

# Exercise 1

## (a) Single gradient descent step and first-order decrease

Current iterate:  $x_k$ . Using fixed stepsize  $\lambda^{-1}$ , one (gradient descent) step gives

$$x_{k+1} = x_k - \lambda^{-1} f'(x_k).$$

Use a first-order Taylor expansion of  $f$  around  $x_k$  to approximate the change in cost:

$$f(x_{k+1}) \approx f(x_k) + f'(x_k)(x_{k+1} - x_k).$$

Substitute  $x_{k+1} - x_k = -\lambda^{-1} f'(x_k)$  to obtain the approximate decrease

$$\Delta f \equiv f(x_{k+1}) - f(x_k) \approx f'(x_k)(-\lambda^{-1} f'(x_k)) = -\lambda^{-1} \textcolor{red}{i}$$

So the expected (first-order) decrease is,

$$\Delta f \approx -\lambda^{-1} \textcolor{red}{i}$$

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## (b) Using the result to adjust stepsize

From part (a), the decrease scales with  $\lambda^{-1} (f')^2$ . To make progress comparable across situations one can

- choose  $\lambda^{-1}$  inversely proportional to  $(f')^2$  (or to a surrogate of it), or
- better: choose  $\lambda^{-1}$  proportional to an estimate of  $1/f''$  so that step length adapts to local curvature.

Practically: monitor  $f'(x_k)$  and set  $\lambda^{-1}$  smaller when  $(f')^2$  (or curvature) is large to keep predictable decreases.

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## (c) Effect of rescaling the independent variable

Define the rescaled cost  $\tilde{f}(x) := f(\alpha x)$  with  $\alpha > 0$ . Its derivative is

$$\tilde{f}'(x) = \frac{d}{dx} f(\alpha x) = \alpha f'(\alpha x).$$

If we perform one gradient step on  $\tilde{f}$  with the same stepsize  $\lambda^{-1}$  starting at  $x_k$ , the expected decrease (by part (a)) is

$$\Delta \tilde{f} \approx -\lambda^{-1} \dot{c}$$

Thus, holding  $\lambda^{-1}$  fixed, the expected decrease is multiplied by  $\alpha^2$ . In other words, rescaling the independent variable changes the magnitude of the predicted cost decrease (so optimization behaviour depends on the unit scale).

## (d) Why $\lambda^{-1} = (\tilde{\lambda} f'')^{-1}$ gives scale invariance

For the scaled cost  $\tilde{f}(x) = f(\alpha x)$ ,  
 $\tilde{f}''(x) = \alpha^2 f''(\alpha x)$ .

Set the stepsize as

$$\lambda^{-1} = (\tilde{\lambda} f'')^{-1}$$

(and for the scaled problem use  $\tilde{f}''$ ).

The predicted decrease becomes

$$[\begin{aligned} \Delta \tilde{f} &\approx -(\tilde{\lambda} f'')^{-1} [\tilde{f}''(\alpha x_k)]^2 \\ &= -\frac{1}{\tilde{\lambda} f''(\alpha x_k)} [\tilde{f}''(\alpha x_k)]^2 \end{aligned}]$$

All factors of  $\alpha$  cancel, so the expected decrease matches the unscaled case.

Thus choosing  $\lambda^{-1} \propto (f'')^{-1}$  yields scale-invariant progress.

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## (e) Carry-over to Gauss–Newton / Levenberg–Marquardt

For a scalar residual  $h(x)$ ,

$$f(x) = h(x)^2,$$

$$f'(x) = 2h(x)h'(x),$$

$$f''(x) = 2h'(x)^2 + 2h(x)h''(x).$$

Gauss–Newton keeps only the dominant term  $2h'(x)^2$ .

Thus the LM stepsize analogue is

$$\lambda^{-1} = \left( \tilde{\lambda} [h'(x)]^2 \right)^{-1}.$$

Under a rescaling  $x \mapsto \alpha x$ ,

$h'(x)$  becomes  $\alpha h'(\alpha x)$ ,

so  $[h'(x)]^2$  gains a factor  $\alpha^2$ .

In the predicted decrease, the term  $[f'(x)]^2$  contains  $[h'(x)]^2$ ,

and the stepsize denominator also contains  $[h'(x)]^2$ .

The  $\alpha^2$  factors cancel, leaving the expected progress unchanged.

Thus LM retains the same scale invariance when using  
 $\lambda^{-1} \propto [h'(x)]^{-2}$ .

## Exercise 2

a)

We used Scipy's implementation of the median filter ([https://docs.scipy.org/doc/scipy-1.11.4/reference/generated/scipy.ndimage.median\\_filter.html](https://docs.scipy.org/doc/scipy-1.11.4/reference/generated/scipy.ndimage.median_filter.html)). The value for "size" parameter was chosen empirically by testing and comparing to the example image from the assignment.

```
from skimage import io, img_as_float
from scipy import ndimage
import matplotlib.pyplot as plt

image = img_as_float(io.imread('brain-noisy.png'))
denoised = ndimage.median_filter(image, size=4)

plt.figure(figsize=(12,6))
plt.subplot(1,2,1)
plt.imshow(image, cmap="gray")
plt.title("Original noisy image")
plt.axis("off")

plt.subplot(1,2,2)
plt.imshow(denoised, cmap="gray")
plt.title("Image after denoising")
plt.axis("off")
plt.show()
```

