**breast cancer dataset**

**Objectives:**

1. **Build a logistic regression model without L2**
2. **Apply L2 regularization**
3. **Evaluate the model using metrics such as accuracy, precision, recall, and F1-score.**

The dataset includes measurements that describe the size, shape, and texture of cell nuclei (the central part of a cell) found in breast cancer tumors. These measurements were taken from images of tissue samples collected using a procedure called Fine Needle Aspiration (FNA), where a thin needle is used to extract cells from a breast lump for analysis.

In simpler terms, scientists used a needle to take tiny samples from breast lumps, took pictures of the cells, and then analyzed those pictures to measure different characteristics of the cells. These measurements help doctors determine whether the tumor is likely to be cancerous (malignant) or not (benign).

**Mean Features:** Provide an average view of the tumor's characteristics.

**Error Features:** Give insight into the variability of the tumor's characteristics.

**Worst Features:** Highlight the most extreme cases, which could be crucial for diagnosis.

**Mean Features (Columns 0-9):**

These features represent the mean value of various attributes calculated from all the cell nuclei in the image.

* **mean radius:** The mean of the distances from the center to points on the perimeter of the cell nuclei.
* **mean texture:** The standard deviation of the gray-scale values in the image, representing the texture.
* **mean perimeter:** The mean perimeter (circumference) of the cell nuclei.
* **mean area:** The mean area of the cell nuclei.
* **mean smoothness:** The mean local variation in radius lengths, indicating how smooth the borders of the cell nuclei are.
* **mean compactness:** The mean perimeter squared divided by the area, subtracting a constant, representing how compact the cell nuclei are.
* **mean concavity:** The mean of the severity of concave portions of the contour, indicating the concave nature of the cell borders.
* **mean concave points:** The mean number of concave portions of the contour, referring to the number of concave points on the boundary.
* **mean symmetry:** The mean symmetry of the cell nuclei.
* **mean fractal dimension:** The mean "coastline approximation" or fractal dimension, representing the complexity of the boundary.

**Error Features (Columns 10-19):**

These features represent the variation or standard error associated with each of the mean features.

* **radius error:** The standard error of the radius measurements.
* **texture error:** The standard error of the texture measurements.
* **perimeter error:** The standard error of the perimeter measurements.
* **area error:** The standard error of the area measurements.
* **smoothness error:** The standard error of the smoothness measurements.
* **compactness error:** The standard error of the compactness measurements.
* **concavity error:** The standard error of the concavity measurements.
* **concave points error:** The standard error of the concave points measurements.
* **symmetry error:** The standard error of the symmetry measurements.
* **fractal dimension error:** The standard error of the fractal dimension measurements.

**Worst Features (Columns 20-29):**

These features represent the worst (or largest) value for each feature across all the cell nuclei in the image.

* **worst radius:** The largest value of the radius across all cell nuclei.
* **worst texture:** The largest value of the texture across all cell nuclei.
* **worst perimeter:** The largest value of the perimeter across all cell nuclei.
* **worst area:** The largest value of the area across all cell nuclei.
* **worst smoothness:** The largest value of the smoothness across all cell nuclei.
* **worst compactness:** The largest value of the compactness across all cell nuclei.
* **worst concavity:** The largest value of the concavity across all cell nuclei.
* **worst concave points:** The largest value of the concave points across all cell nuclei.
* **worst symmetry:** The largest value of the symmetry across all cell nuclei.
* **worst fractal dimension:** The largest value of the fractal dimension across all cell nuclei.

**Target (Column 30):**

* **target:** The label that indicates whether the tumor is benign (0) or malignant (1).