

# Dataset Introduction RT-Gene

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The processed result only contains `.label` file. The image should be read from the path of original `RT-Gene` dataset.

## File Structure

```
RT-Gene
  |-Label
    |-test
    |-train
      |-valid.label
      |-train1.label
      |-train2.label
      |-train3.label
```

## `.label` File Format

Each `.label` file contains the data of one cluster. Each line contains the data of one image. The first line in `.label` file is the name of contained variables. Variables are separated by space. As for variables contain more than one value, values are separated by `,`.

- `Face` - `string` - Path of face image.
- `Left` - `string` - Path of left eye image.
- `Right` - `string` - Path of right eye image.
- `Origin` - `string` - Indicate the original image.
- `3DGaze` - `(3,)` - Ground truth of 3D gaze direction vector.
- `3DHead` - `(3,)` - Ground truth of 3D head orientation vector.
- `2DGaze` - `(2,)` - Ground truth of 2D gaze direction vector *i.e.* yaw and pitch.
- `2DHead` - `(2,)` - Ground truth of 2D head orientation vector *i.e.* yaw and pitch.

## Getting Start.

You could read the line in `.label` file for reading image data. Note that, the image should be read from the path of original `RT-Gene` dataset. Assuming the path of original `RT-Gene` dataset is `/home/RT-Gene`. You could:

```
import os
import cv2

# line; One line in `.label` file.
imroot = '/home/RT-Gene'

face_path = os.path.join(imroot, line.split(' ')[0])
left_path = os.path.join(imroot, line.split(' ')[1])
right_path = os.path.join(imroot, line.split(' ')[2])
```

```
face_image = cv2.imread(face_path)
left_image = cv2.imread(left_path)
right_image = cv2.imread(right_path)

label = line.strip().split(' ')[4].split(",")
label = np.array(label).astype('float')
```