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Instalación de blast

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30 Nov 2017

From January 10-12, 2018, the NCBI will help with a bioinformatics hackathon in

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v.ncbi.nlm.nih.gov/guide/genetics-medicine/

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Data & Software

All Databases

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Databases

[NCBI C++ Toolkit Manual](#)
A comprehensive manual on the NCBI C++ toolkit, including its design and development framework, a C++ library reference, software examples and demos, FAQs and release notes. The manual is searchable online and can be downloaded as a series of PDF documents.

Downloads

[BLAST \(Stand-alone\)](#)
BLAST executables for local use are provided for Solaris, LINUX, Windows, and MacOSX systems. See the README file in the ftp directory for more information. Pre-formatted databases for BLAST nucleotide, protein, and translated searches also are available for downloading under the db subdirectory.

[FTP: BLAST Databases](#)
Sequence databases for use with the stand-alone BLAST programs. The files in this directory are pre-formatted databases that are ready to use with BLAST.

[FTP: CDD](#)
This site provides full data records for CDD, along with individual Position Specific Scoring Matrices (PSSMs), mFASTA sequences and annotation data for each conserved domain. See the README file for full details.

[FTP: ClinVar Data](#)
This site provides full data extractions in XML and summary data in VCF format. It contains files with information about standard terms used in [ClinVar](#), [MedGen](#), and [GTR](#).

[FTP: FASTA BLAST Databases](#)
Sequence databases in FASTA format for use with the stand-alone BLAST programs. These databases must be formatted using formatdb before they can be used with BLAST.

Quick Links

BLAST (Stand-alone)
GenBank: BankIt
GenBank: Sequin
GenBank: tbl2asn
SNP Submission Tool
Basic Local Alignment Search Tool (BLAST)
Cn3D
Conserved Domain Search Service (CD Search)
E-Utilities
Genome Workbench
Primer-BLAST
ProSplign
PubChem Structure Search
Splign
Vector Alignment Search Tool (VAST)

**BLAST®**[Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)**Download BLAST Software and Databases****BLAST+ executables**

Do you have difficulties running high volume BLAST searches? Do you have proprietary sequence data to search and cannot use the NCBI BLAST web site? Do you have access to your own server? Do you have your own research pipeline? Have security or IP concerns about sending searches outside of your organization? If you answered yes to any of these questions, read on!

The NCBI provides a suite of command-line tools to run BLAST called BLAST+. This allows users to perform BLAST searches on their own server without size, volume and database restrictions. BLAST+ can be used with a command line so it can be integrated directly into your workflow.

What are the next steps?

Download and install BLAST+. Installers and source code are available from <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>. Download the databases you need,(see database section below), or create your own. Start searching.

For more details, please see the [BLAST+ user manual](#), the [BLAST Help manual](#), the [BLAST releases notes](#), and the article in BMC Bioinformatics ([PubMed link](#)). See our [versioning policy](#).

The BLAST+ suite is the currently supported package. The older C toolkit executables are no longer supported. See our [versioning policy](#).

We are always listening and welcome your feedback at [BLAST Support Center](#).

Magic-BLAST

Magic-BLAST is a tool for mapping large next-generation RNA or DNA sequencing runs against a whole genome or transcriptome. Read more about Magic-BLAST at <https://ncbi.github.io/magicblast>.

Installers and source code are available from <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/magicblast/LATEST>.

