

## NAME

SequenceFileUtil

## SYNOPSIS

```
use SequenceFileUtil ;

use SequenceFileUtil qw(:all);
```

## DESCRIPTION

SequenceFileUtil module provides the following functions:

AreSequenceLengthsIdentical, CalculatePercentSequenceIdentity, CalculatePercentSequenceIdentityMatrix, GetLongestSequence, GetSequenceLength, GetShortestSequence, IsClustalWSequenceFile, IsGapResidue, IsMSFSequenceFile, IsPIRFastaSequenceFile, IsPearsonFastaSequenceFile, IsSupportedSequenceFile, ReadClustalWSequenceFile, ReadMSFSequenceFile, ReadPIRFastaSequenceFile, ReadPearsonFastaSequenceFile, ReadSequenceFile, RemoveSequenceAlignmentGapColumns, RemoveSequenceGaps, WritePearsonFastaSequenceFile. SequenceFileUtil module provides various methods to process sequence files and retrieve appropriate information.

## FUNCTIONS

## AreSequenceLengthsIdentical

```
$Status = AreSequenceLengthsIdentical($SequencesDataRef);
```

Checks the lengths of all the sequences available in *SequencesDataRef* and returns 1 or 0 based whether lengths of all the sequence is same.

## CalculatePercentSequenceIdentity

```
$PercentIdentity =
  AreSequenceLengthsIdenticalAreSequenceLengthsIdentical(
    $Sequence1, $Sequence2, [$IgnoreGaps, $Precision]);
```

Returns percent identity between *Sequence1* and *Sequence2*. Optional arguments *IgnoreGaps* and *Precision* control handling of gaps in sequences and precision of the returned value. By default, gaps are ignored and precision is set up to 1 decimal.

## CalculatePercentSequenceIdentityMatrix

```
$IdentityMatrixDataRef = CalculatePercentSequenceIdentityMatrix(
  $SequencesDataRef, [$IgnoreGaps,
    $Precision]);
```

Calculate pairwise percent identity between all the sequences available in *SequencesDataRef* and returns a reference to identity matrix hash. Optional arguments *IgnoreGaps* and *Precision* control handling of gaps in sequences and precision of the returned value. By default, gaps are ignored and precision is set up to 1 decimal.

## GetSequenceLength

```
$SequenceLength = GetSequenceLength($Sequence, [$IgnoreGaps]);
```

Returns length of the specified sequence. Optional argument *IgnoreGaps* controls handling of gaps. By default, gaps are ignored.

## GetShortestSequence

```
($ID, $Sequence, $SeqLen, $Description) = GetShortestSequence(
  $SequencesDataRef, [$IgnoreGaps]);
```

Checks the lengths of all the sequences available in *\$SequencesDataRef* and returns *\$ID*, *\$Sequence*, *\$SeqLen*, and *\$Description* values for the shortest sequence. Optional arguments *\$IgnoreGaps* controls handling of gaps in sequences. By default, gaps are ignored.

## GetLongestSequence

```
($ID, $Sequence, $SeqLen, $Description) = GetLongestSequence(
  $SequencesDataRef, [$IgnoreGaps]);
```

Checks the lengths of all the sequences available in *SequencesDataRef* and returns *ID*, *Sequence*, *SeqLen*, and *Description* values for the longest sequence. Optional argument *\$IgnoreGaps* controls handling of gaps in sequences. By default, gaps are ignored.

## IsGapResidue

```
$Status = AreSequenceLengthsIdentical($Residue);
```

Returns 1 or 0 based on whether *Residue* corresponds to a gap. Any character other than A to Z is considered a gap residue.

## IsSupportedSequenceFile

```
$Status = IsSupportedSequenceFile($SequenceFile);
```

Returns 1 or 0 based on whether *SequenceFile* corresponds to a supported sequence format.

**IsClustalWSequenceFile**

```
$Status = IsClustalWSequenceFile($SequenceFile);
```

Returns 1 or 0 based on whether *SequenceFile* corresponds to Clustal sequence alignment format.

**IsPearsonFastaSequenceFile**

```
$Status = IsPearsonFastaSequenceFile($SequenceFile);
```

Returns 1 or 0 based on whether *SequenceFile* corresponds to Pearson FASTA sequence format.

**IsPIRFastaSequenceFile**

```
$Status = IsPIRFastaSequenceFile($SequenceFile);
```

Returns 1 or 0 based on whether *SequenceFile* corresponds to PIR FASTA sequence format.

**IsMSFSequenceFile**

```
$Status = IsClustalWSequenceFile($SequenceFile);
```

Returns 1 or 0 based on whether *SequenceFile* corresponds to MSF sequence alignment format.

**ReadSequenceFile**

```
$SequenceDataMapRef = ReadSequenceFile($SequenceFile);
```

Reads *SequenceFile* and returns reference to a hash containing following key/value pairs:

```
$SequenceDataMapRef->{IDs} - Array of sequence IDs
$SequenceDataMapRef->{Count} - Number of sequences
$SequenceDataMapRef->{Description}{$ID} - Sequence description
$SequenceDataMapRef->{Sequence}{$ID} - Sequence for a specific ID
$SequenceDataMapRef->{Sequence}{InputFileType} - File format
```

**ReadClustalWSequenceFile**

```
$SequenceDataMapRef = ReadClustalWSequenceFile($SequenceFile);
```

Reads ClustalW *SequenceFile* and returns reference to a hash containing following key/value pairs as describes in ReadSequenceFile method.

**ReadMSFSequenceFile**

```
$SequenceDataMapRef = ReadMSFSequenceFile($SequenceFile);
```

Reads MSF *SequenceFile* and returns reference to a hash containing following key/value pairs as describes in ReadSequenceFile method.

**ReadPIRFastaSequenceFile**

```
$SequenceDataMapRef = ReadPIRFastaSequenceFile($SequenceFile);
```

Reads PIR FASTA *SequenceFile* and returns reference to a hash containing following key/value pairs as describes in ReadSequenceFile method.

**ReadPearsonFastaSequenceFile**

```
$SequenceDataMapRef = ReadPearsonFastaSequenceFile($SequenceFile);
```

Reads Pearson FASTA *SequenceFile* and returns reference to a hash containing following key/value pairs as describes in ReadSequenceFile method.

**RemoveSequenceGaps**

```
$SeqWithoutGaps = RemoveSequenceGaps($Sequence);
```

Removes gaps from *Sequence* and return a sequence without any gaps.

**RemoveSequenceAlignmentGapColumns**

```
$NewAlignmentDataMapRef = RemoveSequenceAlignmentGapColumns(
    $AlignmentDataMapRef);
```

Using input alignment data map ref containing following keys, generate a new hash with same set of keys after residue columns containing only gaps have been removed:

```
{IDs} : Array of IDs in order as they appear in file
{Count}: ID count
{Description}{$ID} : Description data
{Sequence}{$ID} : Sequence data
```

**WritePearsonFastaSequenceFile**

```
WritePearsonFastaSequenceFile($SequenceFileName, $SequenceDataRef,
    [$MaxLength]);
```

Using sequence data specified via *SequenceDataRef*, write out a Pearson FASTA sequence file. Optional argument *MaxLength* controls maximum length sequence in each line; default is 80.

#### AUTHOR

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#### SEE ALSO

PDBFileUtil.pm

#### COPYRIGHT

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