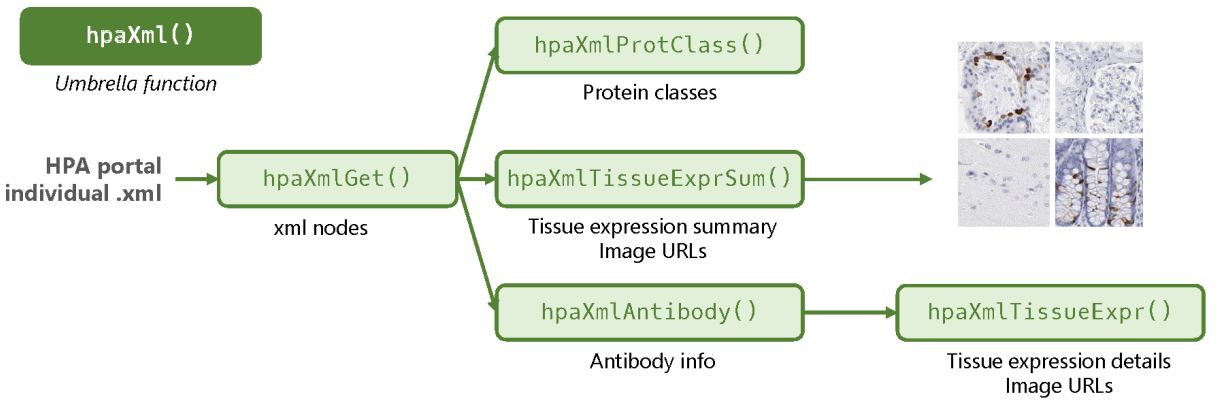
Import, subset and export downloadable datasets



Visualization



Individual XML extraction



Details

Almost everything is documented in vignettes

```
browseVignettes("HPAanalyze")
```

https://doi.org/doi:10.18129/B9.bioc.HPAanalyze

I need some help

- Package testing.
- Reducing dependencies.
- Improving documentation.

Testing

- Package is continuously tested with Travis-CI.
- Do I need testthat?
- How to test a functions whose output is a plot?

Reducing dependencies

- Currently dependent on 60 packages (Bioconductor estimate).
- Imports: dplyr, openxlsx, ggplot2, readr, tibble, xml2, tidyr, stats, utils, hpar, gridExtra
- Should I be worried?

Improving documentation

- Are my vignettes clear enough?
- How do I link my vignettes into a website like this?