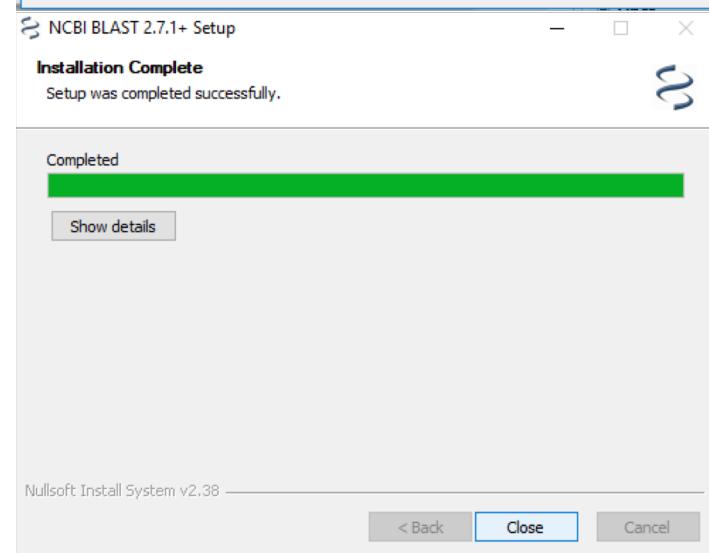
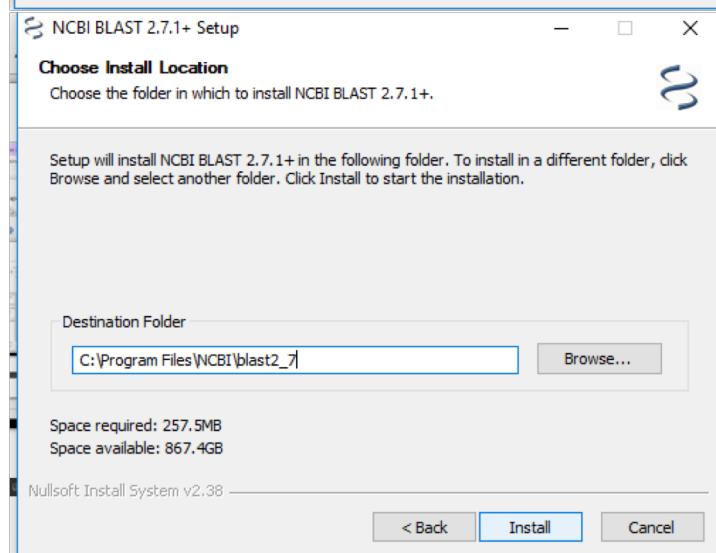
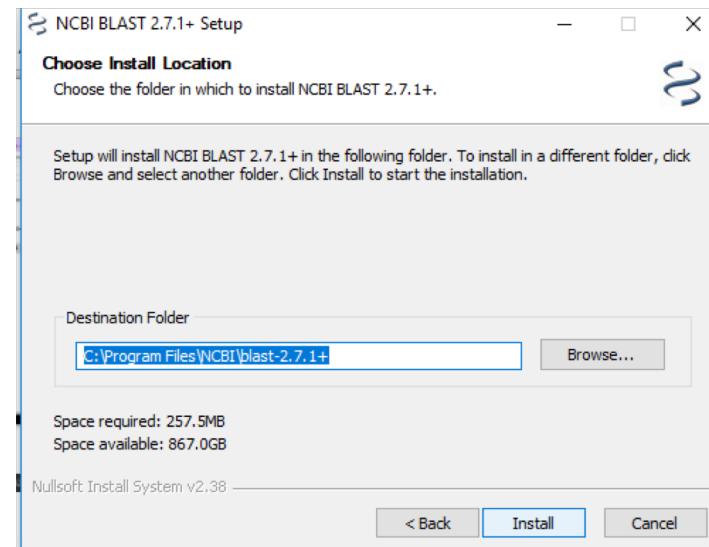
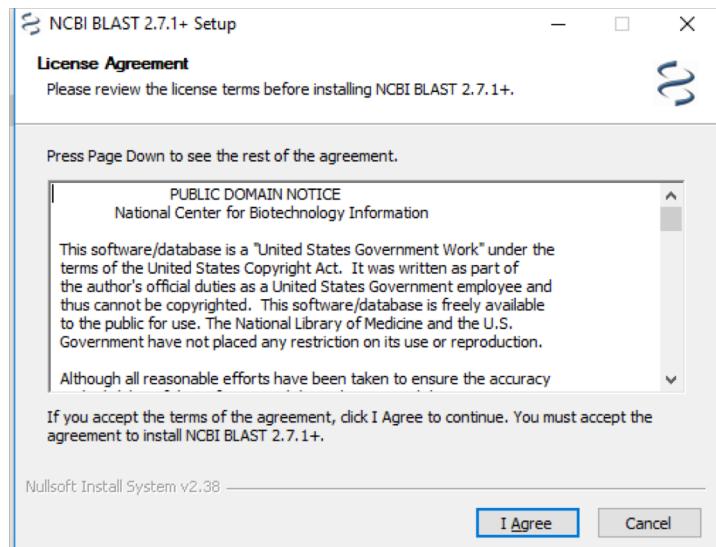
IgBLAST