Original noisy image

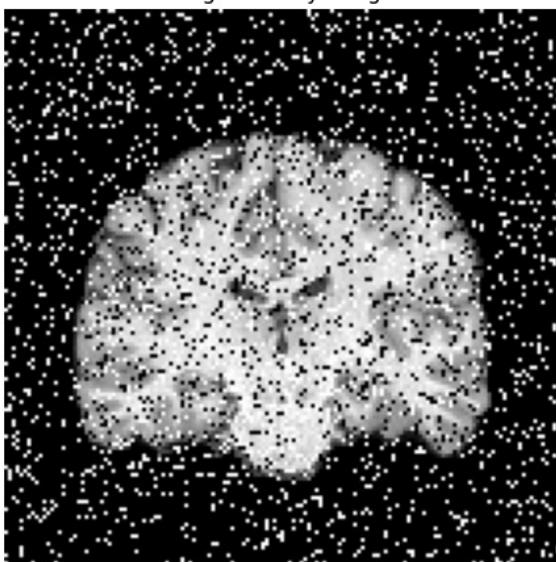
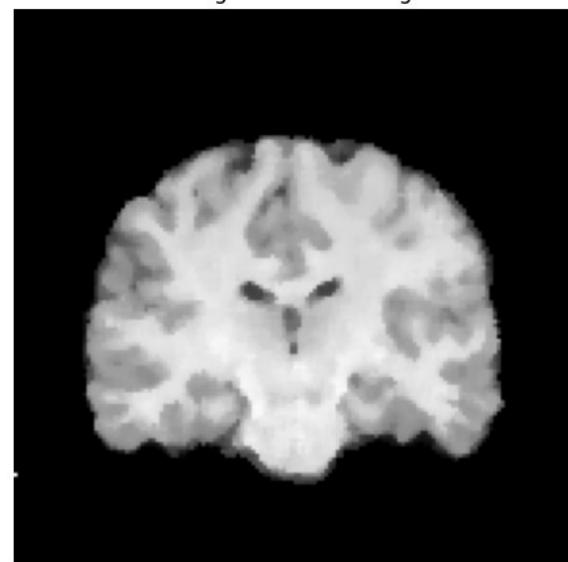


Image after denoising



b)

Looking at the log-scaled histogram we can see 4 distinct peaks. The peak near 0 is probably the background values that were included in the mask (our mask looks to cover a larger area than the denoised image brain). Looking at the other peaks we come up with the intensity value ranges as:

CSF : 0.05-0.5

Gray matter(GM): 0.5-0.75

white matter(WM): 0.75-1

There is definitely overlap between these ranges in the actual values but this is the estimate we could come up with just from looking at the histogram.

To estimate the mixing weights, we used a very rough calculation of area under the curve. For this matter we decided a non-log scaled histogram would be more useful to find the heights. For this we just use area of a rectangle with width=the intensitiy range and height=visually average count. Therefore using the assumptions :

CSF -> width=0.45 height=10 area=4.5

GM -> width=0.25 height=70 area=17.5

WM -> width=0.25 height=120 area=30

This gives:

$$\text{CSF} = 4.5/52 = 0.086$$

$$\text{GM} = 17.5/52 = 0.34$$

$$\text{WM} = 30/52 = 0.57$$

We approximate mixing weights (to sum=1):

