

BIOF3 FIGCODE · SCI 绘图代码集

# GO 条形图 (GO Bar Plot)

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获取文章完整内容，分享生物信息学最新知识。

分类: 功能富集 | 依赖包: ggplot2

## 解决的生物学问题

差异基因在生物过程、分子功能和细胞组分三个维度分别富集了哪些功能？

## 应用场景

- GO 三大类别全景展示
- 对比 BP/MF/CC 富集差异
- 文章 figure 综合功能注释
- 多组差异基因功能对比

## 输入数据格式

enrichGO 结果 (分别跑 BP/MF/CC 后合并)

## 关键参数

- showCategory 每类展示数 (5-10)
- ont 本体类型 (ALL / BP / MF / CC)
- pvalueCutoff 阈值
- facet 是否分面展示
- color 着色变量 (p.adjust / Count)

## 快速开始

### 1. 直接在线运行

打开 [FigCode 在线绘图](#)，点击本工具卡片的"在线绘图"按钮即可用内置示例数据出图，零环境配置。

下载脚本和示例数据，本地 RStudio 运行：

```
# CRAN 包
install.packages(c("ggplot2"))

# Bioconductor 包 (如需)
# BiocManager::install(c())
```

```
library(ggplot2)

# --- Demo data ---
set.seed(42)

bp_terms <- c("Cell division", "DNA repair", "Apoptotic process", "Signal transduction", "Protein binding", "ATP binding", "Kinase activity", "DNA binding", "Regulation of enzyme activity", "Cell cycle", "Cell growth", "Cell death", "Cell differentiation", "Cell migration", "Cell adhesion", "Cell communication", "Cell signaling", "Cell metabolism", "Cell homeostasis", "Cell development", "Cell differentiation", "Cell migration", "Cell adhesion", "Cell communication", "Cell signaling", "Cell metabolism", "Cell homeostasis", "Cell development")
mf_terms <- c("Protein binding", "ATP binding", "Kinase activity", "DNA binding", "Regulation of enzyme activity", "Cell cycle", "Cell growth", "Cell death", "Cell differentiation", "Cell migration", "Cell adhesion", "Cell communication", "Cell signaling", "Cell metabolism", "Cell homeostasis", "Cell development", "Cell differentiation", "Cell migration", "Cell adhesion", "Cell communication", "Cell signaling", "Cell metabolism", "Cell homeostasis", "Cell development")
cc_terms <- c("Nucleus", "Cytoplasm", "Membrane", "Mitochondrion", "Extracellular")

go_df <- data.frame(
  Description = c(bp_terms, mf_terms, cc_terms),
  Count = sample(5:35, 15),
  p.adjust = runif(15, 0.0001, 0.04),
  ONTOLOGY = rep(c("BP", "MF", "CC"), each = 5)
)

# --- Plot ---
ggplot(go_df, aes(x = reorder(Description, Count), y = Count, fill = p.adjust)) +
  geom_col(width = 0.7) +
  coord_flip() +
  facet_grid(ONTOLOGY ~ ., scales = "free_y", space = "free_y") +
  scale_fill_gradient(low = "#dc2626", high = "#93c5fd") +
  labs(x = NULL, y = "Gene Count", title = "GO Enrichment (BP/MF/CC)", fill = "p.adjust") +
  theme_classic() +
  theme(strip.text = element_text(face = "bold"))
```

## 替换为自己的数据

脚本中以 `# --- Demo data ---` 标注的段落是示例数据生成代码。替换为自己的数据时，**保持列名一致**即可：

- 输入格式：enrichGO 结果（分别跑 BP/MF/CC 后合并）
- 使用 `read.csv()` / `readRDS()` 读取本地文件

## 延伸阅读

- 相关教程：[GO 条形图 完整流程](#)
- 出现 bug？欢迎在 [FigCode 页面](#) 点击对应卡片，在评论区留言。