Índice de <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>

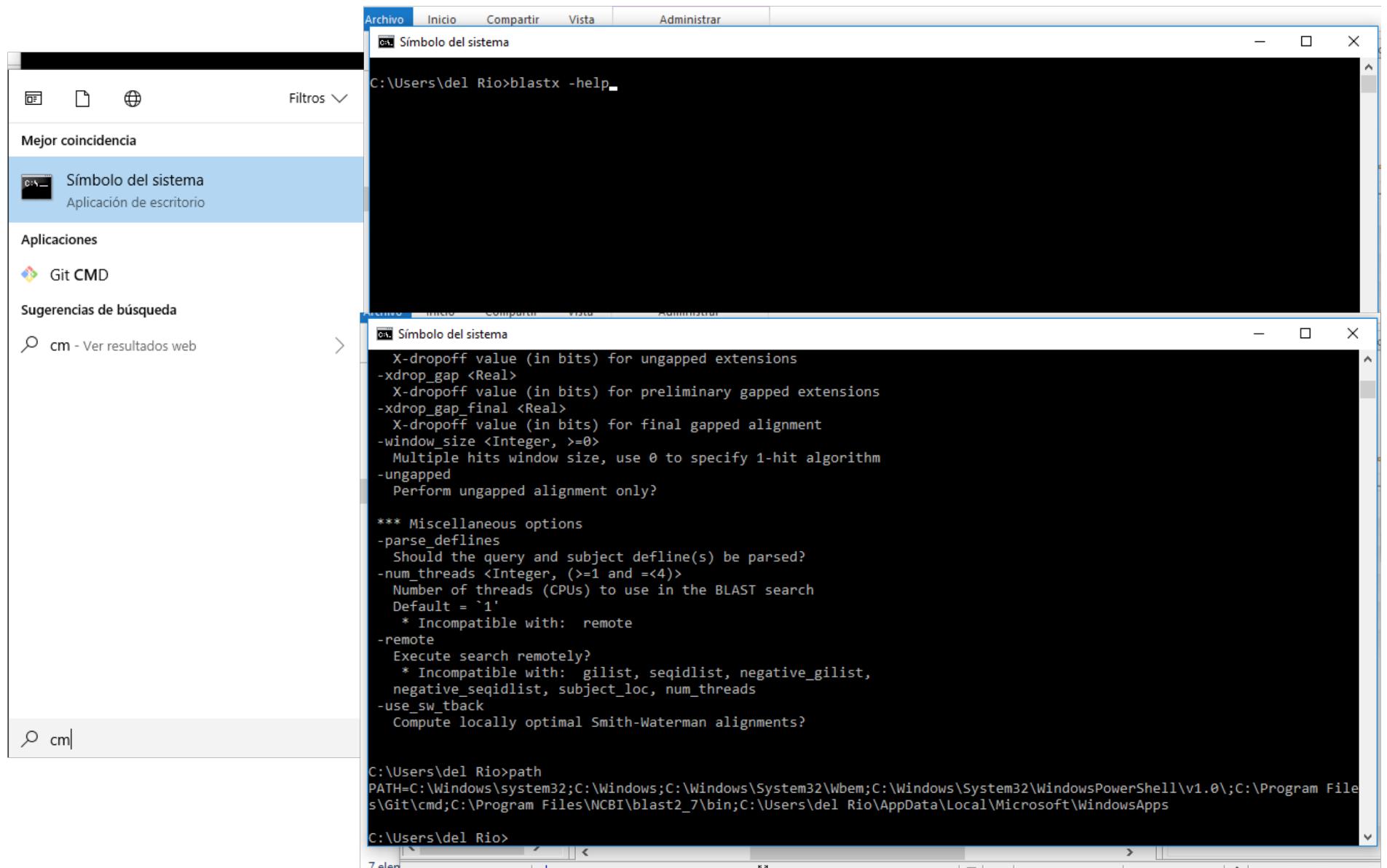
[Subir al directorio superior.](#)

Nombre	Tamaño	Última modificación
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Instalación



Corroborar la instalación



Editor de texto

Notepad ++

The image displays five windows from the Notepad++ v7.5.1 setup process:

- Bienvenido al Asistente de Instalación de Notepad++**: Welcome screen with a green lizard logo and instructions to click Next.
- Acuerdo de licencia**: License Agreement screen showing the GNU General Public License (GPL) terms. It includes a large text area with legal text, a checkbox for accepting the license, and buttons for Back, Accept, and Cancel.
- Elegir lugar de instalación**: Installation Path selection screen. It shows the default destination as C:\Program Files\Notepad++ and provides an "Examinar..." button to change it. It also displays storage requirements: 8.4MB required, 866.8GB available.
- Selección de componentes**: Component Selection screen. It lists optional components like Localization, Auto-completion Files, Themes, Context Menu Entry, Plugins, and Auto-Updater. Under "Don HO", there are checkboxes for "Don't use %APPDATA%" (unchecked), "Allow plugins to be loaded from %APPDATA%\notepad++\plugins" (unchecked), and "Create Shortcut on Desktop" (checked).
- Completando el Asistente de Instalación de Notepad++ v7.5.1**: Completion screen. It shows the Notepad++ logo, a message stating the program is installed, and a checkbox for "Ejecutando Notepad++ v7.5.1" (checked). It includes buttons for Back, Finish, and Cancel.