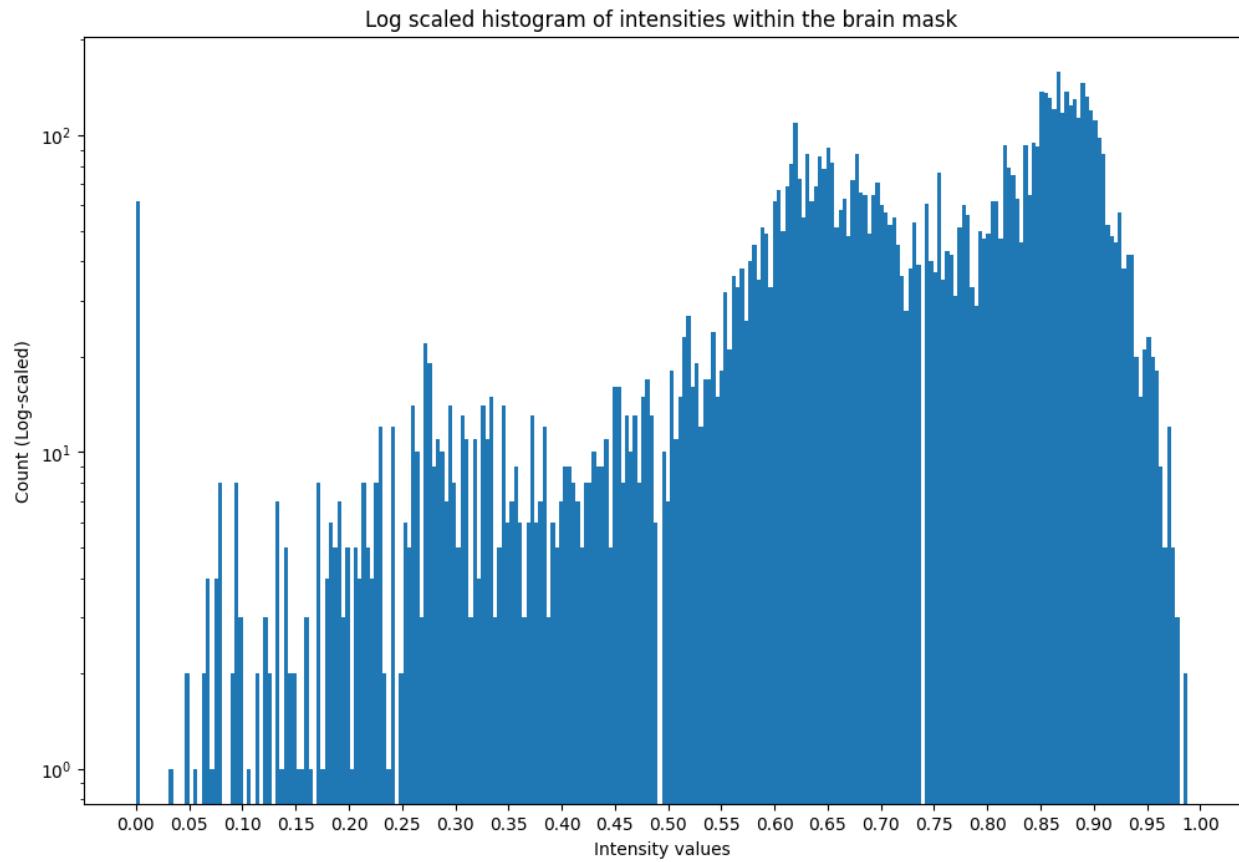
$$\text{Pi\_csf}=0.09$$

$$\text{Pi\_GM}=0.34$$

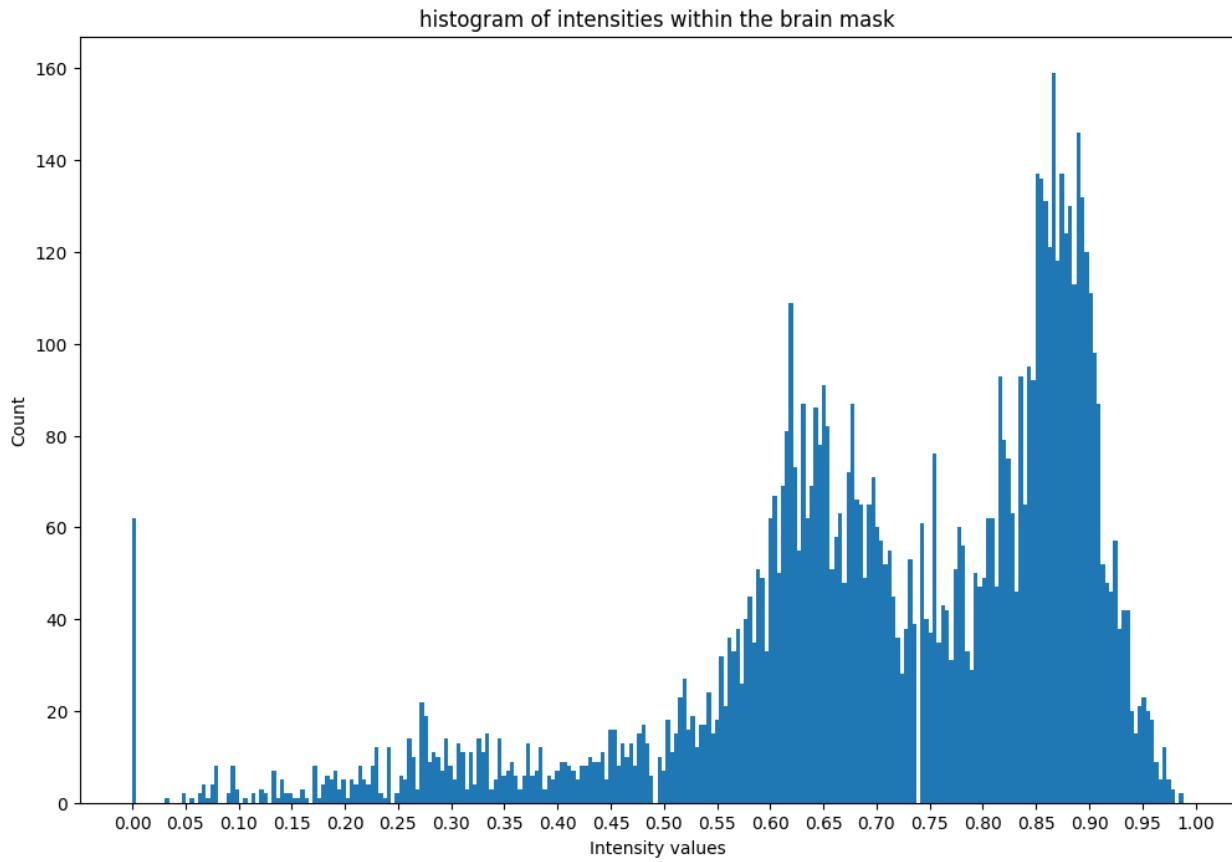
$$\text{Pi\_WM}=0.57$$

```
import numpy as np
from matplotlib.ticker import MultipleLocator

mask_image=io.imread("mask.png")
mask= mask_image > 0
brain_vals = denoised[mask]
plt.figure(figsize=(12,8))
plt.hist(brain_vals,bins=256)
plt.yscale('log')
ax = plt.gca()
ax.xaxis.set_major_locator(MultipleLocator(0.05))
plt.title("Log scaled histogram of intensities within the brain mask")
plt.xlabel("Intensity values")
plt.ylabel("Count (Log-scaled)")
plt.show()
```



```
plt.figure(figsize=(12,8))
plt.hist(brain_vals,bins=256)
ax = plt.gca()
ax.xaxis.set_major_locator(MultipleLocator(0.05))
plt.title("histogram of intensities within the brain mask")
plt.xlabel("Intensity values")
plt.ylabel("Count")
plt.show()
```



C)

The mixing weights were already estimated in b.

to estimate mean we just visually choose the intensity values where the peaks are visible:

mean\_CSF : 0.27

mean\_Gray matter(GM): 0.63

mean\_white matter(WM): 0.87

to estimate variance we use the 68-95-99 rule of normal distribution. We assume that the tails of the distributions are overlapping so we use the estimate that the range values of each group should fall within 2 sigma of the mean from both side so 4 sigma overall. Using the ranges from b and the estimated means we get:

