***In silico* analysis of the PTCome distribution (Kernel plots)**

1. Potential PTCome
    a. To obtain the potential PTCome, extract from Gene database (NCBI, https://www.ncbi.nlm.nih.gov/gene/) the cDNA sequence of the desired gene. Copy it in a text document.
    b. Import the text document in the PTCMAKER program or run the online code.
    c. Run the code in (https://github.com/leiretorices/Kernel-plots, section 1) to obtain unique potential PTC residues.
2. Germline-associated PTCome
    a. To obtain the germline-associated PTCome, browse for the desired PTP in the HGMD database (https://www.hgmd.cf.ac.uk). HGMD displays a data frame with missense and nonsense mutations together.
    b. Import the downloaded file in RStudio by File > Import Dataset > From Excel, or using the *read_excel()* function.
    c. Run the code in (https://github.com/leiretorices/Kernel-plots, section 2) to obtain unique PTC mutated residues.
3. Kernel plot representation
    a. Insert the amino acid length and the name of your protein of interest.
    b. Run the code in (https://github.com/leiretorices/Kernel-plots, section 3) to obtain a kernel plot representation. The three vectors (potential PTCome, cancer-associated PTCome and germline-associated PTCome) are rescaled to 100 to facilitate comparisons between proteins. Mirror vectors are generated to avoid bias at boundaries and a density is calculated of sum of the parental vector and the mirror vectors. The final plot contains black, and blue curves, which represent the potential PTCome and the germline-associated PTCome, respectively. Cancer-associated PTCome (COSMIC database) can be obtained from https://github.com/leiretorices/Kernel-plots section 4.