

Cogent™ NGS Discovery Software v1.5 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 v1.5 User Manual](#).

Before you begin

- A. Supported operating systems
 - Windows 7, Windows 10
 - macOS Mojave (10.14) 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 4.0.0 or higher
 - For Windows: [RTools](#), version compatible with R 4.x (e.g., rtools40)
 - For MacOS: [clang-7.0.0.pkg](#)
 - [RStudio](#) (IDE for R)
 - R [devtools](#) 2.4.2 or higher

Required input files

CogentDS can take either of the following options for input (choose one):

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

Installation

1. [Sign up](#) to download the installation package from our website.
2. Run RStudio.
3. (Uninstall previous software versions): If you have an older versions of CogentDS or the Takara Bio hanta software installed, type the following command(s) at the RStudio prompt to uninstall them:

CogentDS: `remove.packages("CogentDS")`

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

4. Type the following command at the RStudio prompt (all one line) to install CogentDS:

```
devtools::install_local("<PATH>/Cogent_NGS_Discovery_Software_v1.5.zip")
```

<PATH> will be replaced by the full path where the installation ZIP file is stored on the target server.

Example:

```
devtools::install_local("C:/temp/Cogent_NGS_Discovery_Software_v1.5.zip")
```

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, 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 to test the CogentDS installation can be downloaded from the *Example data link on the *Select Input Data* window. The file is called `analysis_demo.rda`.

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Click [Submit] to go to the next step.

- If the “Use previous settings and calculations” option is selected, skip to Step 8, *Cluster Analysis*.
- If the “Select new settings and run all calculations” option is selected and transcript analysis was performed in CogentAP, continue to Step 5, *Select data to use for clustering*.
- If the “Select new settings and run all calculations” option is selected and transcript analysis was **not** performed in CogentAP, go to Step 6, *Quality control*.

5. *Select data to use for clustering*: If transcript analysis was performed on the data in CogentAP (e.g., full-length applications), you will be prompted to choose one of the two options:

- ‘Use transcript counts’ to review transcript-level expression in CogentDS
- Otherwise, select ‘Use gene counts’ (default behavior)

6. *Quality control*:

NOTE: First-time users should start by using the default settings for the quality control options.

- QC Filter: Select how to filter non-informative cells and genes from the gene-count matrix.
- Click the [Next: Norm/Log] button when finished.

7. *Normalization and Transformation*: Select how you would like to normalize and/or transform the data. Click [Next: Clustering] to continue.

8. *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.

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