var\_CSF :  $(0.45/4)^2 = (0.1125)^2 = 0.0126$

var\_Gray matter(GM):  $(0.25/4)^2 = (0.0625)^2 = 0.0039$

var\_white matter(WM):  $(0.25/4)^2 = (0.0625)^2 = 0.0039$

```
N = brain_vals.shape[0]
K = 3
responsibility = np.zeros((N, K), dtype=float)
means = np.array([0.27, 0.63, 0.87], dtype=float)
vars = np.array([0.0126, 0.0039, 0.0039], dtype=float)
mix = np.array([0.09, 0.34, 0.57], dtype=float)
```

```

def normal_pdf(x, mu, var): # this is  $N(xi | \mu_k, \sigma^2_k)$ 
    return (1.0 / np.sqrt(2.0 * np.pi * var)) * np.exp(-0.5 * (x - mu)**2 / var)

def E_step(img_data, responsibility):
    for i in range(N):
        x_i = img_data[i]
        denominator = 0
        for k in range(K):
            denominator += mix[k] * normal_pdf(x_i, means[k], vars[k])
        for k in range(K):
            numerator = mix[k] * normal_pdf(x_i, means[k], vars[k])
            responsibility[i, k] = numerator / denominator

E_step(brain_vals, responsibility)
print(responsibility)

[[1.00000000e+00 9.75738846e-21 1.47696033e-40]
 [1.00000000e+00 9.75738846e-21 1.47696033e-40]
 [1.00000000e+00 9.75738846e-21 1.47696033e-40]
 ...
 [9.99947271e-01 5.27290141e-05 3.99094198e-16]
 [9.99947271e-01 5.27290141e-05 3.99094198e-16]
 [9.99992790e-01 7.20961796e-06 1.28261208e-17]]

```

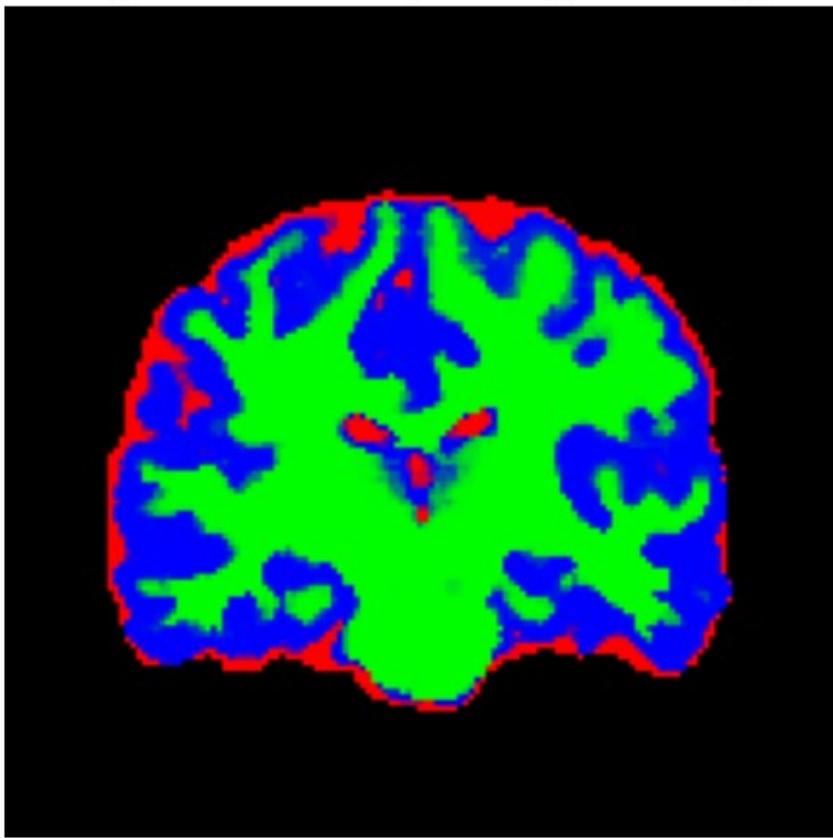
d)

```

H, W = denoised.shape
result= np.zeros((H, W, 3), dtype=float) #the 3rd dimension is for
#rgb so height x weight x rgb
result[..., 0][mask] = responsibility[:, 0]
result[..., 2][mask] = responsibility[:, 1]
result[..., 1][mask] = responsibility[:, 2]
plt.figure()
plt.imshow(result)
plt.title("Segmentation result (After only one E-step)")
plt.axis("off")
plt.tight_layout()
plt.show()

```

Segmentation result (After only one E-step)



e)

```
def M_step(img_data,responsibility):
    for k in range(K):
        num_mu=0
        num_var=0
        N_k=0
        for i in range(N):
            num_mu += responsibility[i,k]*img_data[i]

            N_k += responsibility[i,k]
        mean=num_mu/N_k
        means[k]=mean
        mix[k]=N_k/N
        for i in range(N):
            num_var += responsibility[i,k]*pow((img_data[i] - mean),2)
        vars[k]=num_var/N_k

M_step(brain_vals,responsibility)
print("re-computed means:", np.round(means, 3))
print("re-computed variances:", np.round(vars, 3))
print("re-computed mixing weights:", np.round(mix, 3))
```

```
re-computed means: [0.288 0.637 0.854]
re-computed variances: [0.019 0.004 0.003]
re-computed mixing weights: [0.095 0.39 0.515]
```

f)

