







Functional analysis





Miscellaneous



Quality control



Relative  
quantification



MS  
stats









Input Files

keys.txt





evidence.txt

<http://mstats.org/>

Developed by Mena Choi from Olga Vittek Lab



Bioconductor

OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

It uses a family of **linear mixed models** that attempts to:

- minimize bias and inefficiencies in spectrometry-based proteomics,
- distinguish the systematic variation from random artifacts,
- maximize the reproducibility of the results

**MSstats is an open-source R package for statistical relative quantification of proteins and peptides in global, targeted, and data-independent proteomics.**

Used in



Skyline

**artmsQuantification()**



The logo features the letters 'MS' in a large, blue, serif font. The 'M' is stylized with multiple overlapping, slightly offset outlines, creating a sense of depth or motion. To the right of the 'MS' is the word 'stats' in a smaller, grey, sans-serif font. The entire logo is set against a white background with a light grey shadow at the bottom.

MS  
stats

# artMS

**Analytical R Tools  
for Mass Spectrometry**

<http://artms.org>



# artMS

Analytical R Tools  
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<http://msstats.org/>

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# artMS

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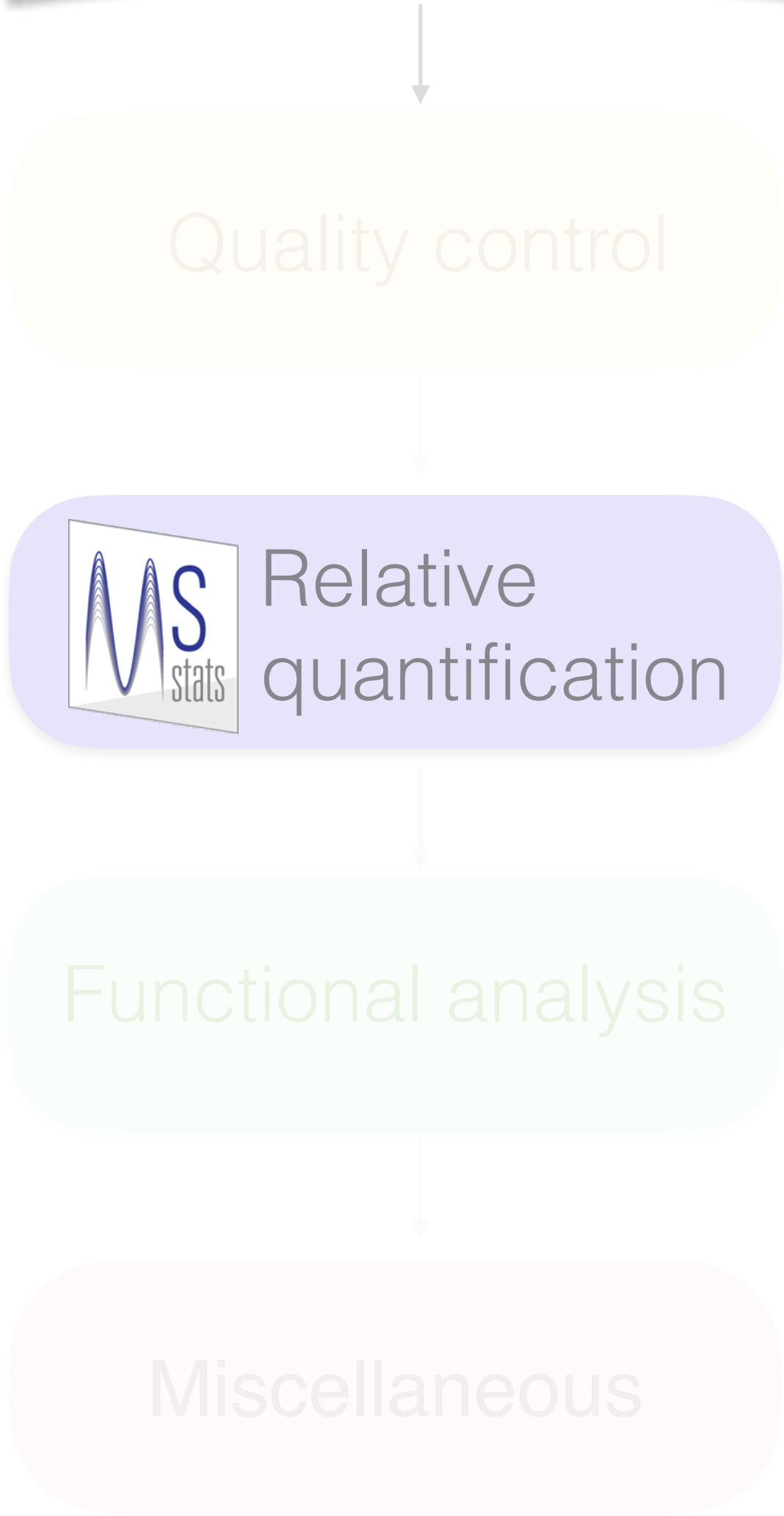
Input Files

 evidence.txt

keys.txt

contrast.txt

config.yaml



**artmsQuantification("config.yaml")**

Console Terminal x

~/

> artmsQuantification(yaml\_config\_file = "config-phglocal.yaml")