Prerequisite:

- ➢ Discovery Studio+ installed on your PC.

Prerequisite terminologies:

In order to have a thorough understanding of our main topic, you should have the basic concept of the following terminologies:

- ➢ Drug Designing.
- ➢ Ligand.
- ➢ Binding pockets of proteins.
- ➢ Binding affinities.
- ➢ Biological receptors.

Introduction:

Discovery studio software can be used for several calculations in computer-aided drug design. Additionally, this software suite can be used for analyzing and modeling molecular structures, sequences, and other data which are of uttermost relevance to life science research. Also, this software provides functionality to enable us to view and edit data as well as perform basic data analysis.

Steps:

- **Download Discovery Studio:**
  - Click on the link given below to download the tool: https://3dsbiovia.com/resource-center/downloads/
- After downloading the tool, install it on your PC to get started with Discovery Studio.
- Open Discovery Studio, in the GUI of Discovery Studio, it provides:

Tools name	Description
Menu Bar:	➔ It grants users access to commonly used tools, such as file access, editing, and viewing commands.
Tool Set Bar:	➔ It is used to display different groups of related analysis tools in the Tools Explorer.
Toolbar:	➔ It grants access to commonly used tools for viewing and editing data.
Feature Search Box:	➔ It is used to search and open functionality.
Tools Explorer:	➔ It is used to locate and open data files.
Windows Tab:	➔ It allows you to work with data in a variety of windows without this data interfering.
Status Bar:	➔ It provides information on current activities being run on the software.

- Here are some of the functions of the Tool Set Bar:

Tab Names	Description
Macromolecules:	➔ It is used to build and edit nucleic acid as well as proteins. To superimpose two proteins,

	analyze their sequence and generate a report of the proteins using this tab.
Simulation tab:	➔ It is used to run simulations like Molecular dynamics, Calculate DMP, ENERGY using quantum mechanical calculations.
Receptor-Ligand Interaction:	➔ It is used for performing molecular docking, You can display the receptor surface and also visualize the 2D interactions and analyze ligand process.
Pharmacophore:	➔ It aids in building a database of available drugs or lead compounds manually or automatically.
Small molecule:	➔ It helps in drawing ligand structure, to minimize ligands, align two or more molecules, to calculate molecular properties and also create QSAR models, to design and analyze the building library.
X-rays Tab:	➔ It helps to build and validate protein structure.

- To **upload your already docked file from PyRx** and to visualize the 2D interaction as well as to calculate basic properties of this interaction:
    - Click the ‘File’ tab from the menu bar.
      [This will enable you to search and locate the complex (Protein-Ligand) in whichever folder you must have saved it.]
    - Once that is done you will see your protein and ligand complex displayed on your screen. It’ll display the protein structure in Ribbon like representation and the Ligand appears to be stick-like. You can turn it around also by right-clicking and then using the mouse to turn in round and round.
    - To **view the 2D interaction**, click on the ‘Receptor-Ligand Interactions’ button.
        - It’ll display two options, one is the ‘View interaction’ button and the second one is the ‘Define and edit binding site’ button’.

        - Click on the ‘View Interaction’ button, and then click on the ‘Ligand Interaction’ button.
          [So, once you click it, you get to see dotted lines which are indicative of the Interactions that exist between your complex.]
        - To view the 2D interaction, click on the tab with the ‘2D diagram’ indication.
          [It’ll display the 2D interaction in a separate window.]

Note: From the complex, you can see more of hydrogen bonds which are actually very important and crucial in drug design mainly because they help in the specificity of protein-ligand interactions by stabilizing the ligand in the binding pockets.

- There might be some unfavorable bonds which will be displayed in red color. [This is indicative of a force of repulsion between the complex and reduced stability in the receptor complex and might potentially ensue into adverse reaction.]
- To save the image of the resulting complex, for the sake of reporting the 2D/3D interaction, click on the image in the window, then go to ‘File’, click on ‘Save as…’, then locate a folder where you want to save and save it as an image file.

- To **calculate and visualize basic chemical properties**, click on the 3D interaction window, then click on ‘Chemistry’, it’ll display a list of instructions, then go to ‘Calculate Basic Properties’, it’ll display a pop-up window below the 3D interaction window.
  - Click on the top arrow to expand this pop-up window.
    [It’ll provide you the properties of the interaction.]
  - Then click on ‘Non bond’.
    [It’ll display the non bond interaction which is our primary concern.]
  - You can maximize the tab to get information about the interacting residues, the distance between them, the type of bonds and categories, and other relative additional information.
- To save this file, click on ‘File’, then ‘Save as…’.
  [You can only save this file in CSF format as this format is compatible with Excel.]

Summary:

In this video tutorial of Molecular Docking, we learned to analyze an already docked receptor-ligand complex using the Discovery Studio+ tool.

We also got to know how to visualize the interactions between the docked ligand and receptor molecules, as well as we learned how to analyze and calculate the basic chemical properties of the docked receptor-ligand complex using the Discovery Studio+ software.