why I decided to include the statements used in each function:
In the read_file() function I've included the input statement, because this way the user can check the Gene Expression
levels from multiple files, by specifying each time which file to look through, shortly it improves accessibility.
I've used the read_csv file because this is the easiest way to read the files including additional specifications, like
setting the dataframe index and specifying which are the separators when reading the file.
And I returned the dataframe, because we need to work with it for the following tasks and, also, one of the requirements
is to have a function that returns a variable and I thought this is the perfect function to do so as the next functions
only display data on the screen, without storing it.
In the plot_boxplots function, all the methods from the matplotlib.pyplot package were used to create and show the plot,
as well as improving it's readability by adding the title and labels. And the boxplot() method was used in order to
specify which dataframe are we working with.
In the plot_users_gene() function I've added the input statement so the user can check any Gene that he wants.
Afterwards I checked if the inputted Gene Name is valid or not so we won't have any unexpected behaviour.
Lastly, I've used the methods from the matplotlib.pyplot package to create and show the plot on user's screen, as well
as improving clarity by adding the title ant the labels again.

why I divided the program into these functions:
I tried to divide the program in a way that each function fulfills a requirement, except for the second task, because
the describe() method it's a function itself and I didn't see the point in implementing a function that contains only
other function. In conclusion, the plot_boxplots() function does the job for the first task, plot_user_gene() does the
job for the third task and read_file() does the job for the main request. All of them completing the following
requirements as well, by having 2+ functions developed by myself, one of them returning a variable.

why I think these functions are good for solving the problem:
I think these functions are very simple and efficient, each one does it's functionality and nothing more, the functions
don't require a lot of resources and are easy to understand in case other developers want to work on them. The functions
contain everything needed and are very flexible, giving users the opportunity to check for desired Genes in desired
files.