

# Analyse case7 npgamma 29-11-2016

November 29, 2016

Use npgamma to compare HN Case 7 dose data. See <https://github.com/SimonBiggs/npgamma/blob/master/Module%20usage%203D.ipynb>

```
In [1]: import dicom
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline

from npgamma import calc_gamma

In [2]: dcm_ref = dicom.read_file("Case7_dose_AAA.dcm")
dcm_evl = dicom.read_file("Case7_dose_Dm.dcm")

In [3]: # The x, y, and z defined here have not been sufficiently verified
# They do not necessarily match either what is within Dicom nor what is with
# TPS. Please verify these and see if they are what you expect them to be.

# If these functions are incorrect or there is a better choice of dimension
# please contact me by creating an issue within the github repository:
#   https://github.com/SimonBiggs/npgamma/issues

# If you are able to validate these functions please contact me in the same

# Imports the dose in matplotlib format, with the following index mapping:
#   i = y
#   j = x
#   k = z

# Therefore w
def load_dose_from_dicom(dcm):
    """Imports the dose in matplotlib format, with the following index mapping:
    i = y
    j = x
    k = z

    Therefore when using this function to have the coords match the same as
    ie. coords_reference = (y, x, z)
```

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        """
        pixels = np.transpose(
            dcm.pixel_array, (1, 2, 0))
        dose = pixels * dcm.DoseGridScaling

    return dose

def load_xyz_from_dicom(dcm):
    """Although this coordinate pull from Dicom works in the scenarios test
    this is not an official x, y, z pull. It needs further confirmation.
    """
    resolution = np.array(
        dcm.PixelSpacing).astype(float)
    # Does the first index match x?
    # Haven't tested with differing grid sizes in x and y directions.
    dx = resolution[0]

    # The use of dcm.Columns here is under question
    x = (
        dcm.ImagePositionPatient[0] +
        np.arange(0, dcm.Columns * dx, dx))

    # Does the second index match y?
    # Haven't tested with differing grid sizes in x and y directions.
    dy = resolution[1]

    # The use of dcm.Rows here is under question
    y = (
        dcm.ImagePositionPatient[1] +
        np.arange(0, dcm.Rows * dy, dy))

    # Is this correct?
    z = (
        np.array(dcm.GridFrameOffsetVector) +
        dcm.ImagePositionPatient[2])

    return x, y, z

dose_reference = load_dose_from_dicom(dcm_ref)
dose_evaluation = load_dose_from_dicom(dcm_ev1)

x_reference, y_reference, z_reference = load_xyz_from_dicom(dcm_ref)
x_evaluation, y_evaluation, z_evaluation = load_xyz_from_dicom(dcm_ev1)

In [7]: # Input coordinates need to match the same order as the dose grid in
        # index reference order.

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coords_reference = (
    y_reference, x_reference, z_reference)

coords_evaluation = (
    y_evaluation, x_evaluation, z_evaluation)

In [8]: distance_threshold = 3
        distance_step_size = distance_threshold / 10

        dose_threshold = 0.03 * np.max(dose_reference)
        lower_dose_cutoff = np.max(dose_reference) * 0.2
        maximum_test_distance = distance_threshold * 2
        max_concurrent_calc_points = 10000000

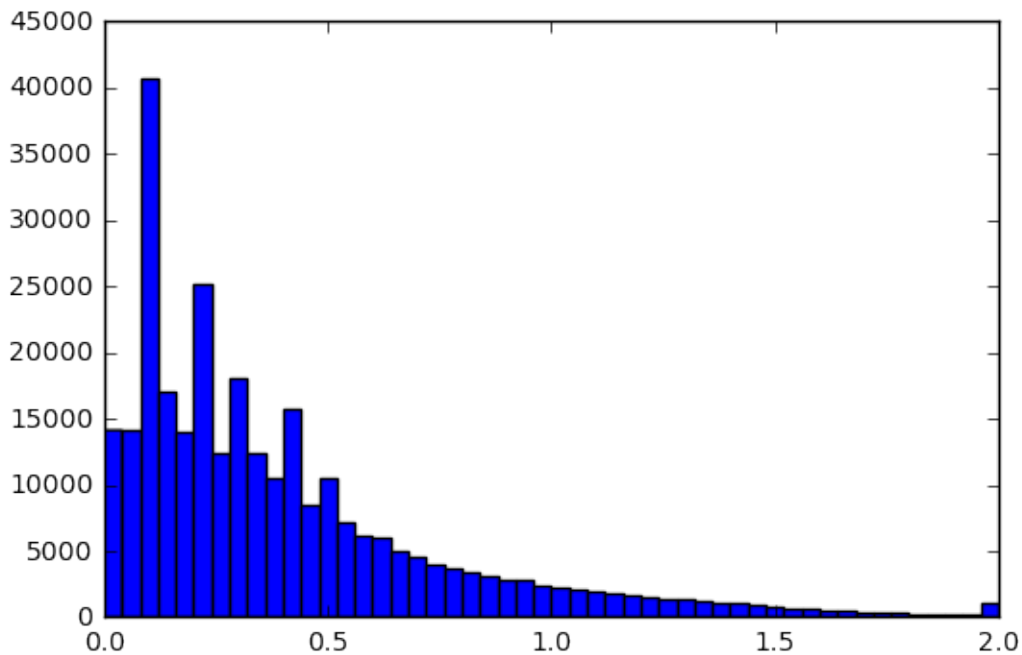
In [9]: gamma = calc_gamma(
        coords_reference, dose_reference,
        coords_evaluation, dose_evaluation,
        distance_threshold, dose_threshold,
        lower_dose_cutoff=lower_dose_cutoff,
        distance_step_size=distance_step_size,
        maximum_test_distance=maximum_test_distance,
        max_concurrent_calc_points=max_concurrent_calc_points)

In [10]: valid_gamma = gamma[~np.isnan(gamma)]
         valid_gamma[valid_gamma > 2] = 2

In [11]: plt.hist(valid_gamma, 50);
         plt.xlim([0,2])

