

# Parallel-Meta Suite

The Installation Guide



# 准备工作

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Parallel-META Suite (以下简称**PMS**) 由C++和R开发。

在开始安装前，需要先安装**R**和**g++**编译器。

```
# For macOS user
## install g++ compiler
brew install gcc
## install R
brew install homebrew/science/r

# For linux user
## g++ compiler is already integrated into the system
## install R
apt-get install r-base

# Verify R installation
R --version
```



# 下载安装包

1 打开浏览器，并访问网页：

<https://github.com/qdu-bioinfo/parallel-meta-suite>

2 点击 “Installation Guide” (安装指南)

3 选择与您的操作系统相匹配的版本来下载

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## Parallel-Meta Suite Users' Manual

Version 3.7 Release date Nov. 16, 2021

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## Installation guide

The latest released package:

For Linux/Win10 WSL, the source code package is [here](#).

For MAC, the source code package is [here](#).

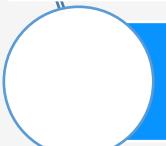
# 安装 (以WSL为例)

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移动安装包

- mv /mnt/e/Downloads/parallel-meta-suite-3.7-src.tar.gz /



解压安装包



进入软件目录

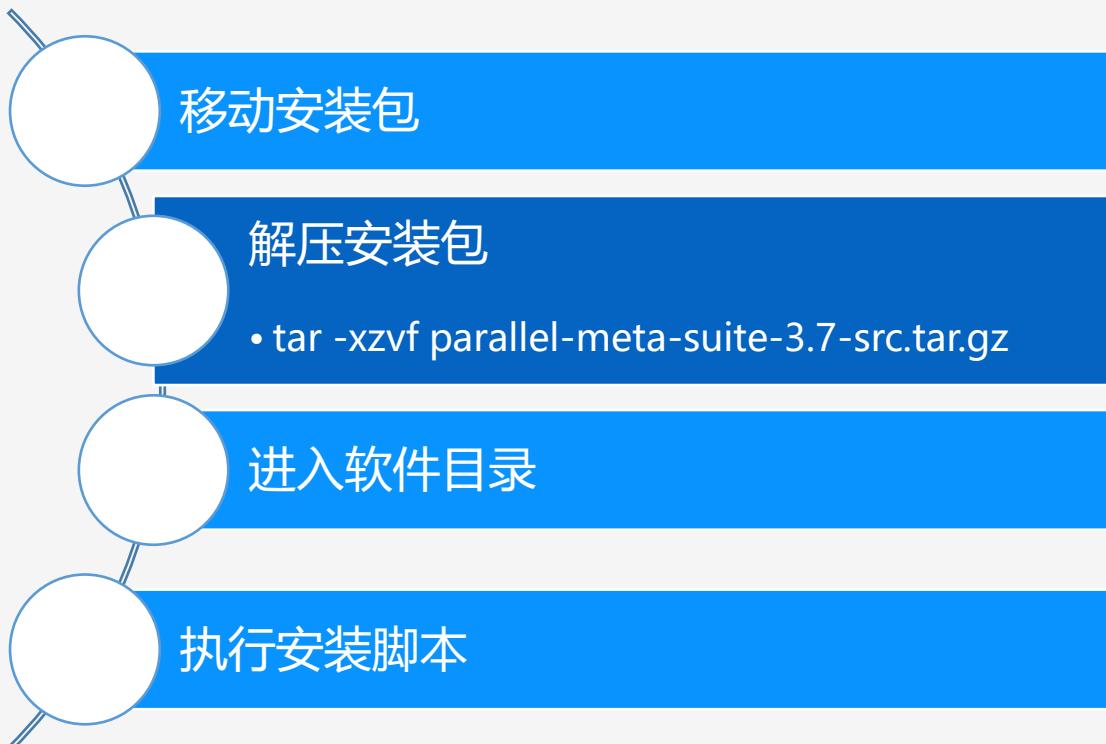


执行安装脚本

**提示：**该操作是可选的，非必须执行

# 安装 (以WSL为例)

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# 安装 (以WSL为例)

