Step 1, visit UMARS via http://musk.ibms.sinica.edu.tw/UMARS/

UMARS

Un-Mappable Reads Solution

miRNA Series

- VirMir
- ZooMir
- UMARS
- UMARS:EEJ
- UMARS:Vir

Links

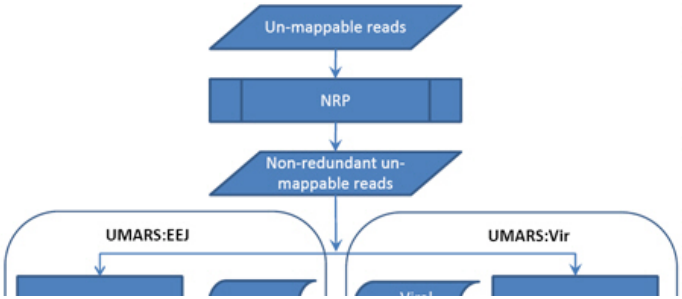
- UCSC Genome Browser
- miRBase
- FASTA Format
- NCBI BLAST
- srnaloop
- LIBSVM
- RepeatMasker

Welcome to UMARS Server

UMARS Recently, next generation sequencing (NGS) technology, including Roche 454, Illumina GA and ABI SOLiD platforms etc, emerged as a powerful tool for generating high-throughput sequencing data. In a typical analysis pipeline, the generated NGS sequence reads were first subject to adaptor trimming and mapping back to reference sequences, including genomes, scaffolds or transcripts. However, a fraction of sequence reads can not be mapped back to the reference sequences. These un-mappable reads were usually discarded without further consideration. It is of our interest to examine the possible biological relevance of un-mappable reads. Therefore, we have developed Un-MAppable Reads Solution (UMARS) pipeline to solve such problem. UMARS focuses on the scanning of viral genome (UMARS:Vir) or novel splicing junction (UMARS:EEJ) from un-mappable reads.

The first step of UMARS is to deal with the redundancy problem of NGS reads. For convenience and efficiency, we developed an in-house tool, called Non-redundant Reads Producer (NRP), to solve such a problem. The reads uploaded to UMARS must be processed by NRP in advance or be presented as the format of NRP output. Then, the un-redundant reads can be processed by either UMARS:Vir or UMARS:EEJ.

UMARS Flowchart & Services



Step 2, visit UMARS:Vir by clicking UMARS:Vir

UMARS

Un-Mappable Reads Solution

miRNA Series

- VirMir
- ZooMir
- UMARS
- UMARS:EEJ
- UMARS:Vir

Links

- UCSC Genome Browser
- miRBase
- FASTA Format
- NCBI BLAST
- srnaloop
- LIBSVM
- RepeatMasker

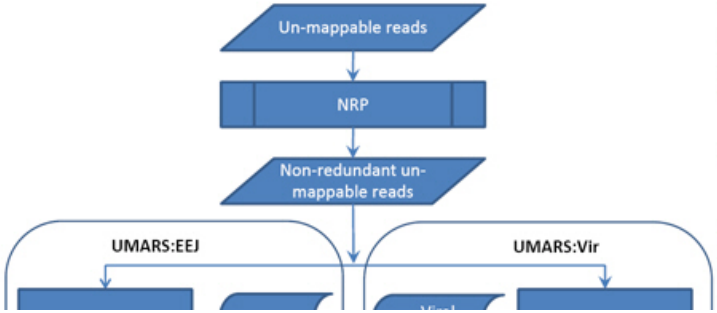
Welcome to UMARS Server

UMARS

Recently, next generation sequencing (NGS) technology, including Roche 454, Illumina GA and ABI SOLiD platforms etc, emerged as a powerful tool for generating high-throughput sequencing data. In a typical analysis pipeline, the generated NGS sequence reads were first subject to adaptor trimming and mapping back to reference sequences, including genomes, scaffolds or transcripts. However, a fraction of sequence reads can not be mapped back to the reference sequences. These un-mappable reads were usually discarded without further consideration. It is of our interest to examine the possible biological relevance of un-mappable reads. Therefore, we have developed Un-MAppable Reads Solution (UMARS) pipeline to solve such problem. UMARS focuses on the scanning of viral genome (UMARS:Vir) or novel splicing junction (UMARS:EEJ) from un-mappable reads.

The first step of UMARS is to deal with the redundancy problem of NGS reads. For convenience and efficiency, we developed an in-house tool, called Non-redundant Reads Producer (NRP), to solve such a problem. The reads uploaded to UMARS must be processed by NRP in advance or be presented as the format of NRP output. Then, the un-redundant reads can be processed by either UMARS:Vir or UMARS:EEJ.

UMARS Flowchart & Services



Step 3, visit UMARS:Vir upload page