

## Cogent™ NGS Discovery Software v1.0 Quick Start Guide

The following information is provided as a high-level introduction to the software, also referred to as CogentDS. For more detailed information, please see the [Cogent NGS Discovery Software User Manual](#).

### Before you begin

- A. Supported operating systems
  - Windows 7, Windows 10
  - macOS Sierra (10.12) or higher
  - Linux CentOS 6.9 or higher
- B. Hardware requirements
  - Standard Laptop/Desktop (or server)
  - Memory: 8 GB RAM or higher
  - Free disk space: 2 GB or higher
- C. Additional dependencies
  - Internet connectivity on the computer
  - [R](#) version 3.6.0 or higher
    - For Windows: [RTools](#) software
    - For MacOS: [clang-7.0.0.pkg](#)
  - [RStudio](#) (IDE for R)
  - [R devtools](#) 2.1.0 or higher

### Required input files

CogentDS can take either of the following options for input:

1. `CogentDS.analysis.rda`, an R-object file output from [Cogent NGS Analysis Pipeline](#) (CogentAP)
2. Raw gene-count matrix and stats/metadata files

### Installation

1. [Sign up](#) to obtain the installation command from our website. You will receive an email automatically after signing up that will contain an authorization code you will need in Step 4.
2. Run RStudio
3. (Uninstall the previous version): To uninstall the previous version (called hanta), type the following command at the RStudio prompt:
 

```
remove.packages("hanta")
```

4. (Install the new version): Type the following command at the RStudio prompt (all one line):

```
devtools::install_github("takarabiosa/CogentDS", auth_token = "<AUTHCODE>")
```

<AUTHCODE> will be replaced by the authorization code, without the brackets (<>), sent in the sign-up confirmation email.

Example:

```
devtools::install_github("takarabiosa/CogentDS", auth_token = "abcde12345")
```

### To run Cogent NGS Discovery Software

1. Run RStudio
2. At the RStudio prompt, run the command:

```
CogentDS::launch()
```

The CogentDS user interface (GUI) will display in the default browser for the workstation or server.

**NOTE:** If prompted to download updates for R modules and additional guidance is needed, please refer to the [Cogent NGS Discovery Software notices page](#).

3. Click the [Get Started] button in the GUI.
4. *Select Input Data:* Upload the required input files by selecting one of the options from the drop-down.

**NOTE:** A mini dataset that can be used to test the CogentDS functionality can be downloaded as a zip file from the *\*Example data* link on this page. Unzip the file before using.

Click [Submit] to go to the next step.

- If the input is a `Cogent.analysis.rda` file, skip to step 7 on the next page.
- If the input is raw gene-count and stats files, continue to step 5.

5. *Quality control:*

**NOTE:** First-time users should start by using the default settings on the following two pages.

- a. QC Filter: Select how to filter non-informative cells and genes from the gene-count matrix. Click the [Next: Norm/Log] button when finished.
- b. Normalization and Transformation: Select how you would like to normalize and/or transform the data. Click [Next: Clustering] to continue.

6. *Cluster Analysis:* Adjust the gene filter method, number of variable genes to cluster by, and the reduction method (either UMAP or tSNE). Click [Launch Analysis] button to run the analysis. This step typically takes about a minute to complete.
7. *Discover:* The main/center section of the screen typically shows the results of graph-based clustering. The User Controls and Formatting menu options in the sidebar panel to the left of the screen can be used to modify how the graph displays.

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United States/Canada: +1.800.662.2566 • Asia Pacific: +1.650.919.7300 • Europe: +33.(0)1.3904.6880 • Japan: +81.(0)77.565.6999

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This document has been reviewed and approved by the Quality Department.

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