Out[11]: (0, 2)

```



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In [12]: np.sum(valid_gamma <= 1) / len(valid_gamma)

Out[12]: 0.9152553510103717

In [13]: relevant_slice = (
    np.max(dose_evaluation, axis=(0, 1)) >
    lower_dose_cutoff)
slice_start = np.max([
    np.where(relevant_slice)[0][0],
    0])
slice_end = np.min([
    np.where(relevant_slice)[0][-1],
    len(z_evaluation)])

In [17]: max_ref_dose = np.max(dose_reference)

cut_off_gamma = gamma.copy()
greater_than_2_ref = (cut_off_gamma > 2) & ~np.isinf(cut_off_gamma)
cut_off_gamma[greater_than_2_ref] = 2

for z_i in z_evaluation[slice_start:slice_end:5]:
    i = np.where(z_i == z_evaluation)[0][0]
    j = np.where(z_i == z_reference)[0][0]
    print("=====")
    print("Slice = {0}".format(z_i))

    plt.contourf(
        x_evaluation, y_evaluation, dose_evaluation[:, :, j], 30,
        vmin=0, vmax=max_ref_dose, cmap=plt.get_cmap('gist_heat'))
    plt.title("AXB Dm") # Evaluation -
    plt.colorbar()
    plt.show()

    plt.contourf(
        x_reference, y_reference, dose_reference[:, :, j], 30,
        vmin=0, vmax=max_ref_dose, cmap=plt.get_cmap('gist_heat'))
    plt.title("AAA") # Reference -
    plt.colorbar()
    plt.show()

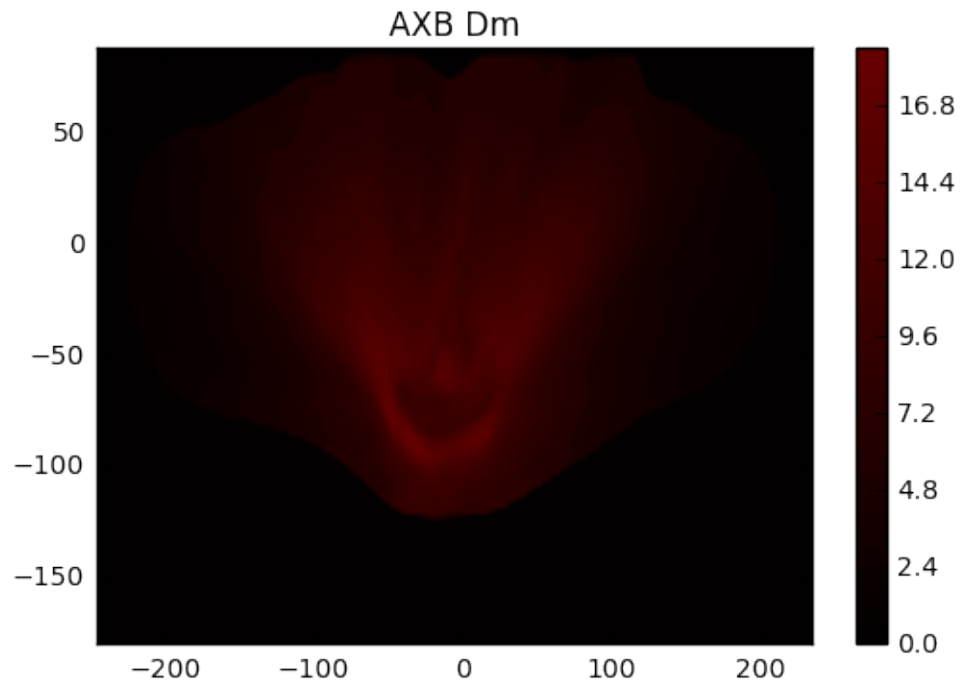
    plt.contourf(
        x_evaluation, y_evaluation, cut_off_gamma[:, :, i], 30,
        vmin=0, vmax=2, cmap=plt.get_cmap('bwr'))
