BLAST+

BLAST+ is a widely used bioinformatics tool and algorithm for exploring sequence information in biological sequences such as amino acids or DNA. It was developed by people at the US National Institutes of Health.

**1. Print something if no parameters are supplied**

If no parameters are used BLAST directs you to the user manual.

**2. Always have a “-h” or “--help” switch**

BLAST has a -h switch for a brief USAGE summary and a -help switch for more in-depth descriptions.

**3. Have a “-v” or “--version” switch**

BLAST has a -version switch which prints the version and build date.

**4. Do not use stdout for messages and errors**

BLAST uses stderr for log-files.

**5. Always raise an error if something goes wrong**

BLAST exits with ‘0’ for success and ‘1’ when there is an error.

**6. Validate your parameters**

BLAST catches invalid parameters.

**7. Don’t hard-code any paths**

BLAST uses relative pathing.

**8. Don’t pollute the PATH**

BLAST uses a few master-commands (e.g. ‘blastn’ for ‘nucleotide’ searches, ‘blastp’ for ‘protein’) which is then used to invoke sub-commands.

**9. Check that your dependencies are installed**

Unsure how BLAST handles dependencies.

**10. Don’t distribute bare JAR files**

BLAST is not distributed as bare JAR files.