We really couldn't figure out why our final segmentation is not as smooth as the example picture in the assignment. There are more red (CSF) patches in the blue (GM) area. We even lowered the tolerance and ran it for longer until convergence but no immediate improvements. It might be due to our initialization values.

```
N = brain_vals.shape[0]
K = 3
responsibility = np.zeros((N, K), dtype=float)
means = np.array([0.27, 0.63, 0.87], dtype=float)
vars = np.array([0.0126, 0.0039, 0.0039], dtype=float)
mix = np.array([0.09, 0.34, 0.57], dtype=float)
max_iter = 500
tol = 1e-10

for iter in range(max_iter):
    old_means = means.copy()
    old_vars = vars.copy()
    old_mix = mix.copy()
    E_step(brain_vals, responsibility)
    M_step(brain_vals, responsibility)

    diff_means = np.max(np.abs(means - old_means))
    diff_vars = np.max(np.abs(vars - old_vars))
    diff_mix = np.max(np.abs(mix - old_mix))
    diff = max(diff_means, diff_vars, diff_mix)

    print(f"Iter {iter:02d}")

    if diff < tol:
        print("Converged.")
        break

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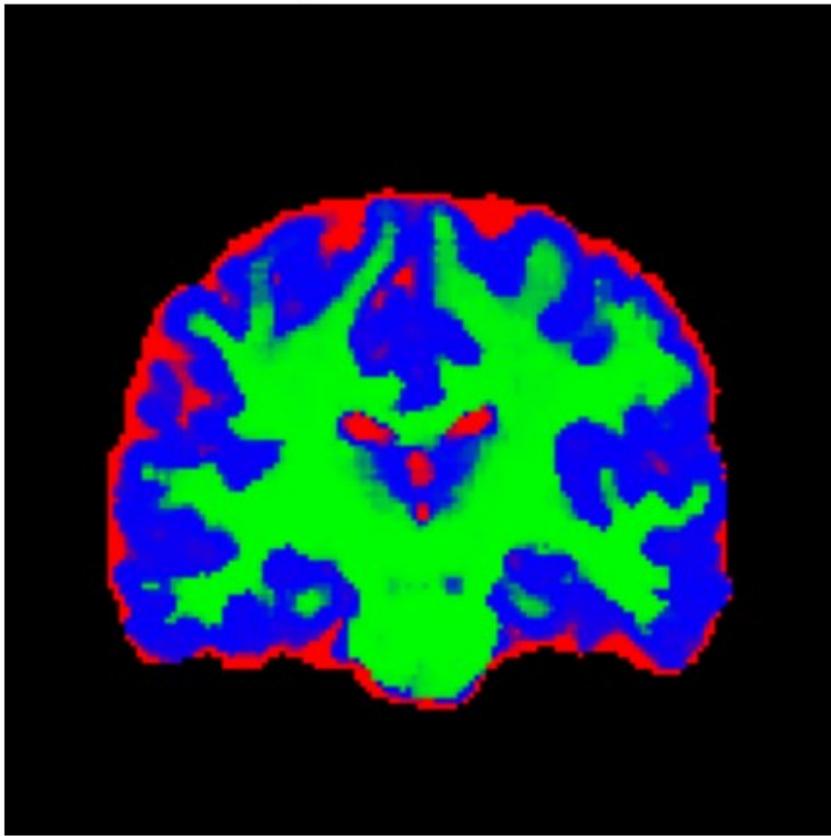
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Converged.

print("final means:", np.round(means, 3))
print("final variances:", np.round(vars, 3))
print("final mixing weights:", np.round(mix, 3))
H, W = denoised.shape
result= np.zeros((H, W, 3), dtype=float)
result[..., 0][mask] = responsibility[:, 0]
result[..., 2][mask] = responsibility[:, 1]
result[..., 1][mask] = responsibility[:, 2]
plt.figure()
plt.imshow(result)
plt.title("Segmentation result")
plt.axis("off")
plt.tight_layout()
plt.show()

final means: [0.351 0.668 0.871]
final variances: [0.031 0.006 0.002]
final mixing weights: [0.12 0.455 0.425]
```

Segmentation result



## Exercise 3

a)

Leaving out the median filtering and running one 1 E-step we get the hard labeled image of the noisy original image.

```
from skimage import io, img_as_float
from scipy import ndimage
import matplotlib.pyplot as plt
import numpy as np
from matplotlib.ticker import MultipleLocator

image = img_as_float(io.imread('brain-noisy.png'))

mask_image=io.imread("mask.png")
mask= mask_image > 0
brain_vals = image[mask]

N = brain_vals.shape[0]
```

```

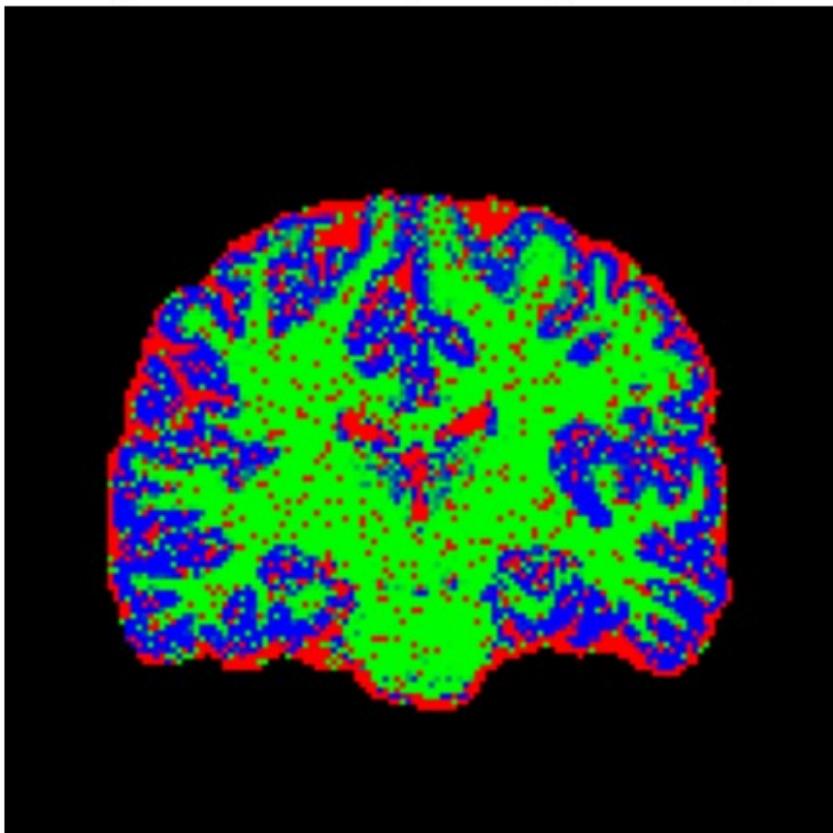
K = 3
responsibility = np.zeros((N, K), dtype=float)
means = np.array([0.27, 0.63, 0.87], dtype=float)
vars  = np.array([0.0126, 0.0039, 0.0039], dtype=float)
mix   = np.array([0.09, 0.34, 0.57], dtype=float)

E_step(brain_vals, responsibility)

H, W = image.shape
result= np.zeros((H, W, 3), dtype=float) #the 3rd dimension is for
rgb so heigh x weight x rgb
result[..., 0][mask] = responsibility[:, 0]
result[..., 2][mask] = responsibility[:, 1]
result[..., 1][mask] = responsibility[:, 2]
plt.figure()
plt.imshow(result)
plt.title("Segmentation result (After only one E-step)")
plt.axis("off")
plt.tight_layout()
plt.show()