    plt.title("Gamma 3%/3mm")
    plt.colorbar()
    plt.show()

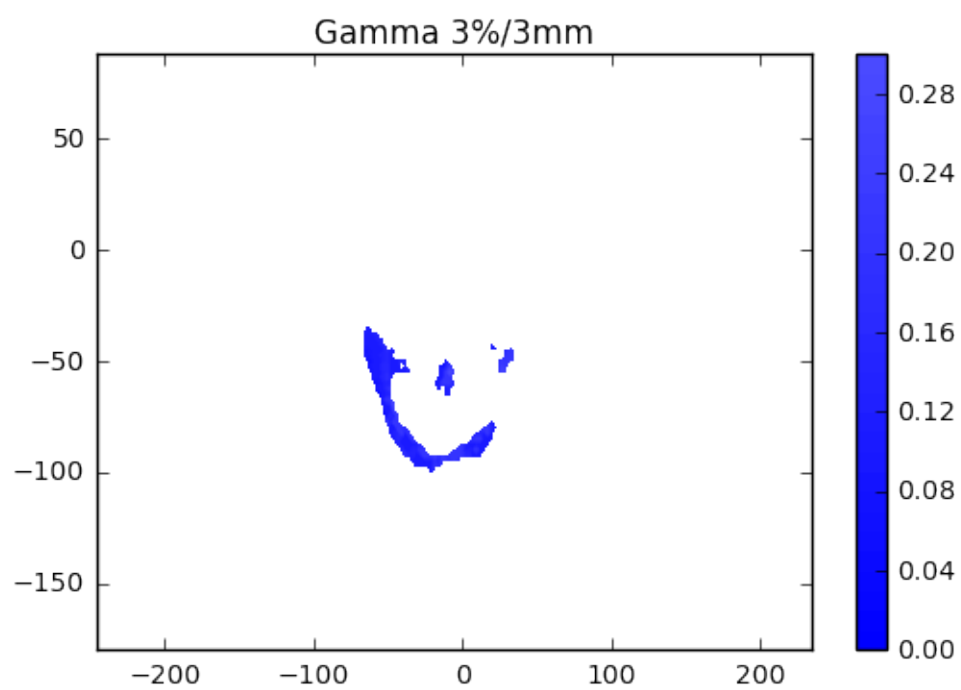
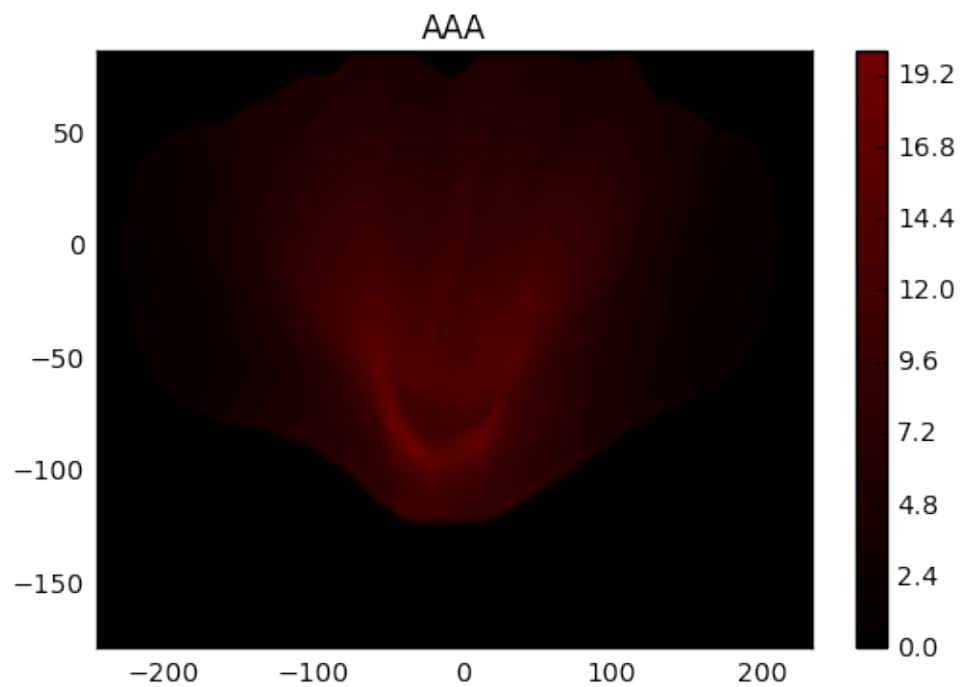
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print("\n")
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C:\Users\RCole02.ROYALSURREY\AppData\Local\Continuum\Anaconda3\lib\site-packages\ip
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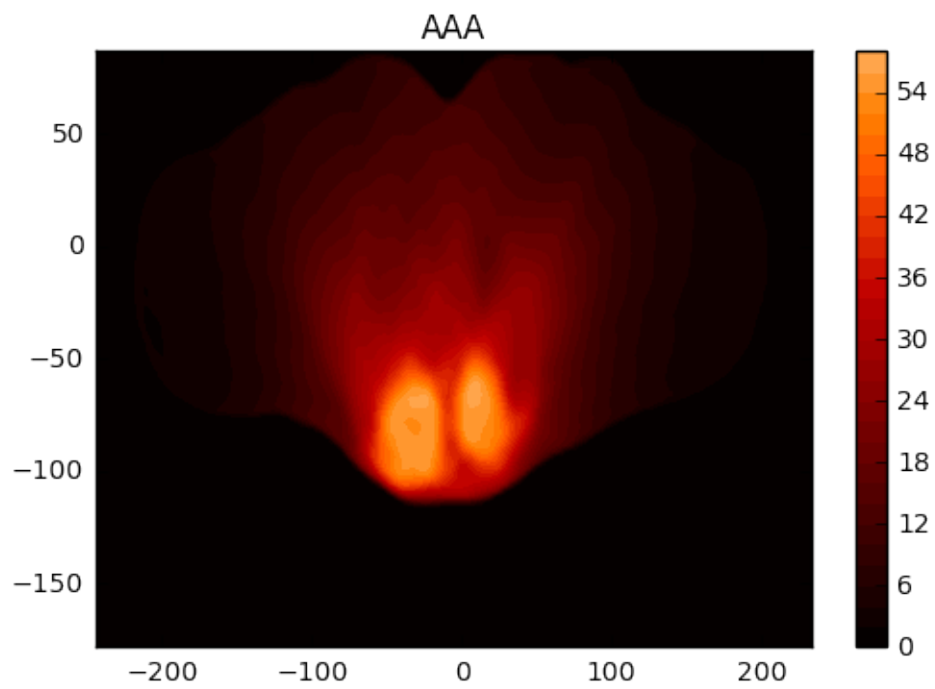
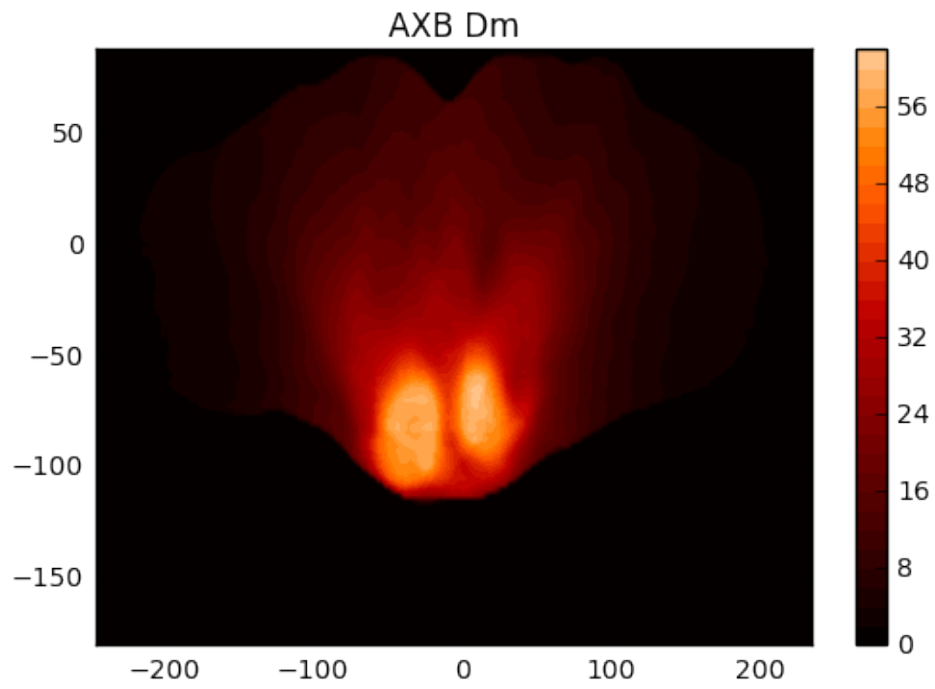
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Slice = -141.25
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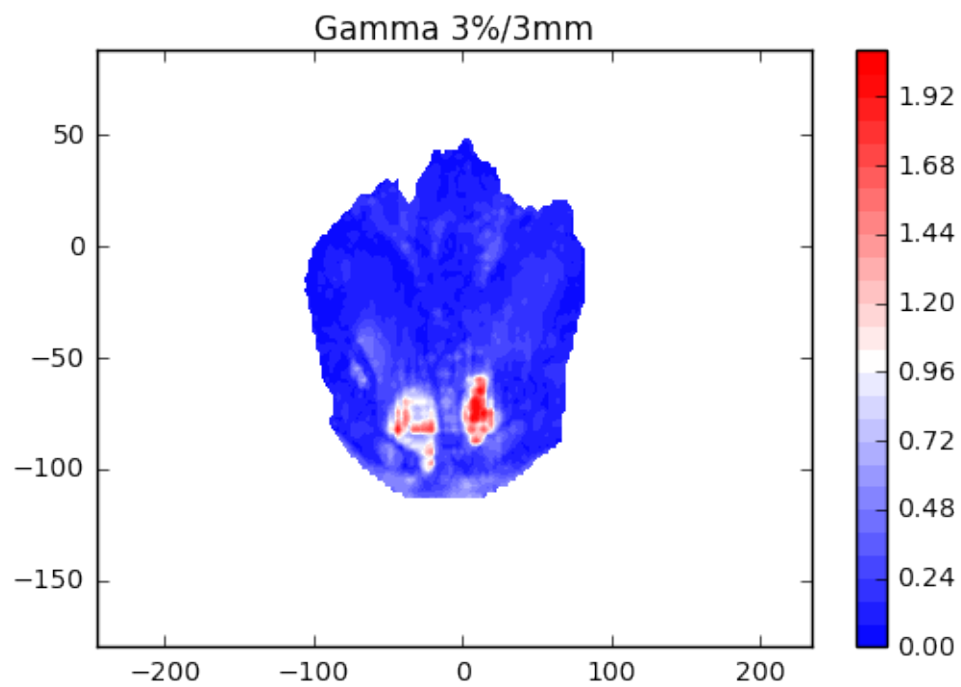




