1.1 -1.4

**2.1**

BlastP: Searching in protein sequence database with protein sequence

BlastN: Searching in nucleotide sequence database with nucleotide sequence

BlastX: Searching in protein sequence database with nucleotide sequence

**2.3.1**

Yes

**2.3.2**

HATPase

**2.4.1**

Similarity: Sequences have segments in common.

Homology: Sequences have some same segments, due to evolution.

**2.4.2**

Both terms describe certain degree of similarity in sequence. However, in homology, these similar sequences are evolutionarily relevant.

**2.4.3**

**3.1**

A sequence search and alignment tool, searching/aligning sequence database for homolog sequences using HMM.

**3.2**

Phmmer: searching for protein sequence against protein sequence database

Hmmscan: searching for protein sequence against profile-HMM database

Hmmsearch: protein alignment or do profile-HMM against protein sequence database

Jackhmmer: iterative search against protein sequence database

**3.3.1**

HMMER advantage:

1. search in a certain taxonomy.

2. Fast search in big database

3. presenting result according to taxonomy and domain. Better visualization method

Regarding algorithm:

1. Gaps are weighted instead of calculating gap open and extend penalty.

2. Using position-specific probabilities instead of BLOSUM

(Ref:

<https://doi.org/10.1093/nar/gkv397>

<https://doi.org/10.1093/nar/gkr367>)

**3.3.2**

**HMMER**

**3.3.3**

Short sequences: BLAST

No taxonomy requirement: BLAST

Others: HMMER

**4.3**

*Time:*

HMMER 19.51s

Jackhmmer (iteration 1) : 19.37s

Blast: 4 minutes

*Output:*

Same between HMMER and Jackhmmer (iteration 1)

**4.4**

Taxonomy-Blast:

A screenshot of a video game

Description generated with high confidence