# Extending Bioconductor to exposome data analysis

Carles Hernandez-Ferrer

July 26th, 2017

Barcelona Institute for Global Health

The exposome encompasses the totality of human environmental [...] exposures from conception onwards, complementing the genome. Dr. Christopher Wild, "Complementing the Genome with an Exposome"



#### Publications containing [term] in title by year

The European Commission awarded two large-grants to pursue exposome-related research (2012):

- The **HELIX project**, lead by *Barcelona Institute for Global Health*, will attempt to develop an early life exposome, noting that the first exposures occur during development.
- The EXPOSOMICS, lead by Imperial College London, will use smartphones that utilize GPS and environmental sensors to assess exposures in adulthood.

Late:

- Health and Environment-Wide Associations based on Large Scale population Surveys (**HEALS**)
- **HERCULES** that aims to provide expertise to develop and refine new tools and technologies to assess the exposome

## The HELIX Project



| Cohort | # Sample |
|--------|----------|
| BIB    | 14 000   |
| EDEN   | 2 000    |
| INMA   | 2 500    |
| KANC   | 4 000    |
| MoBa   | 8 000    |
| RHEA   | 1 500    |

From the total  $(+30\ 000)$ , 1 200 will get omic data

### rexposome project<sup>1</sup>

Aims to incorporate the exposome into Bioconductor ecosystem.

- rexposome (under revision): package for exposome data management, exposome characterization and testing exposome health outcome association.
- omicRexposome (under revision): package for testing exposome - omic association (exposome and exposome cluster) and integration.

<sup>&</sup>lt;sup>1</sup>Hernandez-Ferrer C, et al.; *Comprehensive analysis of the exposome, exposome-health associations and omics intermediates*; [submitted]

### rexposome project





### Any questions?

You can contact me at:

- carles.hernandez@isglobal.org
- http://www.carleshf.com
- @carleshf
- github.com/isglobal-brge

| 1  | data = rnorm(100)   |
|----|---|
| 2  | attempts = 0  |
| 3  | pvalue = 1  |
| 4  | <pre>while( pvalue &gt; 0.05 ){</pre>                         |
| 5  | attempts = attempts + 1                                       |
| 6  | <pre>cases = sample(data,50)</pre>                            |
| 7  | controls = data[!data %in% cases]                             |
| 8  | <pre>pvalue = t.test(cases,controls)\$p.value }</pre>         |
| 9  | <pre>cat("Congratulations! With p =", round(pvalue, 3),</pre> |
| 10 | "you achieved scientific success in",attempts,"attempts\n")   |

How to achieve scientific success in 10 lines of R code!

Leon Eyrich Jessen (@jessenleon) - October 23th, 2016