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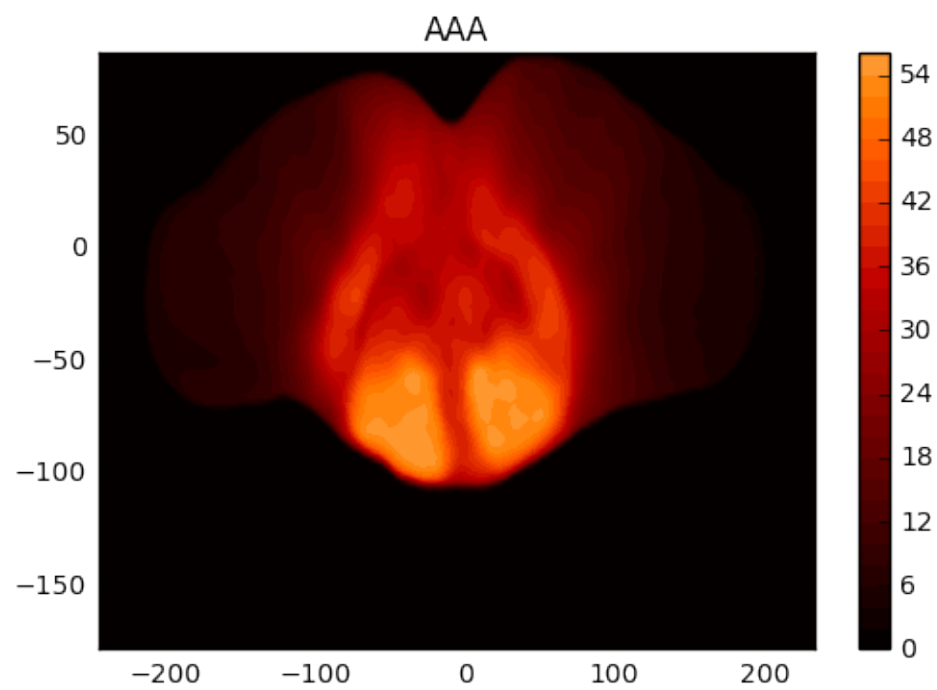
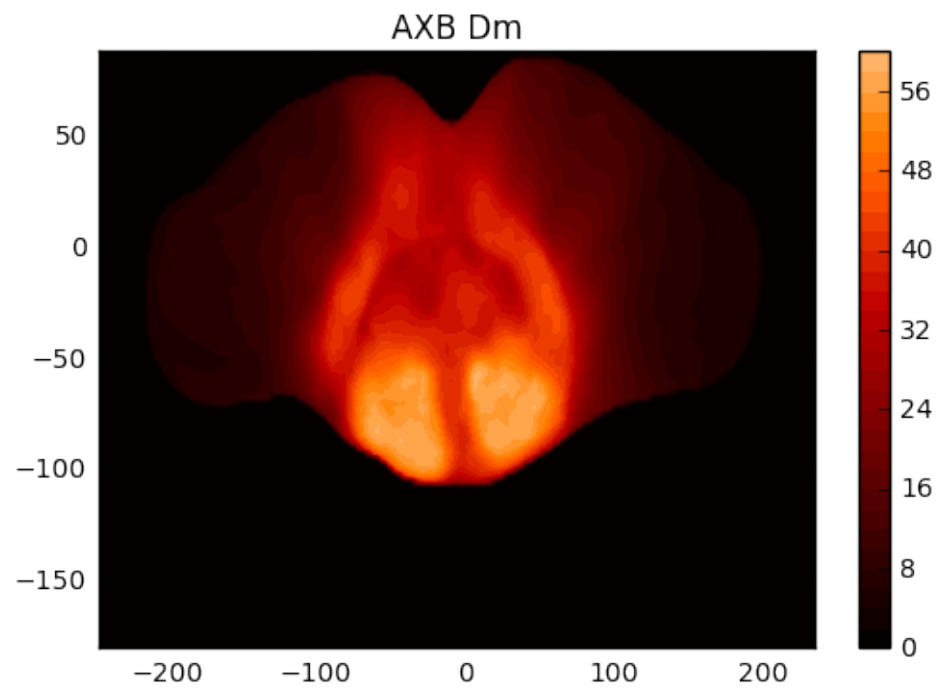
Slice = -128.75

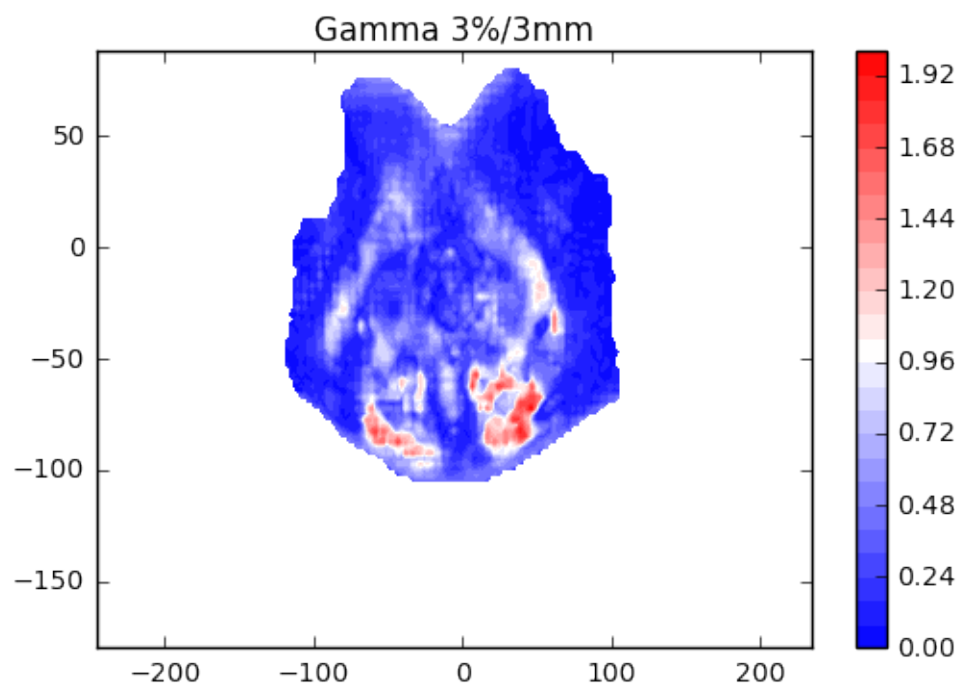




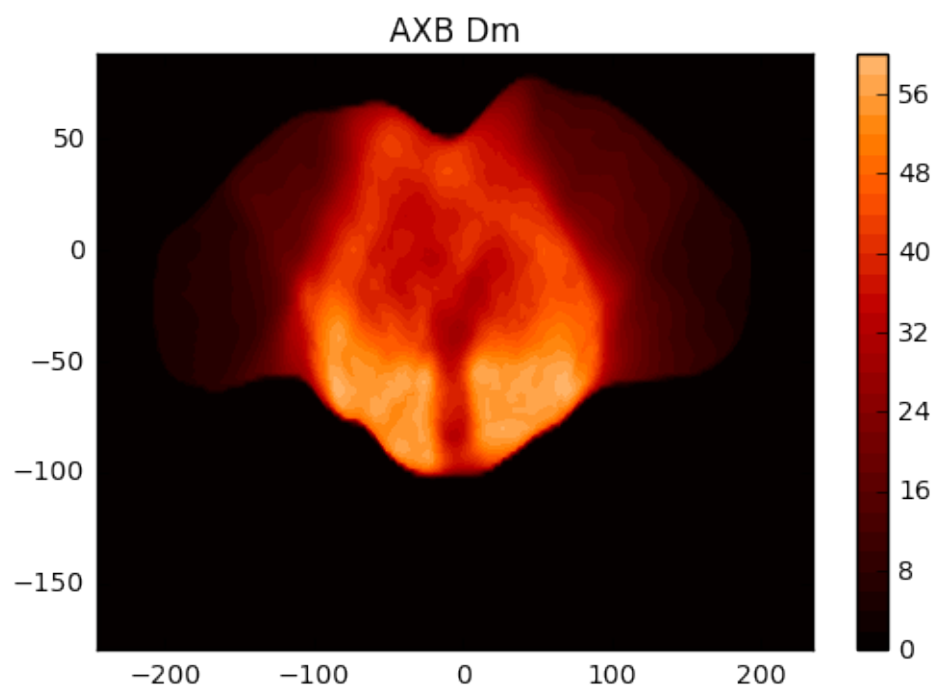
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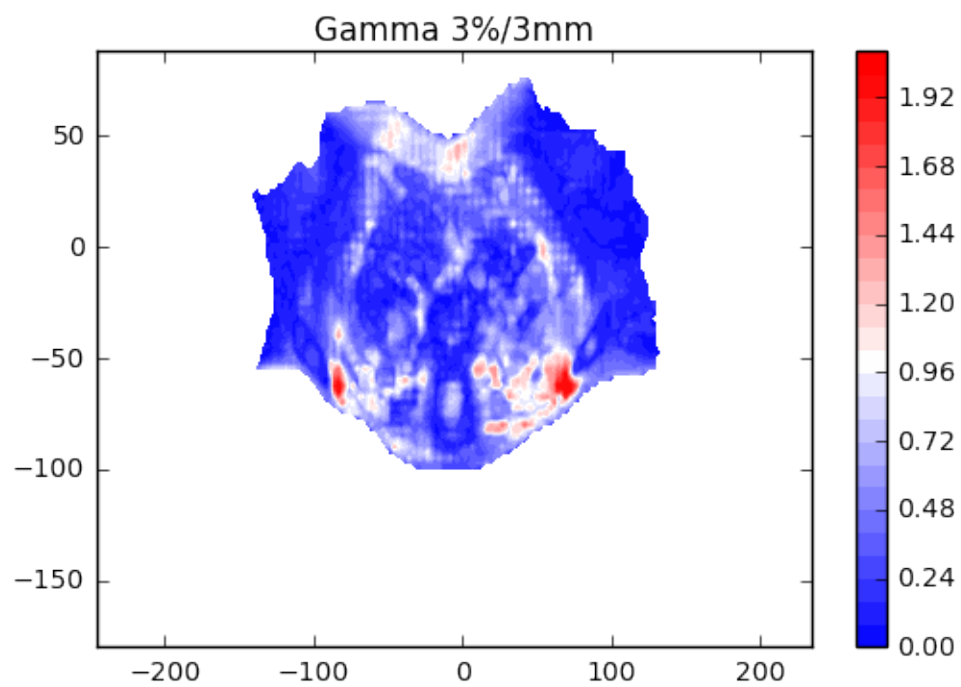
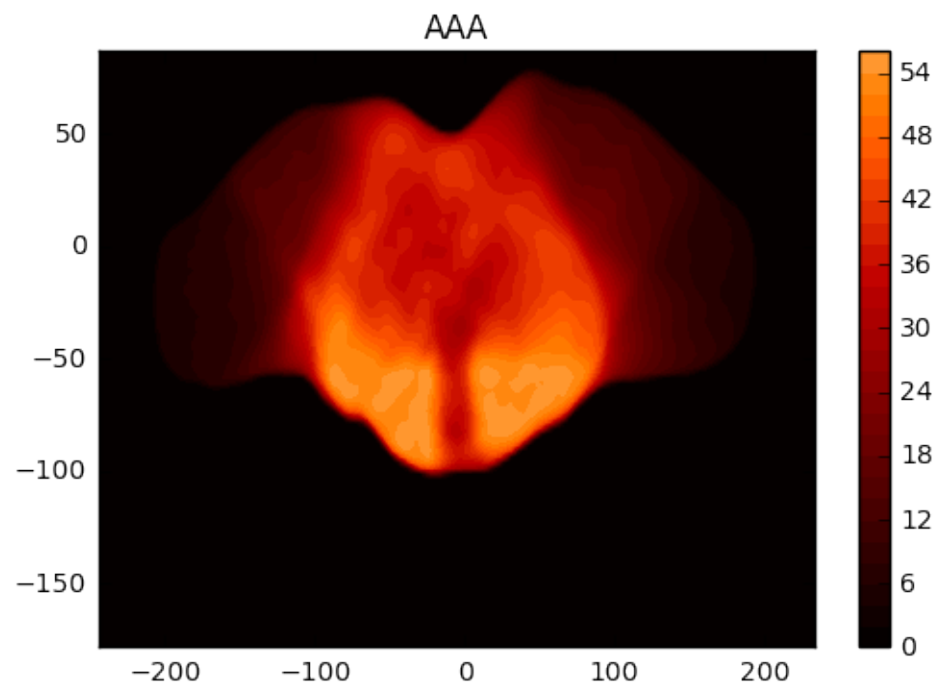






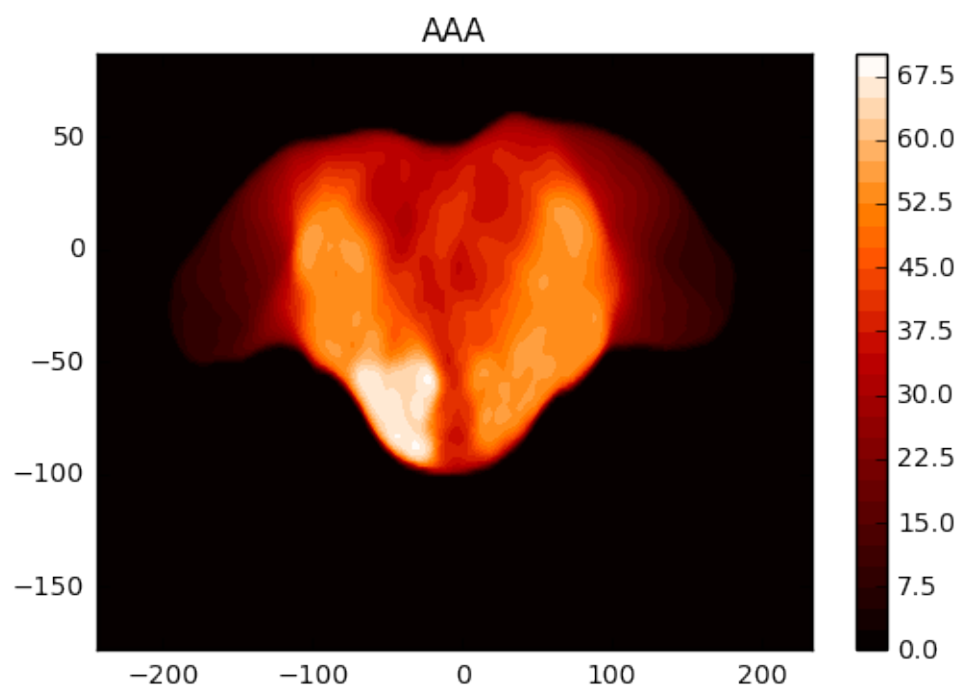
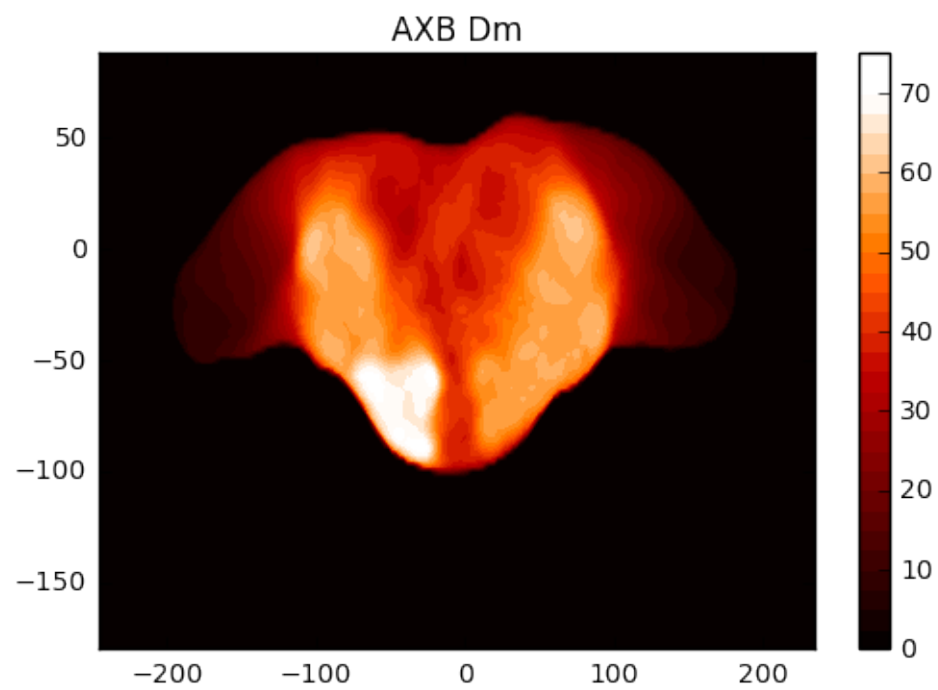
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Slice = -103.75

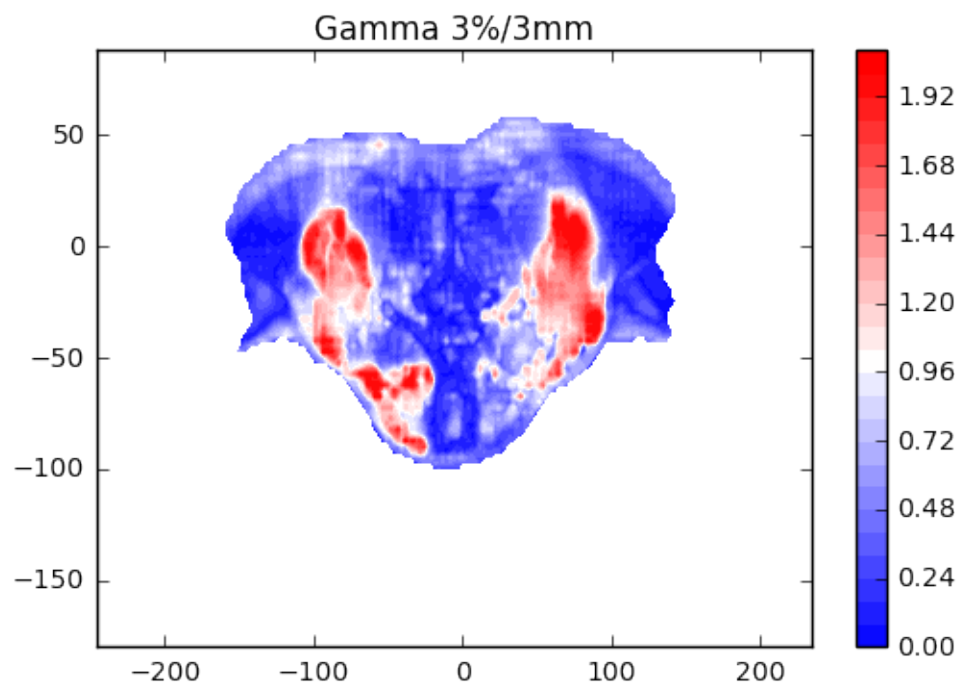




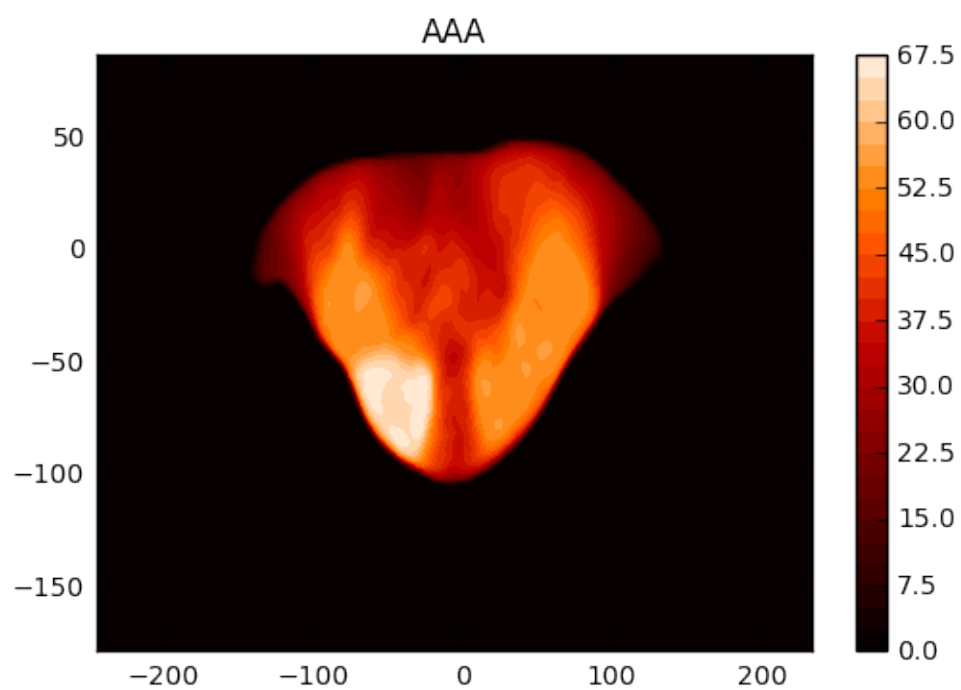
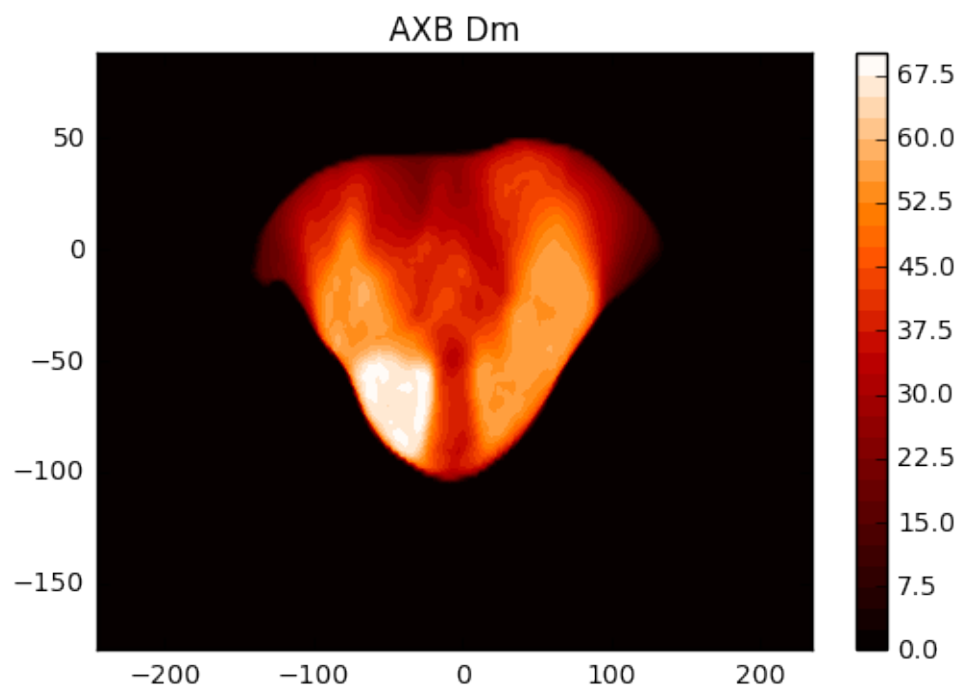
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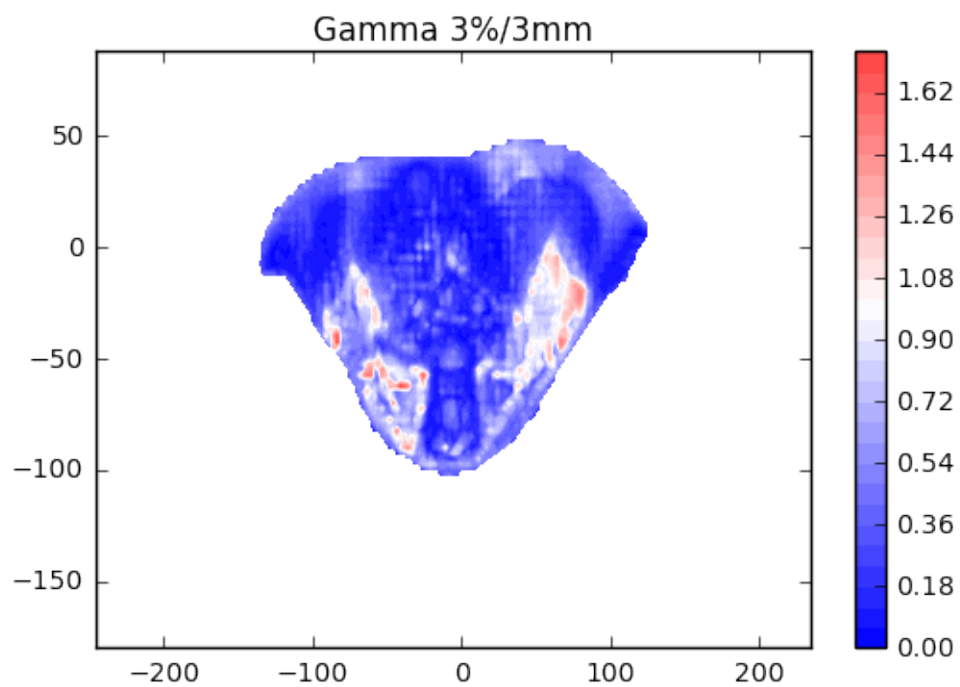
