Quarto example

目录

# 中文支持

yaml头部设置如下：

pdf:  
 include-in-header:  
 text: |  
 \usepackage{ctex}  
 \usepackage{amsthm,mathrsfs}  
 CJKmainfont: KaiTi

# croos reference

引用图片 [图 1](#fig-example) . （注意空行以及空格）

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| |  |  |  | | --- | --- | --- | | |  | | --- | | (a) 图片引用示例a | |  |  |  |  | | --- | --- | | |  | | --- | | (b) 图片应用示例b | |   图 1: 图片example |

引用表格 [表格 1](#tbl-go) .

表格 1: GO富集分析中线粒体相关

| ONTOLOGY | ID | Description | p.adjust |
| --- | --- | --- | --- |
| BP | GO:0051881 | regulation of mitochondrial membrane potential | 0.0215593 |
| CC | GO:0005759 | mitochondrial matrix | 0.0396286 |

引用公式 ([方程式 1](#eq-example))

引用文献[1](#ref-li_exaggerated_2022) ， 这里还有[2](#ref-noauthor_wgcna_nodate) .

# 附录

pdf的输出需要Latex， 用如下命令下载

quarto install

从[这里](https://www.zotero.org/styles)下载csl文件。

# 参考文献

1. Li, Y., Ge, X., Peng, F., Li, W. & Li, J. J. [Exaggerated false positives by popular differential expression methods when analyzing human population samples](https://doi.org/10.1186/s13059-022-02648-4). *Genome Biology* **23**, 79 (2022).

2. [WGCNA: an R package for weighted correlation network analysis BMC Bioinformatics Full Text](https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-9-559).