

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 containg 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.

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SEE ALSO

PDBFileUtil.pm

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