Slice = -91.25



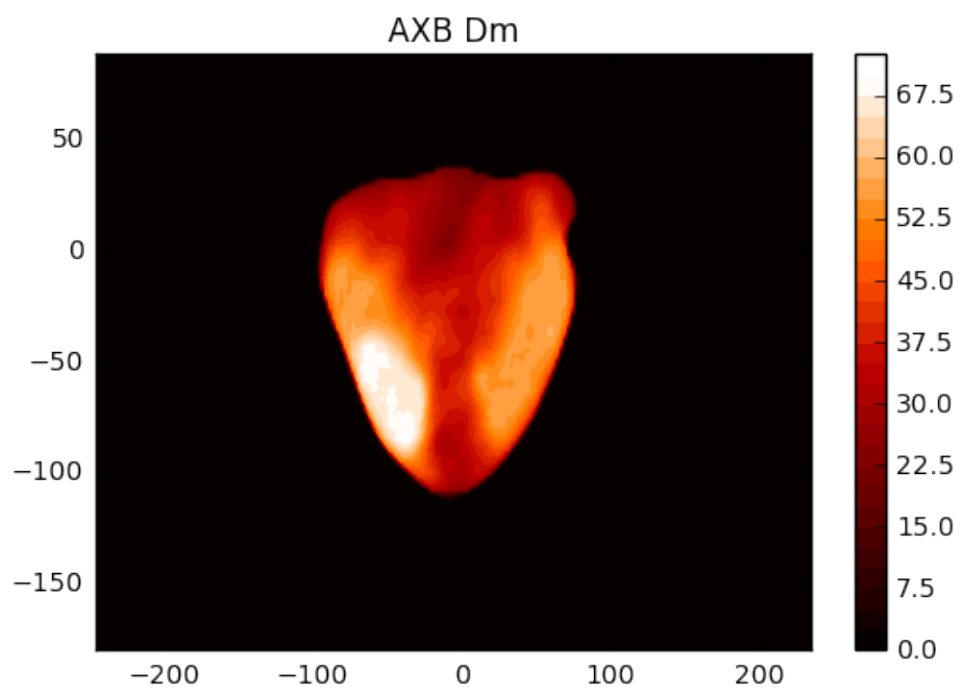


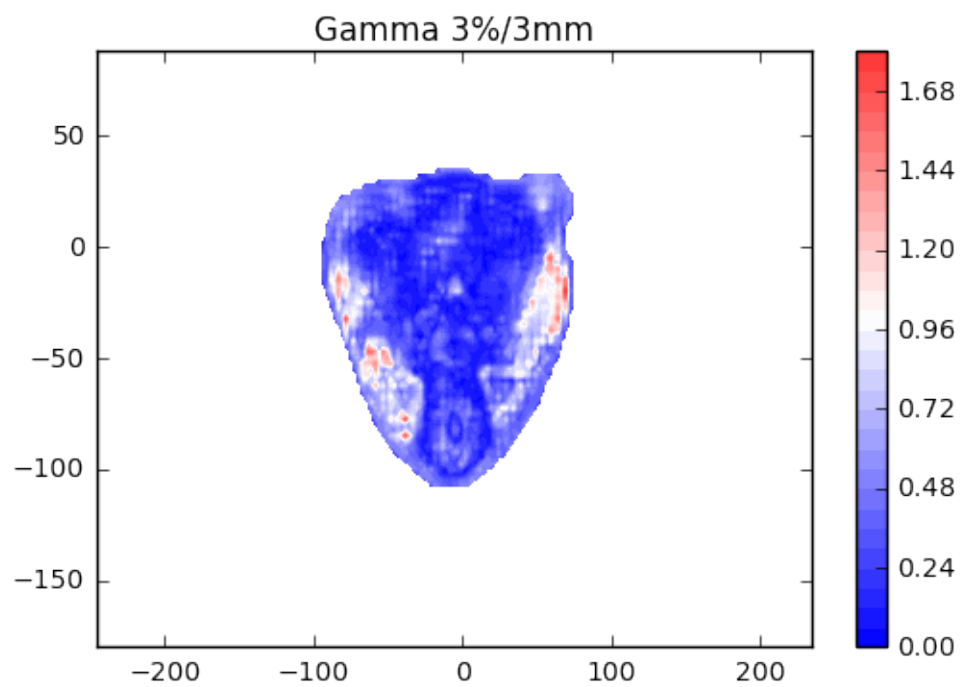
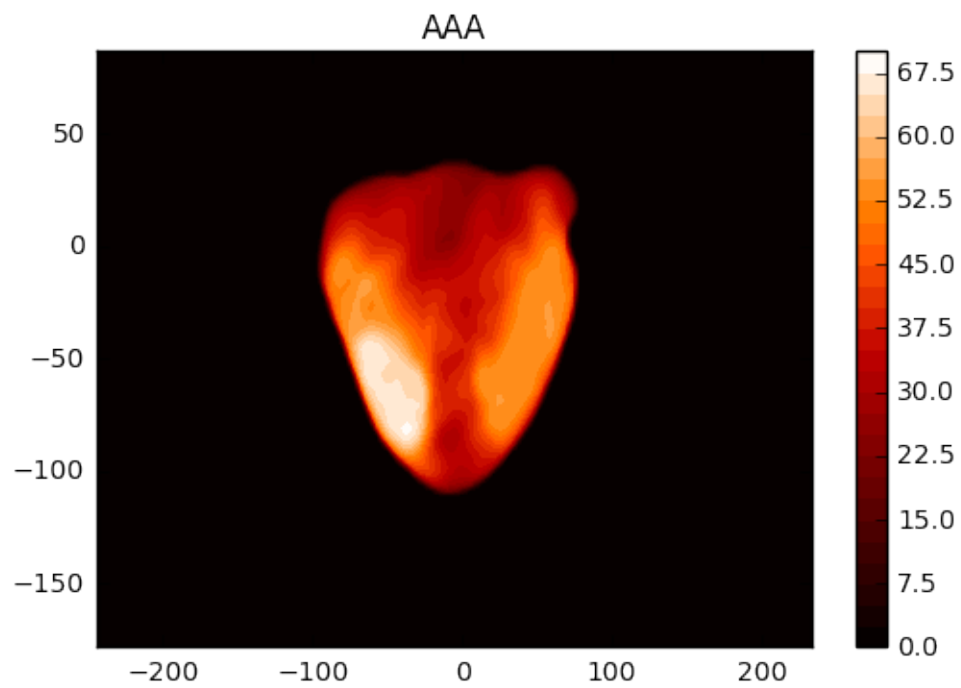
=====  
Slice = -78.75





=====  
Slice = -66.25

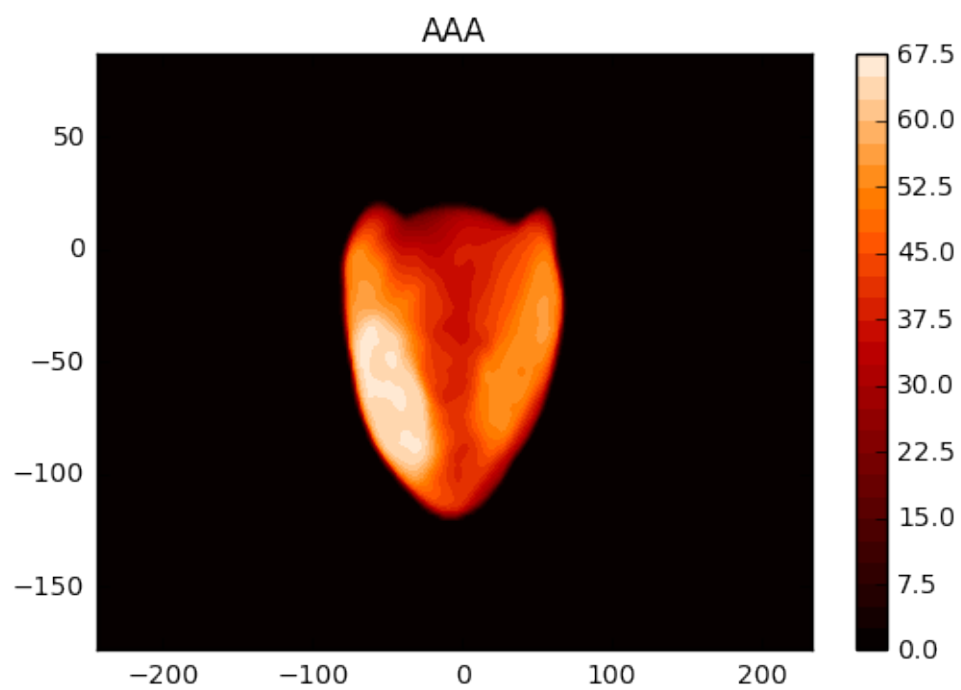
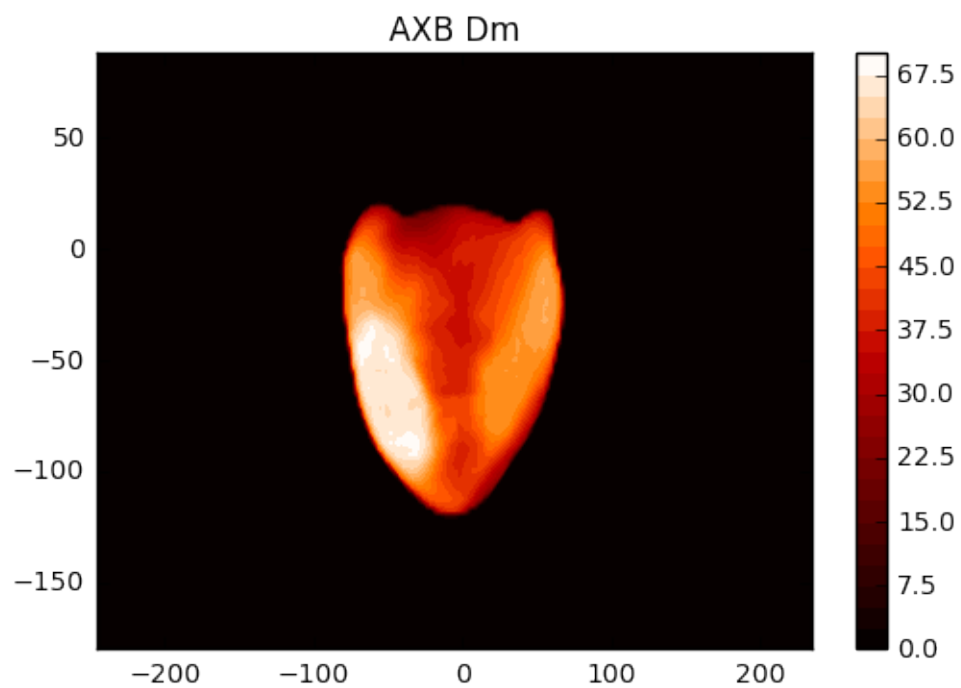


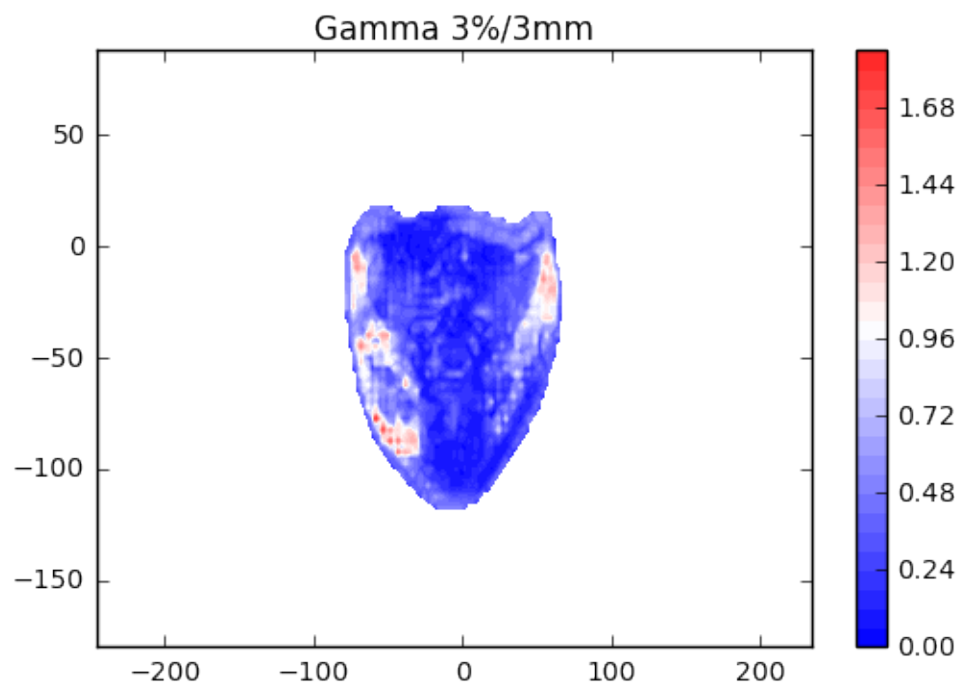




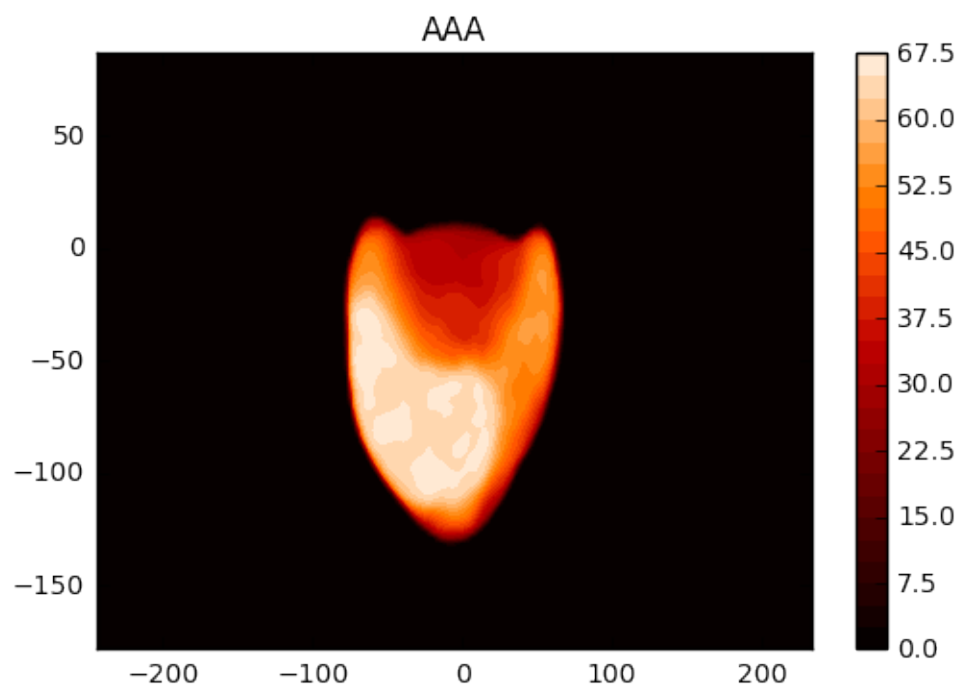
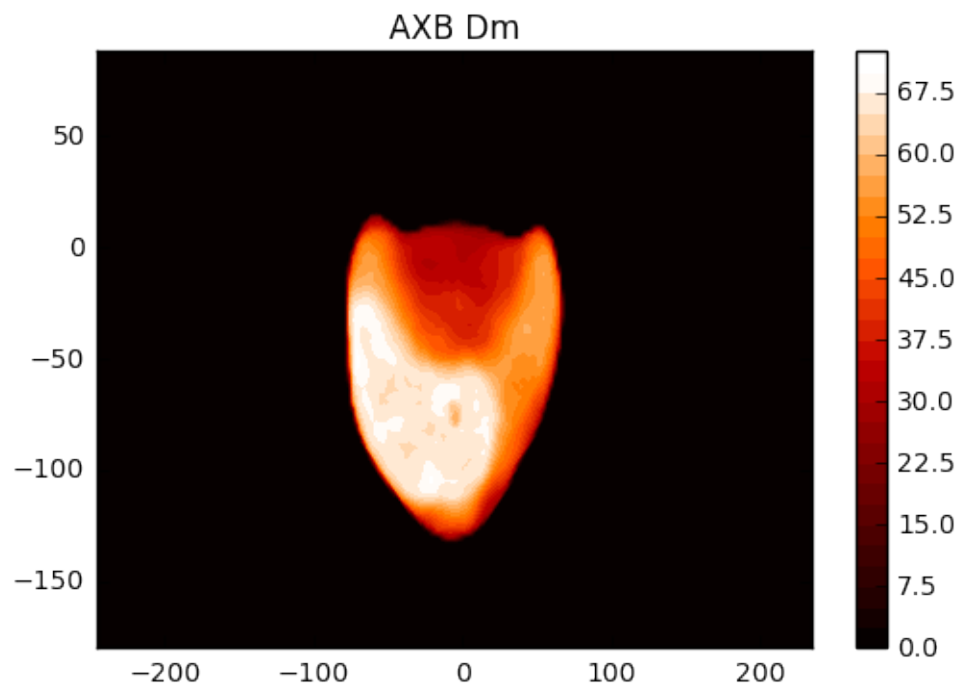
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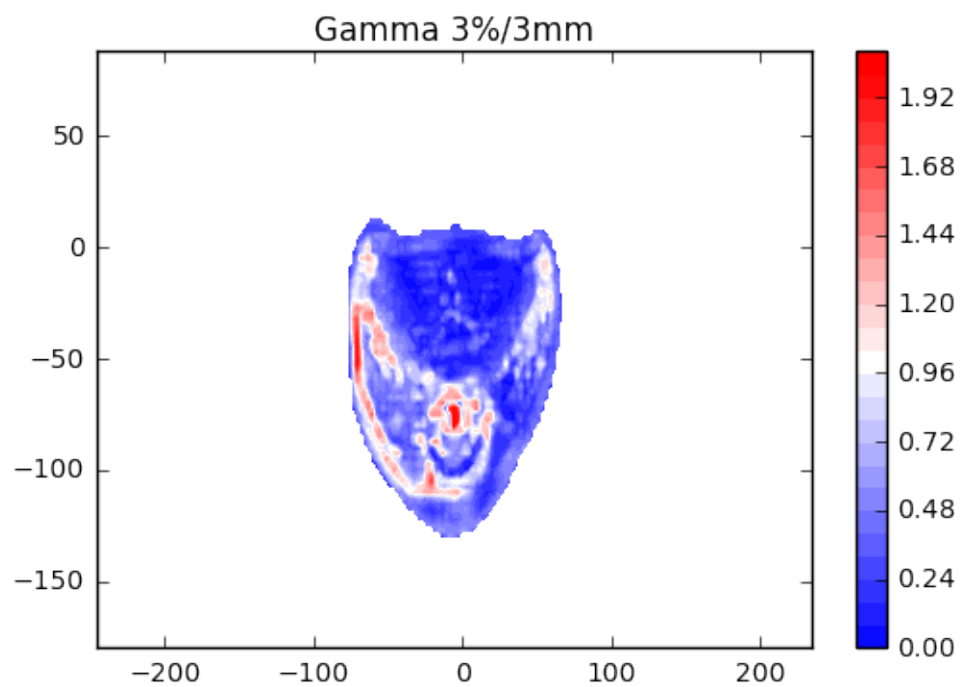
Slice = -53.75



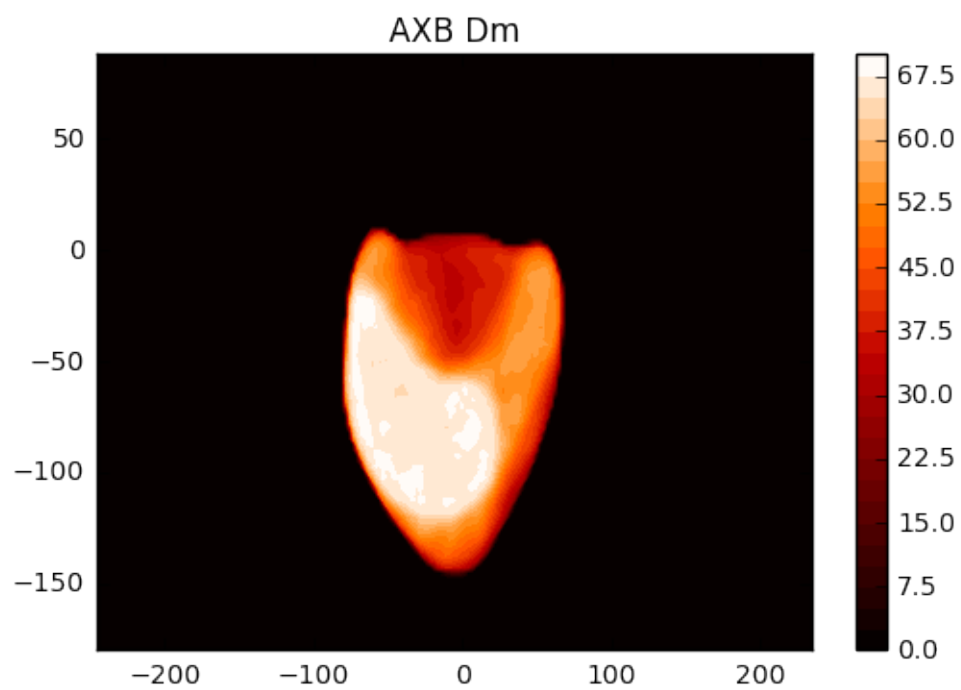


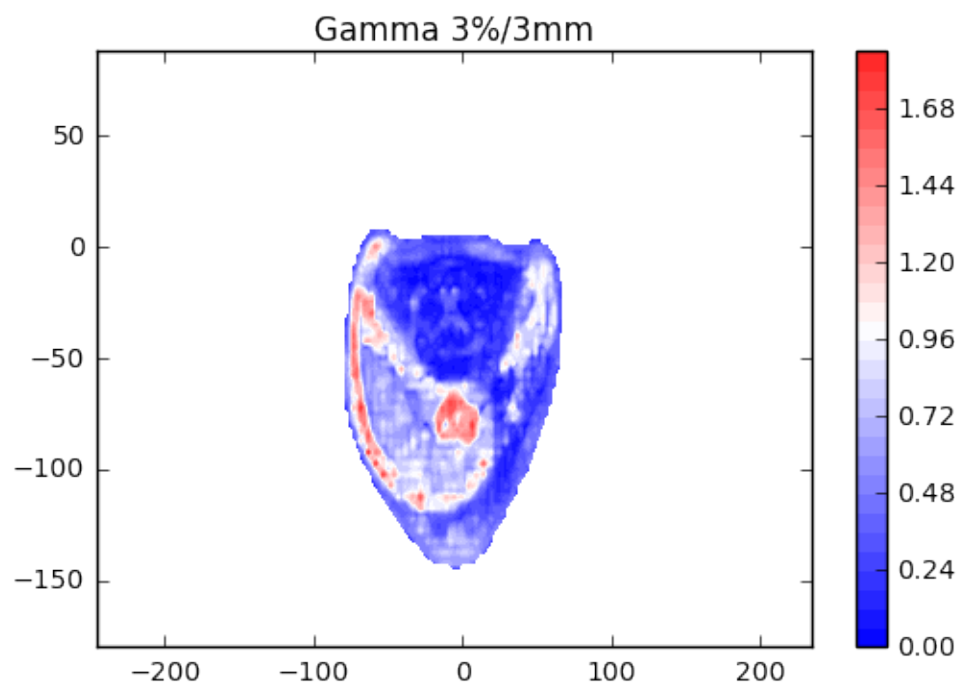
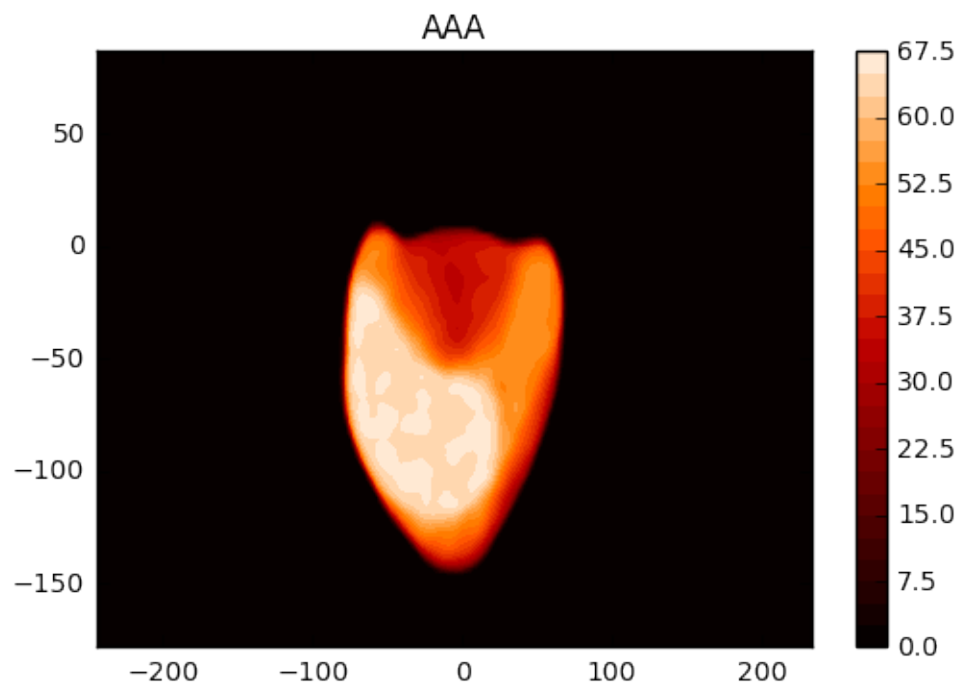
=====  