```

Segmentation result (After only one E-step)



b)

```
import numpy as np
import matplotlib.pyplot as plt

def get_neighbors_indices(row, col, H, W):
    neighbors = []
    deltas = [(-1, 0), (0, 1), (1, 0), (0, -1)]
    for dr, dc in deltas:
        nr, nc = row + dr, col + dc
        if 0 <= nr < H and 0 <= nc < W:
            neighbors.append((nr, nc))
    return neighbors

def compute_unary_potential(pixel_index, label_k, means, vars):
    x_i = brain_vals[pixel_index]
    pdf_val = normal_pdf(x_i, means[label_k], vars[label_k])
    return -np.log(pdf_val + 1e-15)

def compute_pairwise_potential(label_i, label_j, beta):
    return beta if label_i != label_j else 0.0

def ICM_iteration(labels_2D, means, vars, beta, mask, H, W, N, K,
                   brain_vals):
    map_2D_to_1D = -np.ones((H, W), dtype=int)
    map_2D_to_1D[mask] = np.arange(N)

    brain_pixels_coords = np.argwhere(mask)
    new_labels_2D = labels_2D.copy()
    changes = 0

    for r, c in brain_pixels_coords:
        original_label = labels_2D[r, c]
        min_energy = float('inf')
        best_label = original_label
        pixel_1D_index = map_2D_to_1D[r, c]

        for k in range(K):
            # Calculate Unary Potential
            x_i = brain_vals[pixel_1D_index]
            pdf_val = (1.0 / np.sqrt(2.0 * np.pi * vars[k])) * np.exp(-0.5 * (x_i - means[k]) ** 2 / vars[k])
            unary_potential = -np.log(pdf_val + 1e-15)

            # Calculate Pairwise Potential
            pairwise_sum = 0.0
            neighbors_coords = get_neighbors_indices(r, c, H, W)

            for nr, nc in neighbors_coords:
                if mask[nr, nc]:
```

```

        neighbor_label = labels_2D[nr, nc]
        pairwise_sum += beta if neighbor_label != k else
        0.0

    # Total Energy = Unary + Pairwise
    total_energy = unary_potential + pairwise_sum

    if total_energy < min_energy:
        min_energy = total_energy
        best_label = k

    # Update and count changes
    new_labels_2D[r, c] = best_label
    if best_label != original_label:
        changes += 1

return new_labels_2D, changes

gmm_labels_1D = np.argmax(responsibility, axis=1)
labels_2D = np.zeros((H, W), dtype=int)
labels_2D[mask] = gmm_labels_1D

beta = 0.5

labels_after_1_icm, changes = ICM_iteration(labels_2D.copy(), means,
vars, beta, mask, H, W, N, K, brain_vals)

rgb_after_1_icm = np.zeros((H, W, 3), dtype=float)

for r, c in np.argwhere(mask):
    label_k = labels_after_1_icm[r, c]

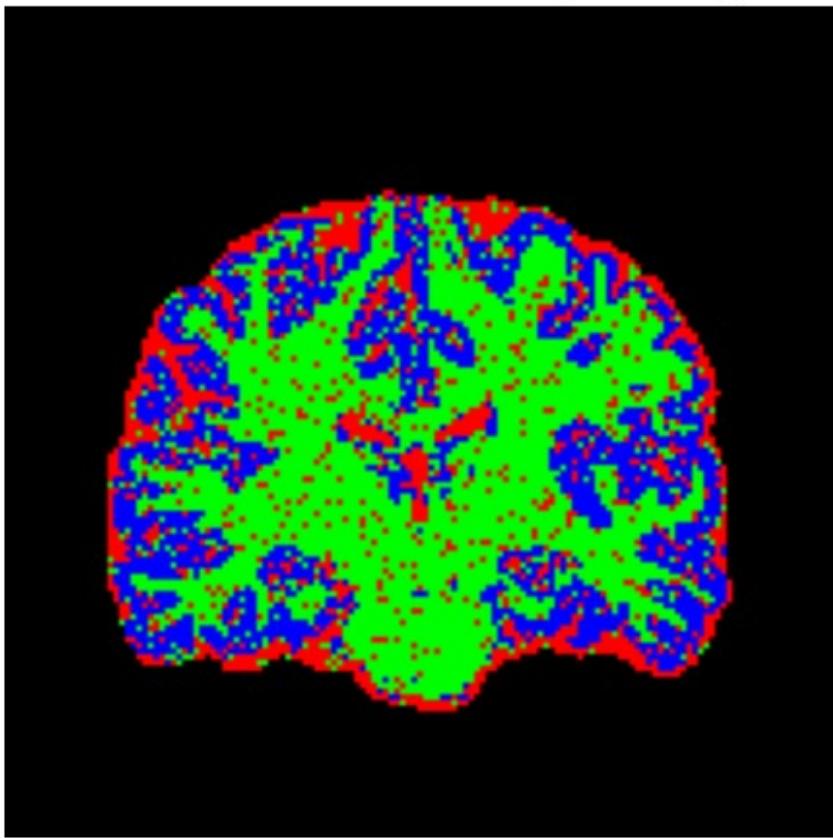
    if label_k == 0:
        rgb_after_1_icm[r, c, 0] = 1
    elif label_k == 1:
        rgb_after_1_icm[r, c, 2] = 1
    elif label_k == 2:
        rgb_after_1_icm[r, c, 1] = 1

plt.figure()
plt.imshow(rgb_after_1_icm)
plt.title(f"Results after 1 ICM iteration (beta={beta})")
plt.axis("off")
plt.tight_layout()
plt.show()

print(f"Pixel labels changed after 1 ICM iteration: {changes}")

