

# OTU ANALYSIS AND TAXONOMY

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## USEARCH

Ultra-fast sequence analysis

USEARCH has been cited by **3,277 papers**  
[Google scholar](#)  
Last updated 24 Jul 2016

**Features**

**Download**

**OTU clustering**

**Documentation**

**10 - 1,250x** BLAST  
**1 - 1,000x** CD-HIT

### High-throughput search and clustering

USEARCH is a unique sequence analysis tool with thousands of users world-wide. USEARCH offers search and clustering algorithms that are often orders of magnitude faster than BLAST.

### Improved productivity and insights

USEARCH combines many different algorithms into a single package with outstanding documentation and support. This cuts your learning curve, reduces the number of steps you need to take for a given task, and slashes compute times. USEARCH will encourage you to explore your data, enabling new insights and suggesting new analyses that you might not have tried with slower tools.

### Free for most users

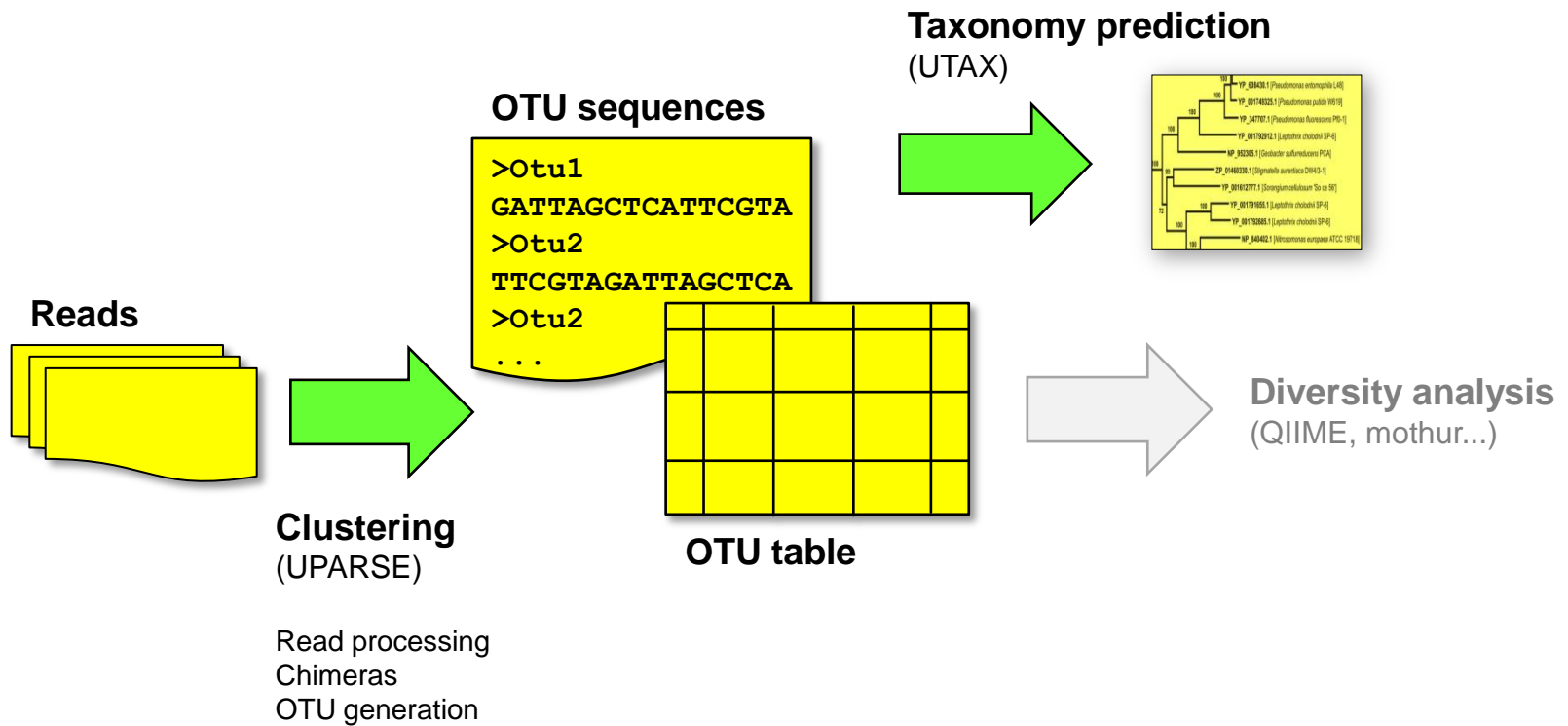
Licenses to use 32-bit USEARCH are offered at no charge for all users, including commercial.

**27,479**  
registered users

### 64-bit users

Joint Genome Institute  
MBL, Woods Hole  
Cornell Univ.  
CNRS (France)  
La Jolla Institute  
Ag. Research (NZ)  
Broad Institute  
Nestle  
LANL  
UC Davis  
UC Berkeley  
NCBI  
NIH  
Monsanto  
Caltech  
Pacific Biosystems  
*and many more.*

# OTU analysis



# Six commands

- Three hours of lectures, six commands
- Few minutes to process millions of MiSeq reads

## 1. Merge pairs

```
$usearch -fastq_mergepairs ../fq/F3D*_R1_*.fastq -fastqout $out/merged.fq \  
-relabel @ -log $out/merge.log
```

## 2. Quality filter

```
$usearch -fastq_filter $out/merged.fq -fastq_maxee 1.0 -fastaout $out/filtered.fa \  
-relabel Filt -log $out/filter.log
```

## 3. Find uniques

```
$usearch -derep_fulllength $out/filtered.fa -sizeout -relabel Uniq \  
-fastaout $out/uniques.fa -log $out/derep.log
```

## 4. Cluster & filter chimeras

```
$usearch -cluster_otus $out/uniques.fa -minsize 2 -otus $out/otus.fa \  
-relabel Otu -log $out/cluster_otus.log
```

## 5. Predict taxonomy

```
$usearch -utax $out/otus.fa -db ../utax/utax_16s_250.udb -strand plus \  
-fastaout $out/otus_tax.fa -utax_cutoff 0.9 -log $out/utax.log
```

## 6. Make OTU table

```
$usearch -usearch_global $out/merged.fq -db $out/otus_tax.fa -strand plus -id 0.97 \  
-log $out/make_otutab.log -otutabout $out/otutab.txt
```