Slice = -41.25





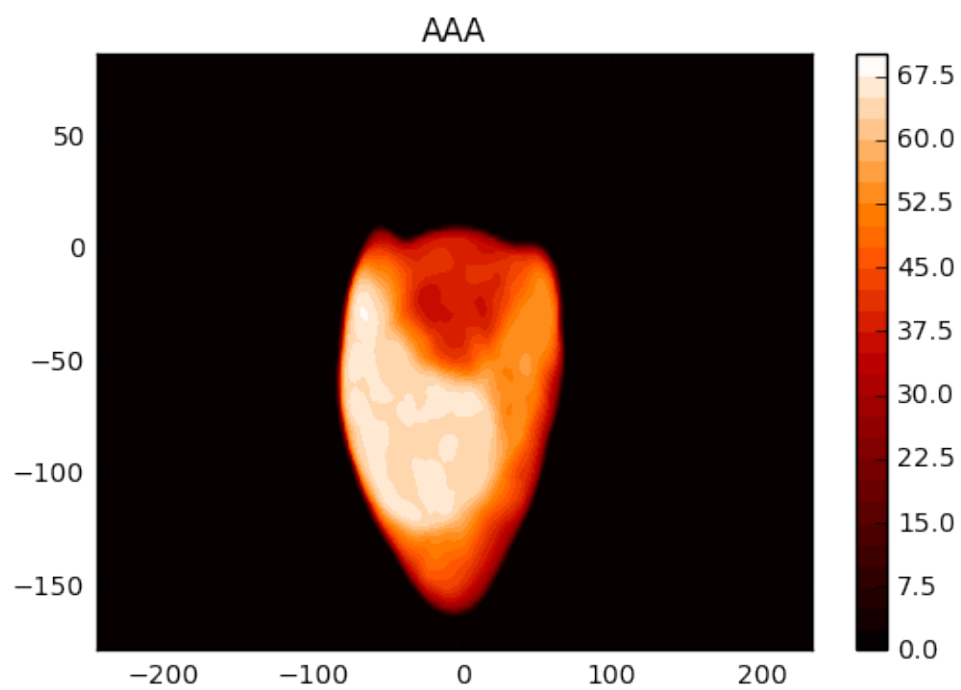
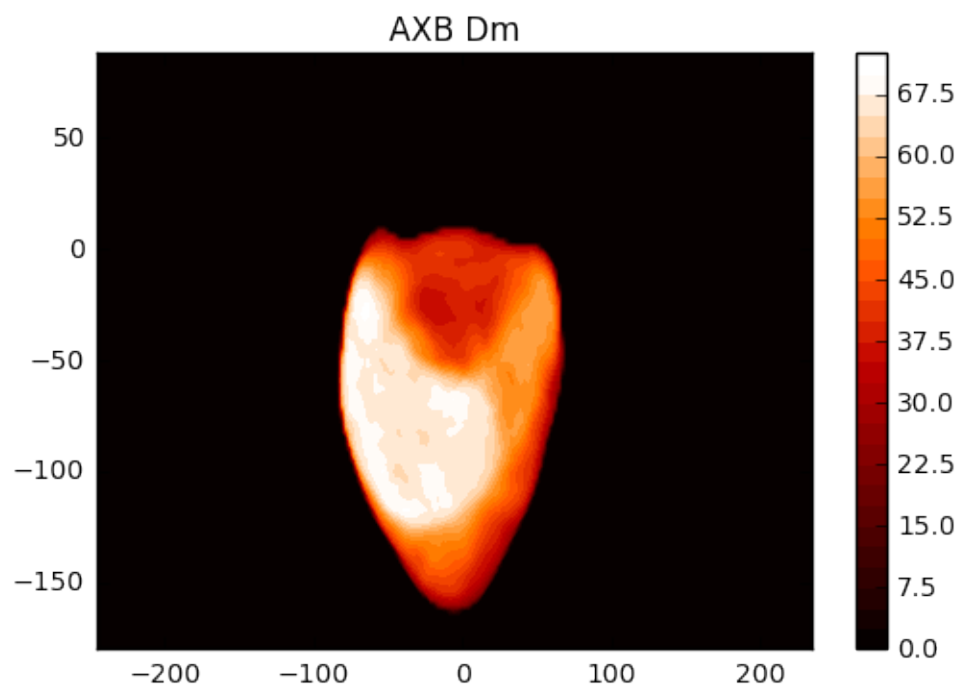
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Slice = -28.75

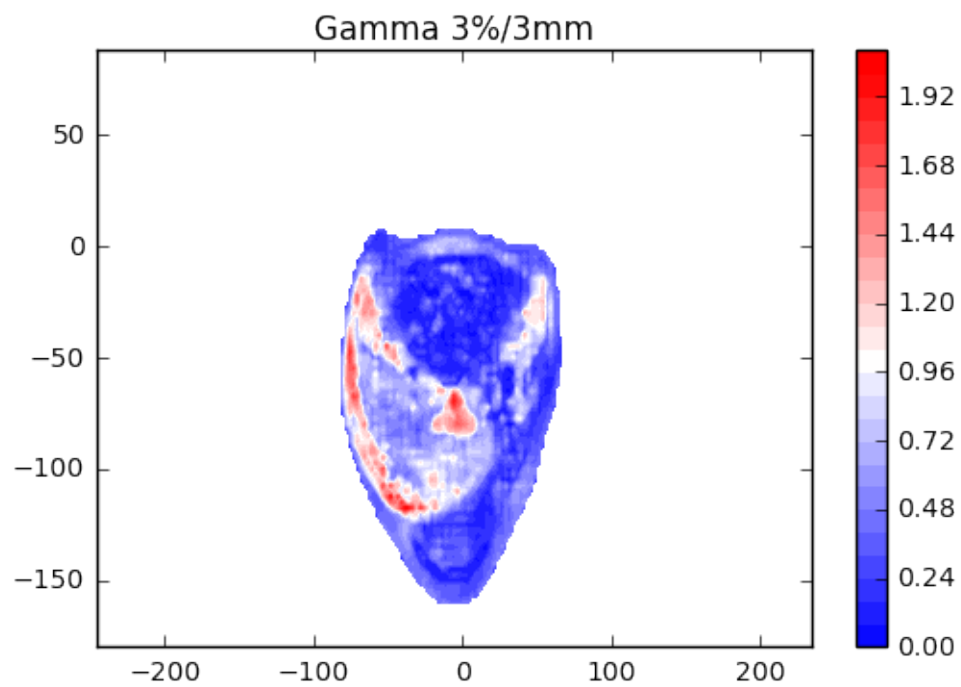




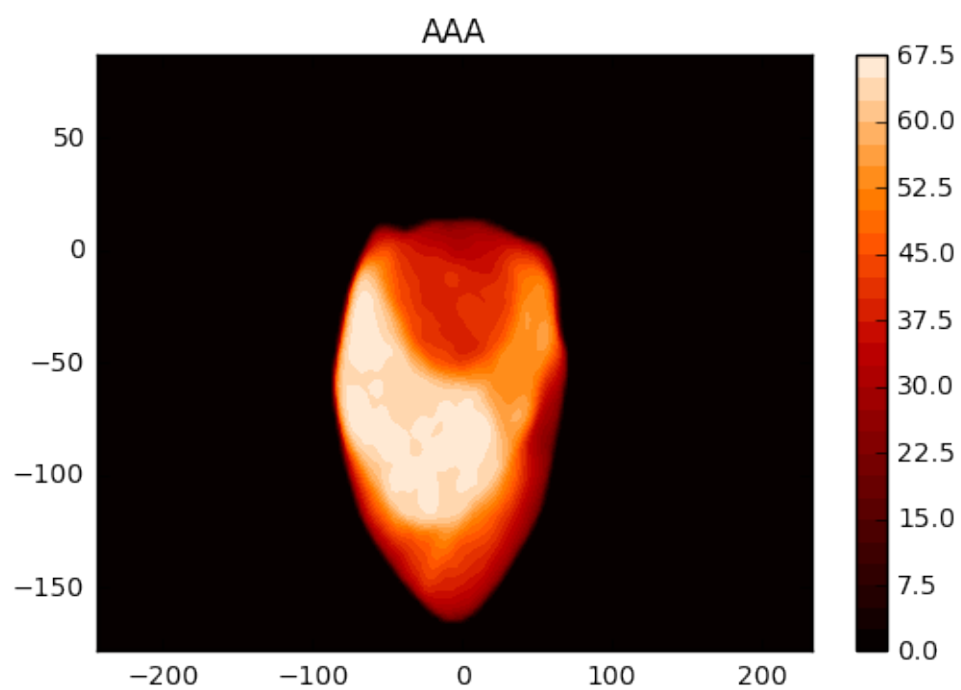
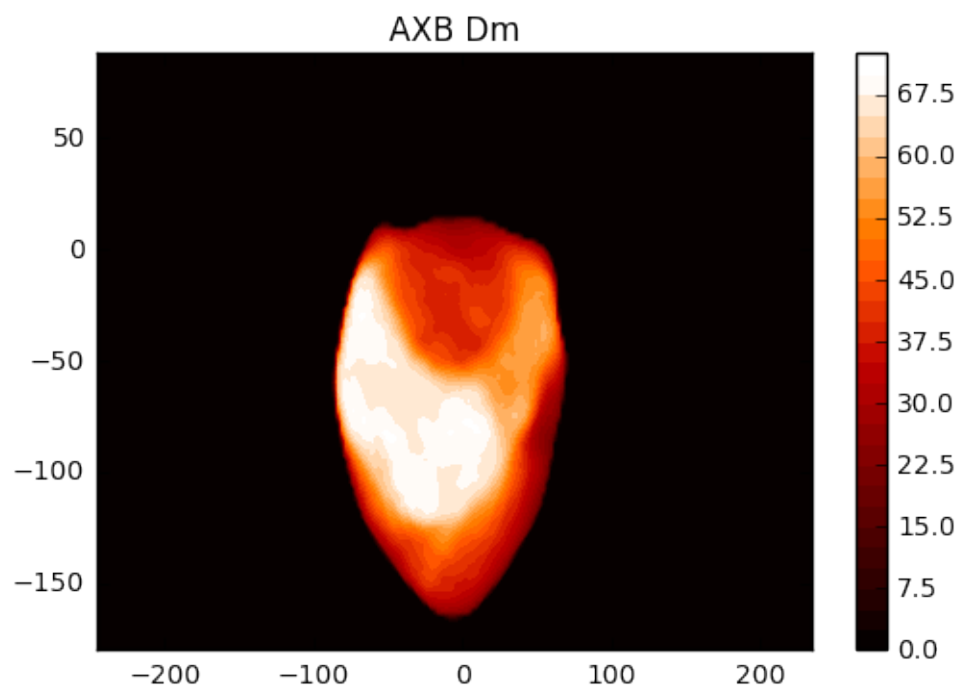
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Slice = -16.25

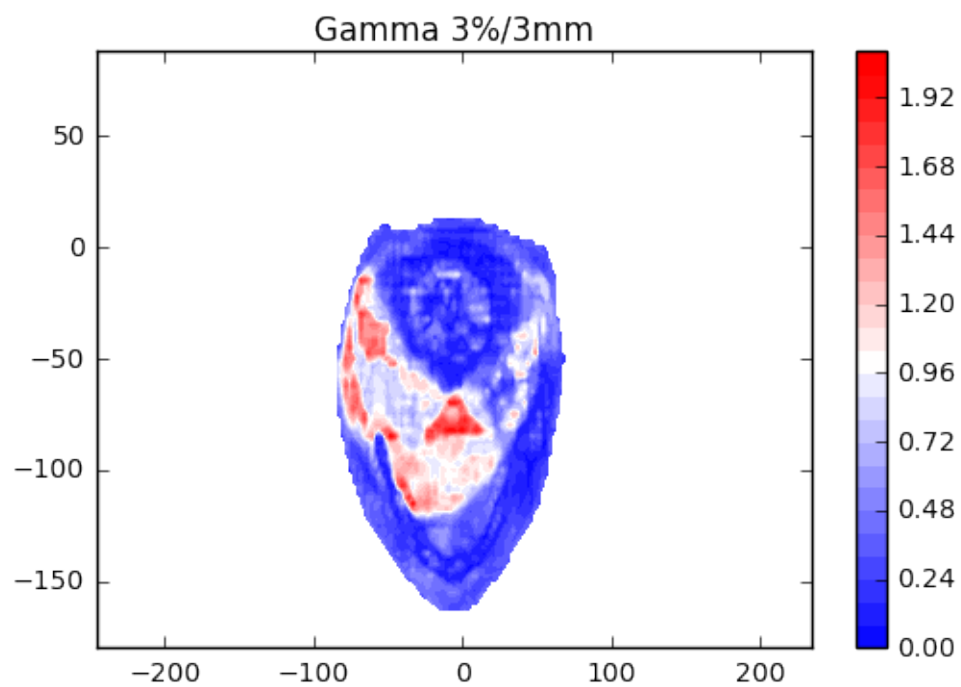




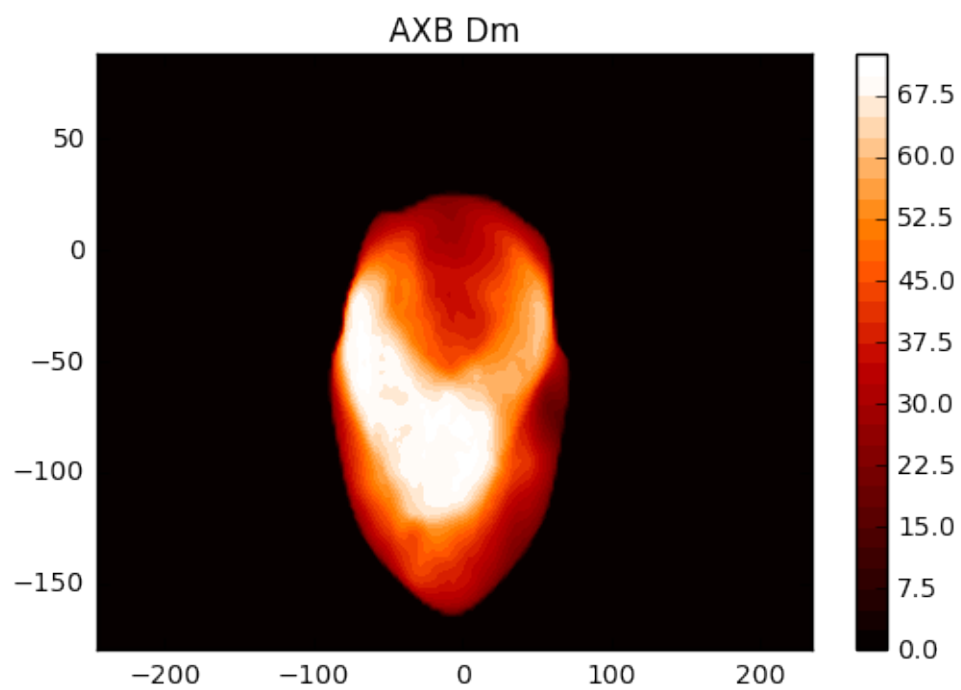
=====  
Slice = -3.75

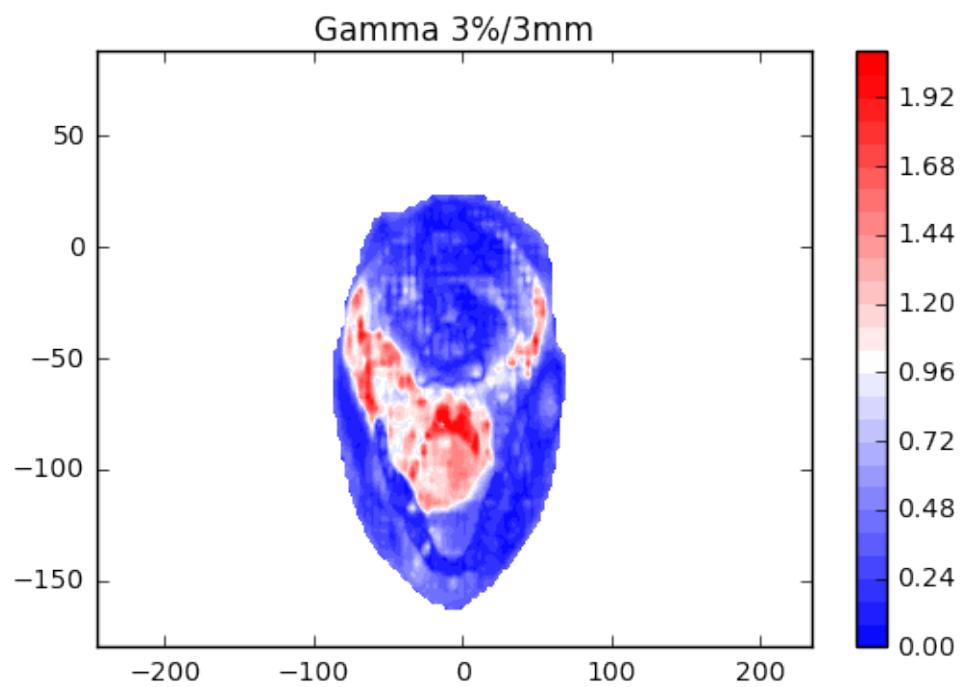
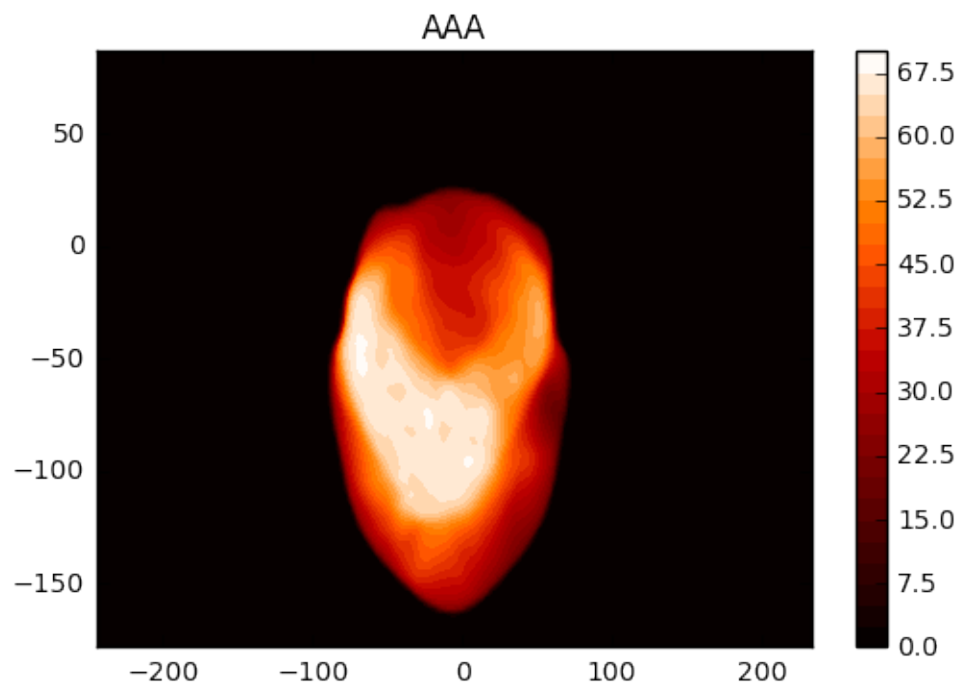






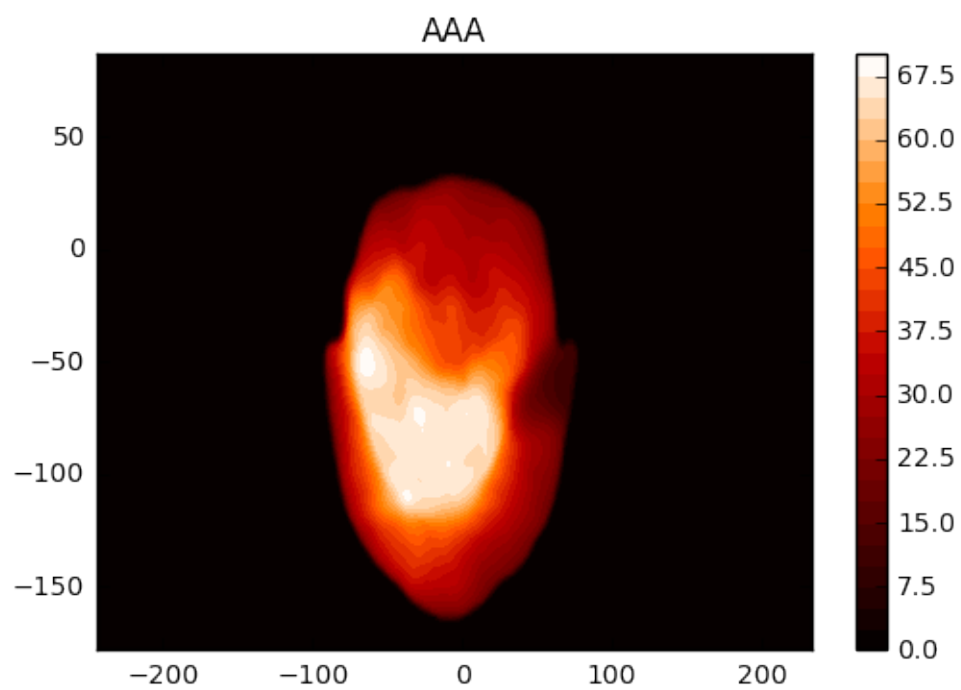
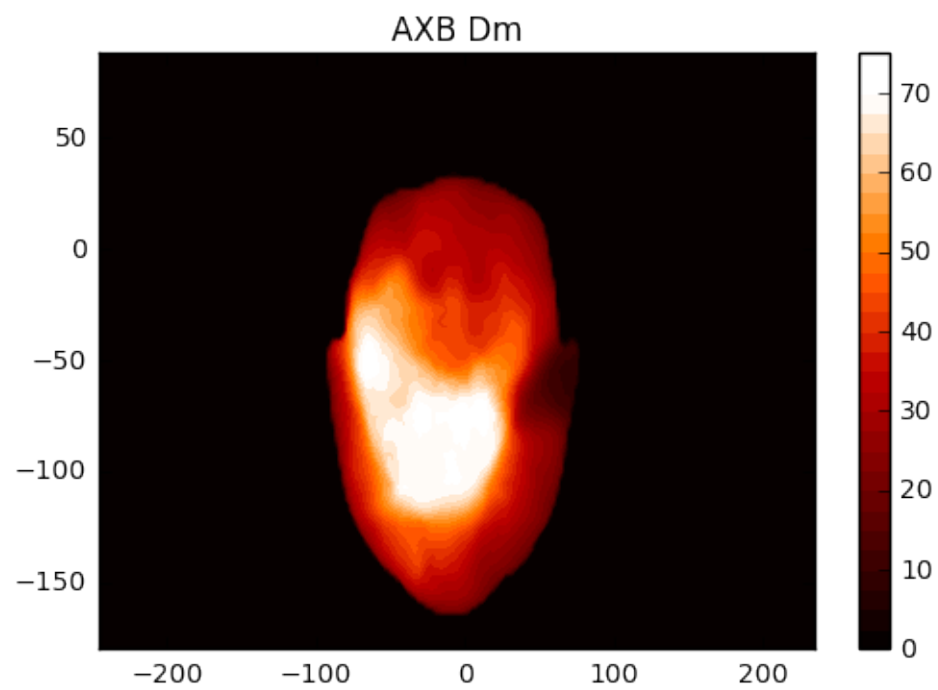
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Slice = 8.75