```

Results after 1 ICM iteration (beta=0.5)



Pixel labels changed after 1 ICM iteration: 149

c)

```
labels_after_5_icm = labels_2D.copy()
beta = 0.5
total_changes = 0

for i in range(5):
    # Perform ICM on the result of the previous iteration
    labels_after_5_icm, current_changes =
    ICM_iteration(labels_after_5_icm, means, vars, beta, mask, H, W, N, K,
    brain_vals)
    total_changes += current_changes
    print(f"ICM Iteration {i+1}: {current_changes} pixels changed.")

rgb_after_5_icm = np.zeros((H, W, 3), dtype=float)
for r, c in np.argwhere(mask):
    label_k = labels_after_5_icm[r, c]

    if label_k == 0:
        rgb_after_5_icm[r, c, 0] = 1
```

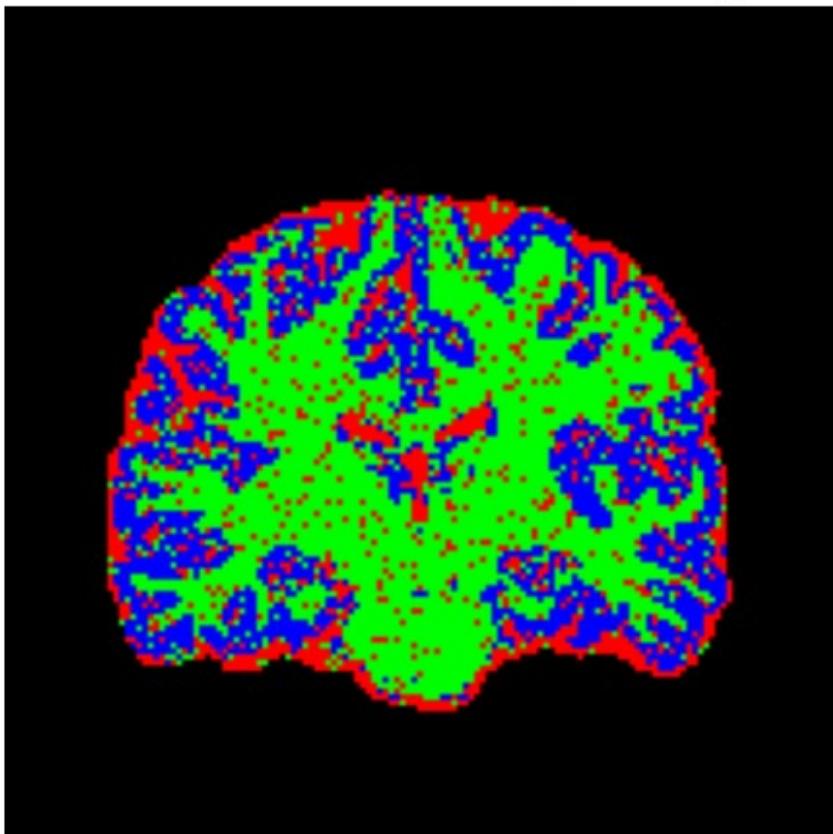
```
        elif label_k == 1:
            rgb_after_5_icm[r, c, 2] = 1
        elif label_k == 2:
            rgb_after_5_icm[r, c, 1] = 1

plt.figure()
plt.imshow(rgb_after_5_icm)
plt.title(f"Results after 5 ICM iteration (beta={beta})")
plt.axis("off")
plt.tight_layout()
plt.show()

print(f"\nTotal pixel labels changed across the 5 ICM iterations:
{total_changes}")

ICM Iteration 1: 149 pixels changed.
ICM Iteration 2: 16 pixels changed.
ICM Iteration 3: 5 pixels changed.
ICM Iteration 4: 4 pixels changed.
ICM Iteration 5: 3 pixels changed.
```

Results after 5 ICM iteration (beta=0.5)



```
Total pixel labels changed across the 5 ICM iterations: 177
```

