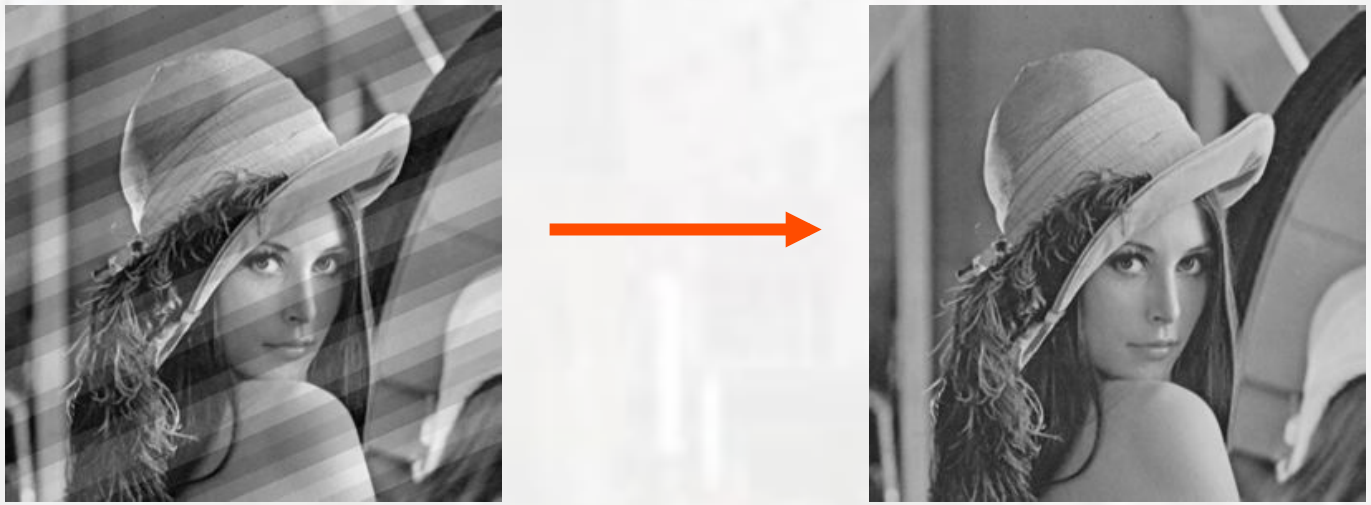
GA Group Projects

- Today we will form teams of several students;
- Each team will implement a GA in Matlab (or C/Java/VB?) to restore a corrupted image:



- Each team should have one good programmer, and access to a notebook computer (preferably with Matlab)!
- You will submit a written report in week 15 and give a short presentation in week 14 (in English)

GA Group Project: details

- The form of the corruption source is additive noise:

  $$N(row,col) = NoiseAmp \times \sin([2\pi \times NoiseFreqRow \times row] + [2\pi \times NoiseFreqCol \times col]))$$

- Teams must code a simple GA that optimises the three unknown constants **NoiseAmp**, **NoiseFreqRow**, and **NoiseFreqCol** such that the restoration error (the difference between the original and GA-optimised restored image) is minimised.
- To make things easy, we will measure the average per-pixel restoration error, thus:

  $$\text{Restoration error} = (I_{original} + Noise^{GA}) - I_{corrupted}$$

  where $I_{original}$ is the original uncorrupted Lena image, $I_{corrupted}$ is the corrupted image (I will give you), and $Noise^{GA}$ is the modelled GA corruption noise using the noise equation above.

GA Group Project: details

- Each iteration of your GA will, *for each gene in the population*:
  - Generate new values for **NoiseAmp**, **NoiseFreqRow**, and **NoiseFreqCol**.
  - Corrupt the original image using the equation

N(row,col)=NoiseAmp×sin([2π×NoiseFreqRow×row]+[2π×NoiseFreqCol×col]))

  - Measure the restoration error (subtract the GA corrupted image from the original corrupted image). This becomes the (inverse of) this gene's fitness
  - Make new child genes using selection, crossover, and mutation functions.
- The search ranges for the three variables are:
  - **NoiseAmp** 0 to 30.0
  - **NoiseFreqRow** 0 to 0.01
  - **NoiseFreqCol** 0 to 0.01
- Each gene encodes all three variables. If you use 1 byte per variable, each gene will be 24-bits, if you use 2-bytes per variable, 48 bits:

10110111 01010001 11001010 (24-bits per gene)

NoiseAmp NoiseFreqRow NoiseFreqCol

- You need to map the (binary) integer values of each gene to floating point values for the variables. I.e, for **NoiseAmp, 00000000=0.0 and 11111111=30.0**