---



# 安装 (以WSL为例)



移动安装包



解压安装包



进入软件目录



执行安装脚本

- source ./install.sh

```
root@DESKTOP-74P0JFM:/mnt  
source install.sh  
**Parallel-Meta Suite Installation**  
**version 3.7**  
  
**Parallel-Meta Suite src package**  
g++ -c -o src/ExtractRNA.o src/ExtractRNA.cpp -Wno-deprecated  
g++ -o bin/PM-parallel-meta src/frame.cpp src/ExtractRNA.o -fopenmp -Wno-deprecated  
g++ -o bin/PM-extract-rna src/ExtractRNA_plus.cpp src/ExtractRNA.o -Wno-deprecated  
g++ -o bin/PM-plot-taxa src/class_tax.cpp -Wno-deprecated -w -ffunction-sections -fdata  
openmp  
g++ -o bin/PM-predict-func src/class_func.cpp -Wno-deprecated -w -ffunction-sections -f  
e -fopenmp  
g++ -o bin/PM-predict-func-nsti src/class_func_nsti.cpp -Wno-deprecated -w -ffunction-s  
ched -msse -fopenmp  
g++ -o bin/PM-predict-func-contribute src/class_func_contribute.cpp -Wno-deprecated -w  
ns -fmodulo-sched -msse -fopenmp  
g++ -o bin/PM-select-taxa src/taxa_sel.cpp -Wno-deprecated -w -ffunction-sections -fdat  
fopenmp  
g++ -o bin/PM-select-func src/func_sel.cpp -Wno-deprecated -w -ffunction-sections -fdat  
fopenmp
```

# 验证安装是否成功

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完成上述步骤后，可以使用以下命令验证软件安装是否成功。

**Command:** PM-pipeline –h

该命令输出PM-pipeline的帮助信息。

在安装成功的情况下，此命令将在终端中打印以下消息。

```
**Parallel-Meta Suite Installation Complete**  
**An example dataset with demo script is available in "example"**
```

# 案例演示

安装成功后，PMS就可以使用了，

我们提供了一个测试案例。

```
root@DESKTOP-74P0JFM:/parallel-meta-suite# ls
INSTALL.txt      Makefile      Parallel-Meta-Suite.md      Rscript
LICENSE          PMS-config    ReleaseNote-3.7.md      databases
root@DESKTOP-74P0JFM:/parallel-meta-suite# |
```

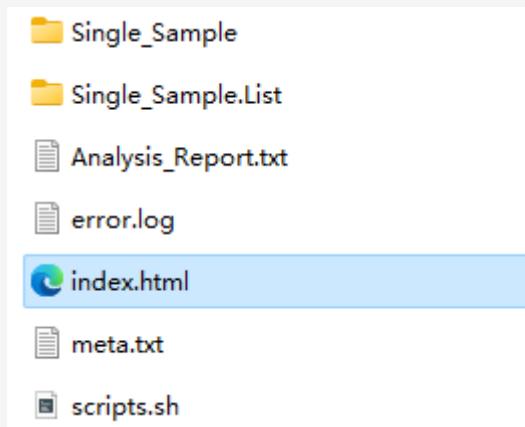
1 该测试案例可以在[parallel-meta-suite](#)文件夹下找到，  
名字是[example](#)

2 这个文件夹下包含了几个简单的  
样本[序列](#)和这些样本的[元数据](#)

3 [PMS-config](#)是帮助理解、  
生成命令的好帮手。

# 结果查看

PMS还提供了图形化的结果展示页面。



A screenshot of the 'Parallel-Meta Suite Results Viewer' software interface. At the top, it says 'PM Suite' and 'Parallel-Meta Suite Results Viewer'. Below that is a section titled 'Analysis Results' with the sub-instruction: 'Most results are listed here Click "More results" for detailed information'. There are six main analysis categories displayed in cards: 1. Taxonomy profile, 2. Relative Abundance, 3. Alpha diversity, 4. Beta diversity, 5. Distance matrix, and 6. Distribution. Each card has a 'View samples' button and a 'More results' link.

1 在结果文件夹中，

可以找到[index.html](#)

2 打开它，

可以找到各种分析的结果

# 如果对PMS的使用仍有疑问：

您可以阅读安装包中的文档

或

[Visit PMS GitHub page](#)



[Contact us](#)

Email: [suxq@qdu.edu.cn](mailto:suxq@qdu.edu.cn)

The screenshot shows a GitHub user profile for 'qdu-bioinfo'. The 'Repositories' tab is selected, displaying three public repositories:

- parallel-meta-suite** (Public)  
C++ | GNU General Public License v3.0 | Updated 6 days ago
- bioconda-recipes** (Public)  
Forked from bioconda/bioconda-recipes  
Conda recipes for the bioconda channel.
- staged-recipes** (Public)  
Shell | 2,044 | Updated 7 days ago