d)

```
def EM_MRF_iteration(img_data, labels_2D, means, vars, mix, beta,
mask, H, W, N, K):
    icm_max_iter = 500
    icm_labels_2D = labels_2D.copy()

    for i in range(icm_max_iter):
        icm_labels_2D, changes = ICM_iteration(icm_labels_2D, means,
vars, beta, mask, H, W, N, K, img_data)
        if changes == 0:
            break

    labels_1D = icm_labels_2D[mask]
    hard_responsibility = np.zeros((N, K), dtype=float)
    for k in range(K):
        hard_responsibility[labels_1D == k, k] = 1.0

    new_means = means.copy()
    new_vars = vars.copy()
    new_mix = mix.copy()

    for k in range(K):
        N_k = np.sum(hard_responsibility[:, k])

        if N_k > 0:
            num_mu = np.sum(hard_responsibility[:, k] * img_data)
            mean = num_mu / N_k
            new_means[k] = mean

            new_mix[k] = N_k / N

            diff_sq = (img_data - mean)**2
            num_var = np.sum(hard_responsibility[:, k] * diff_sq)
            new_vars[k] = num_var / N_k

    return icm_labels_2D, new_means, new_vars, new_mix

gmm_labels_2D = np.zeros((H, W), dtype=int)
gmm_labels_2D[mask] = gmm_labels_1D
em_mrf_labels_2D = gmm_labels_2D.copy()
em_mrf_means = means.copy()
em_mrf_vars = vars.copy()
em_mrf_mix = mix.copy()
beta = 0.5

em_mrf_max_iter = 50
```

```

em_mrf_tol = 1e-6

for iter in range(em_mrf_max_iter):
    old_means = em_mrf_means.copy()
    print(f"EM-MRF Outer Iter {iter:02d}")

    # Perform one iteration
    em_mrf_labels_2D, em_mrf_means, em_mrf_vars, em_mrf_mix =
    EM_MRF_iteration(
        brain_vals, em_mrf_labels_2D, em_mrf_means, em_mrf_vars,
        em_mrf_mix, beta, mask, H, W, N, K
    )

    diff_means = np.max(np.abs(em_mrf_means - old_means))

    if diff_means < em_mrf_tol:
        print("EM-MRF Converged.")
        break
    elif iter == em_mrf_max_iter - 1:
        print("EM-MRF max iterations reached.")

final_em_mrf_rgb = np.zeros((H, W, 3), dtype=float)

for r, c in np.argwhere(mask):
    label_k = em_mrf_labels_2D[r, c]

    if label_k == 0:
        final_em_mrf_rgb[r, c, 0] = 1
    elif label_k == 1:
        final_em_mrf_rgb[r, c, 2] = 1
    elif label_k == 2:
        final_em_mrf_rgb[r, c, 1] = 1

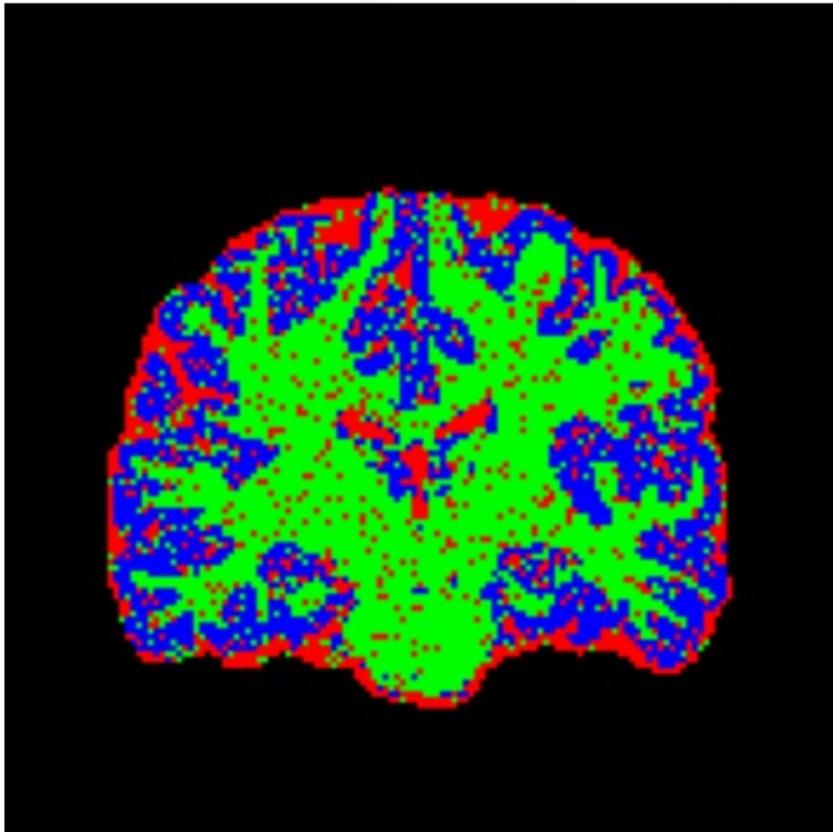
plt.figure()
plt.imshow(final_em_mrf_rgb)
plt.title(f"Final EM-MRF Segmentation (beta={beta})")
plt.axis("off")
plt.tight_layout()
plt.show()

EM-MRF Outer Iter 00
EM-MRF Outer Iter 01
EM-MRF Outer Iter 02
EM-MRF Outer Iter 03
EM-MRF Outer Iter 04
EM-MRF Outer Iter 05
EM-MRF Outer Iter 06

```

```
EM-MRF Outer Iter 07  
EM-MRF Converged.
```

Final EM-MRF Segmentation ( $\beta=0.5$ )



e)

After some tests we noticed that with  $\beta$  in between 3 to 8, the results start to be less noisy, but when it equals 9, the result resembles more to the example image given in the exercise sheet.

```
gmm_labels_2D = np.zeros((H, W), dtype=int)
gmm_labels_2D[mask] = gmm_labels_1D
em_mrf_labels_2D = gmm_labels_2D.copy()
em_mrf_means = means.copy()
em_mrf_vars = vars.copy()
em_mrf_mix = mix.copy()
beta = 9

em_mrf_max_iter = 50
em_mrf_tol = 1e-6

for iter in range(em_mrf_max_iter):
```

```

old_means = em_mrf_means.copy()

print(f"EM-MRF Outer Iter {iter:02d}")

# Perform one iteration
em_mrf_labels_2D, em_mrf_means, em_mrf_vars, em_mrf_mix =
EM_MRF_iteration(
    brain_vals, em_mrf_labels_2D, em_mrf_means, em_mrf_vars,
em_mrf_mix, beta, mask, H, W, N, K
)

diff_means = np.max(np.abs(em_mrf_means - old_means))

if diff_means < em_mrf_tol:
    print("EM-MRF Converged.")
    break
elif iter == em_mrf_max_iter - 1:
    print("EM-MRF max iterations reached.")

final_em_mrf_rgb = np.zeros((H, W, 3), dtype=float)

for r, c in np.argwhere(mask):
    label_k = em_mrf_labels_2D[r, c]

    if label_k == 0:
        final_em_mrf_rgb[r, c, 0] = 1
    elif label_k == 1:
        final_em_mrf_rgb[r, c, 2] = 1
    elif label_k == 2:
        final_em_mrf_rgb[r, c, 1] = 1

plt.figure()
plt.imshow(final_em_mrf_rgb)
plt.title(f"Final EM-MRF Segmentation (beta={beta})")
plt.axis("off")
plt.tight_layout()
plt.show()

EM-MRF Outer Iter 00
EM-MRF Outer Iter 01
EM-MRF Outer Iter 02
EM-MRF Outer Iter 03
EM-MRF Converged.

```

Final EM-MRF Segmentation (beta=9)