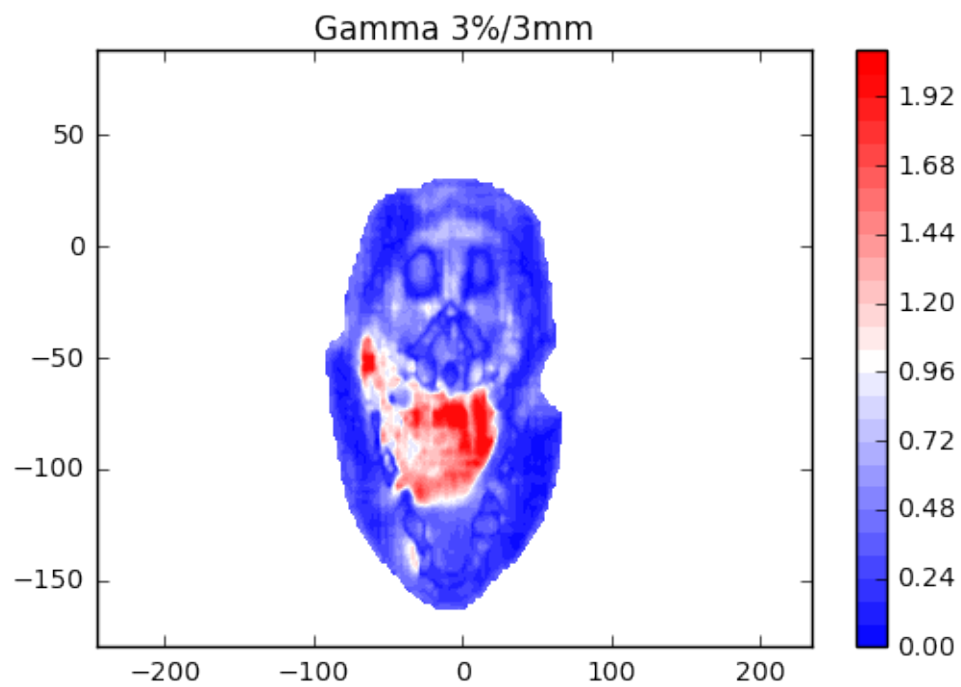




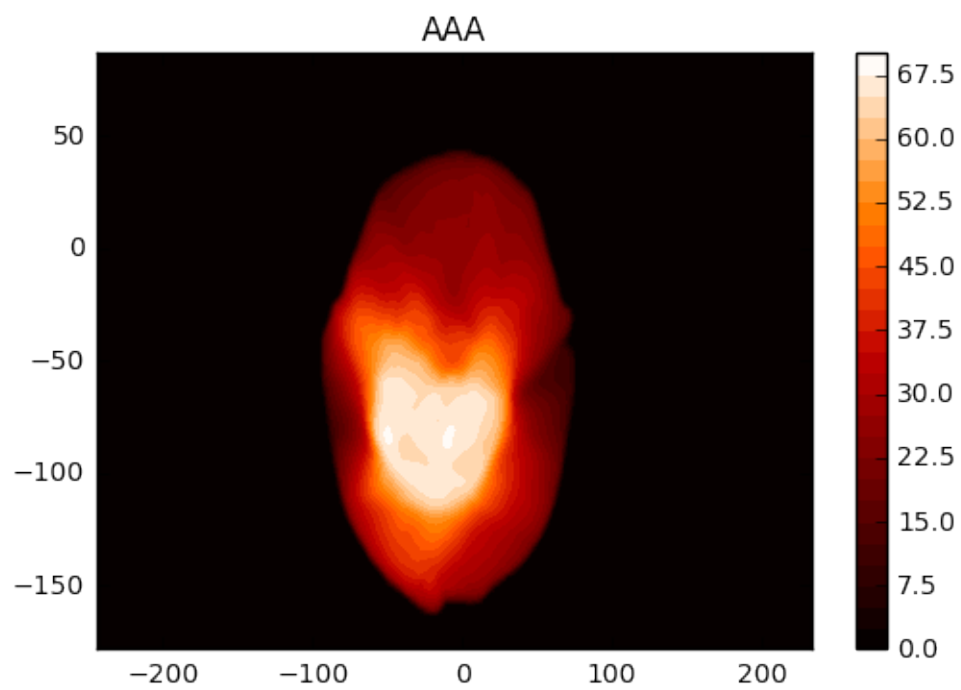
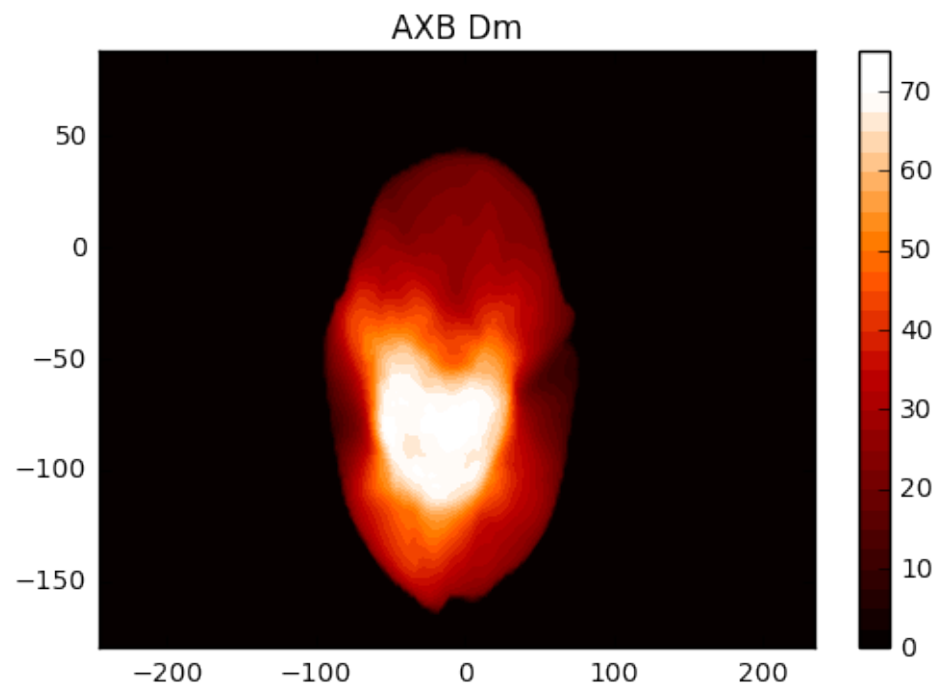
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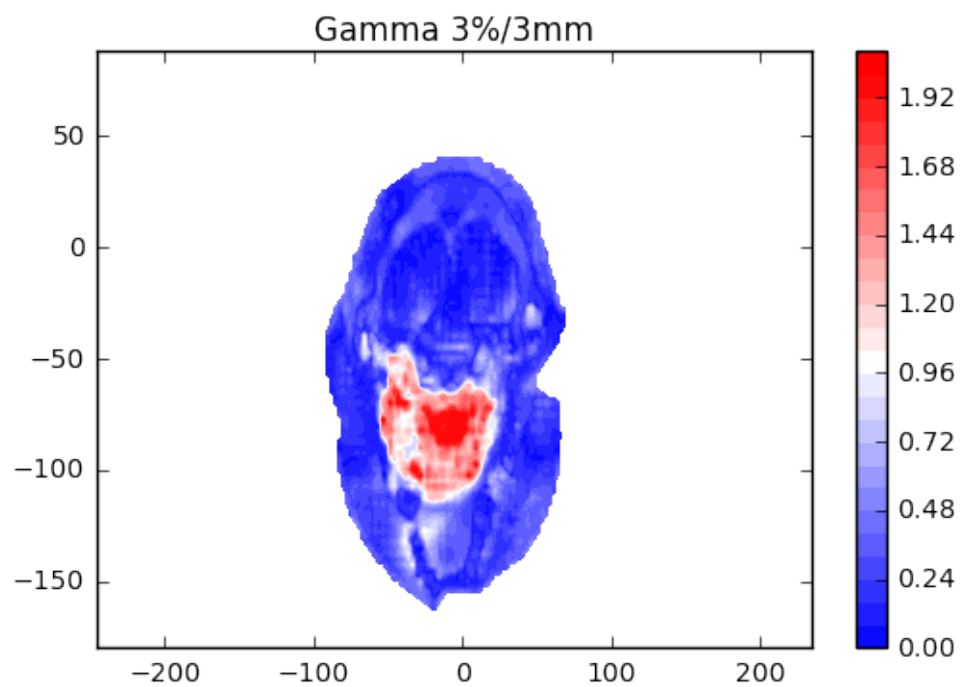
Slice = 21.25



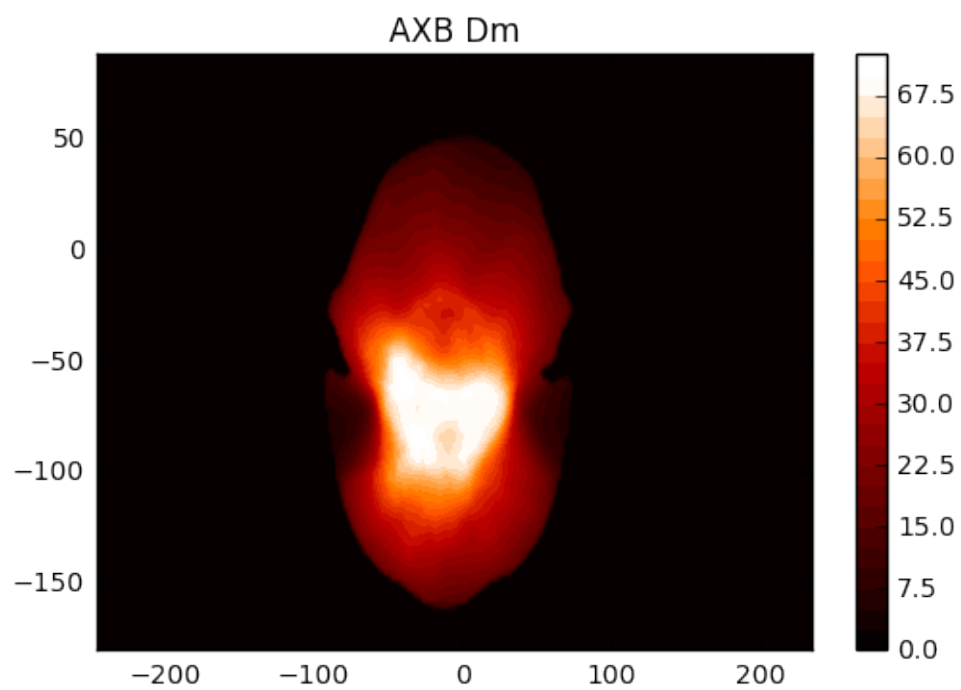


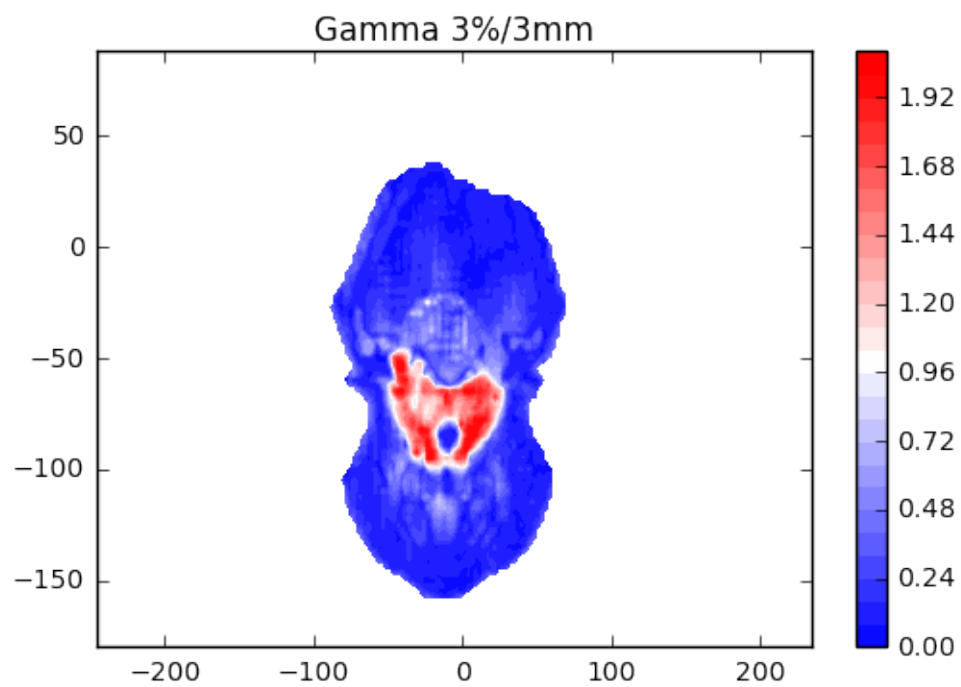
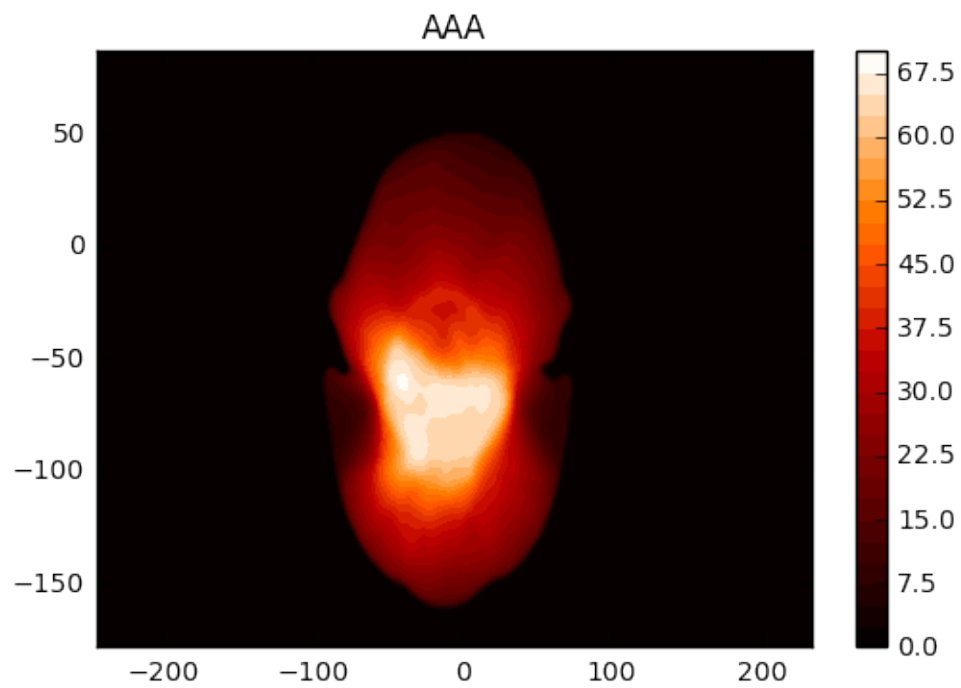
=====  
Slice = 33.75





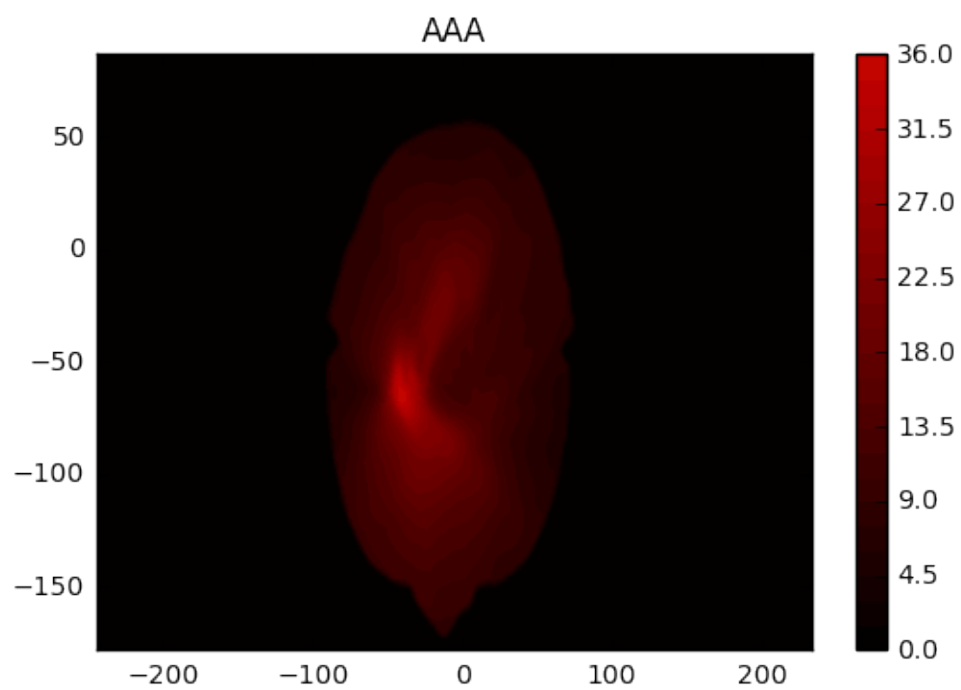
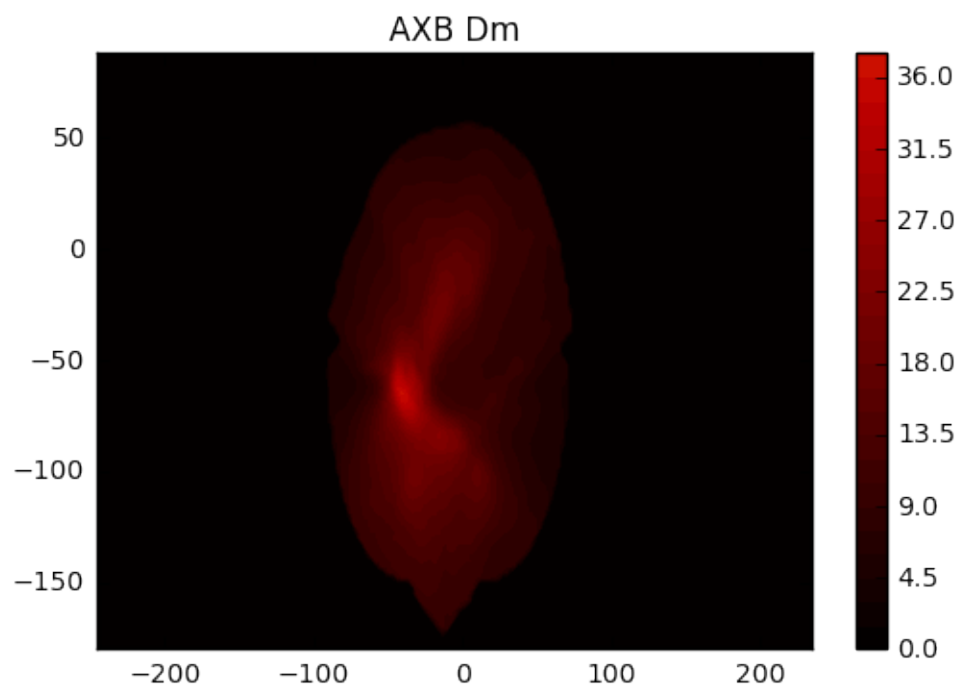
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Slice = 46.25



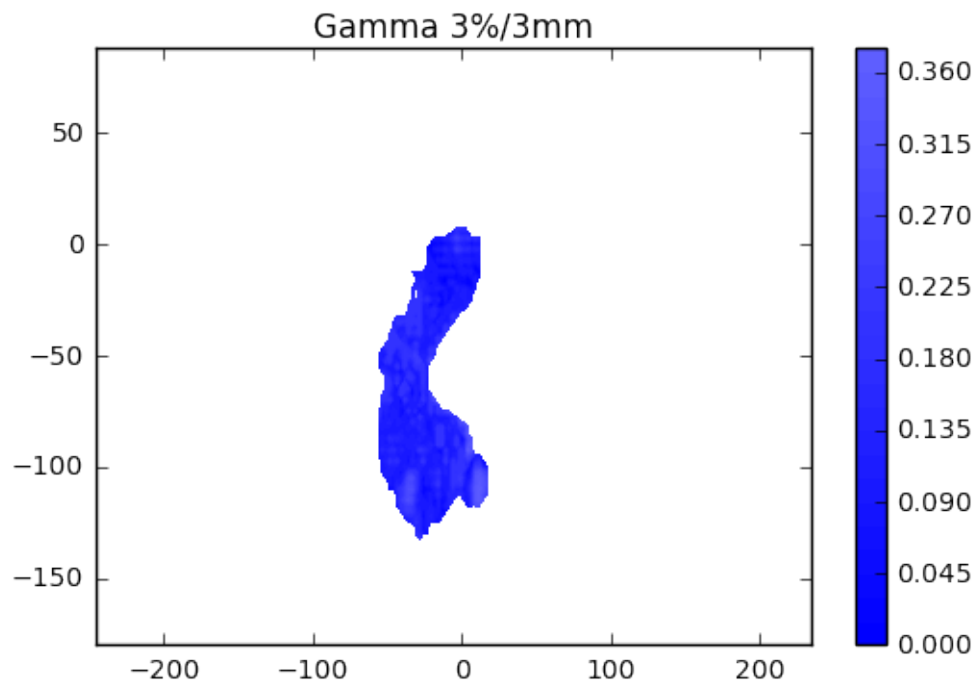


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Slice = 58.75







In [ ]: