Applications of Landmark Localization on Medical Images

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Motivation: Why to locate keypoints?

- Pose estimation
- Object detection & localization
- Object recognition
- 3D Reconstruction
- Testing sufficiency model & dataset



LEFT: Contoured Image of a person



RIGHT: Registered contour image to 3D model created from same person's MRI surface

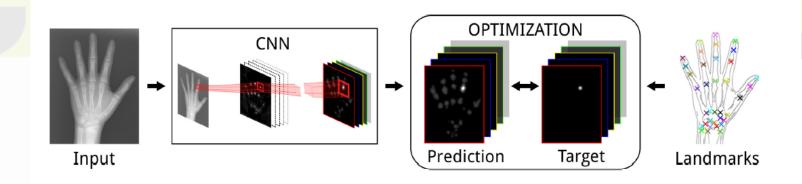
Source: Yetkin, Hamamcı, 2017

Heatmap Regression with Fully Convolutional Network

Regressing Heatmaps for Multiple Landmark Localization using CNNs

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Regression with fully Convolutional Neural Netwok

- It's pretty easy and popular, actually.
- Reduces computational loss.
- Normally, output of last convolution layer is flattened and sent to fully connected neural network layers. Loss is applied to last layer of network.
- But now, instead of fully connected layers, there are convolutional layers with 1x1 kernel size. What they do is producing a single value among feature maps.
- This conv. layers with 1x1 kernel size may have different activation function(sometimes none), and may be tied to different normalization functions.(sometimes none)

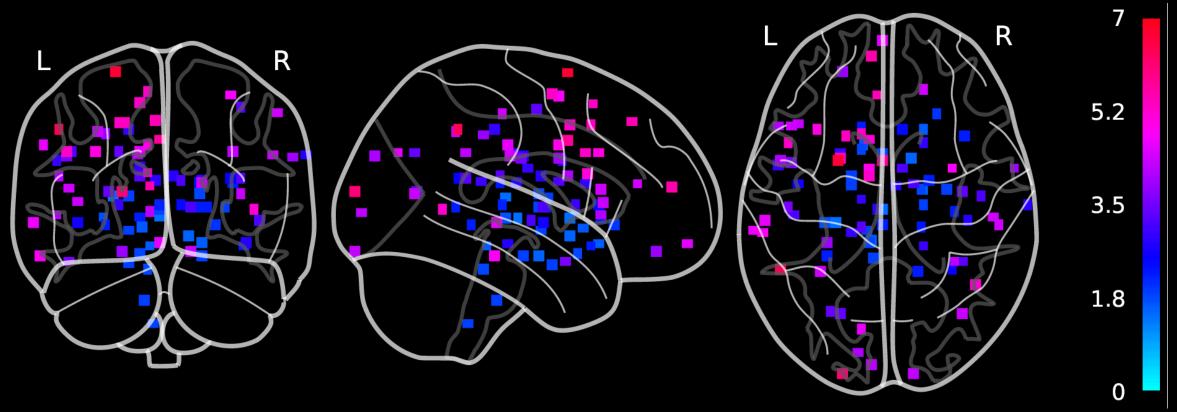
Useful Python Libraries

- SimpleITK: simplified layer built on top of ITK,
- nipy, analysis of structural and functional neuroimaging data.
 - nilearn: fast and easy statistical learning on Neuro-Imaging data,
 - nibabel : Read / write common neuroimaging file formats,
 - ... it goes on and on

Besides, **3D Slicer** is an open source software platform for medical image informatics, image processing, and three-dimensional visualization.

- It has Python wrapper! You can move your own work to Slicer environment as an extension easily.
- The advantage you get by doing this, you could use Slicer's utilities.

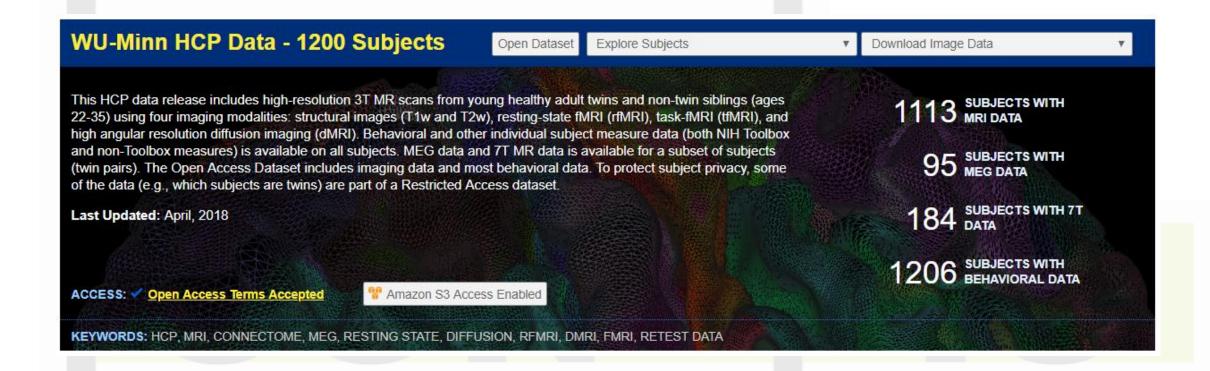
import nilearn.plotting as nip
result = nibabel.Nifti1Image(array,affine)
nip. plot_glass_brain(result,other_parameters)



Source: Yetkin, Hamamcı, 2018

Dataset: Human Connectome Project

db.humanconnectome.org



Network Structure

- Hyperparameters (kernel size, depth of layers, # of layer, Ir, optimizer, loss func.) play key role and are problem specific.
- Write your own loss function? Why not?

```
def my_loss_func_1(y_true, y_pred):
    lmbda = 0.05 ## penalizing factor
    out = K.square(y_true-y_pred)
    return K.mean(out, axis=1) * lmbda
```

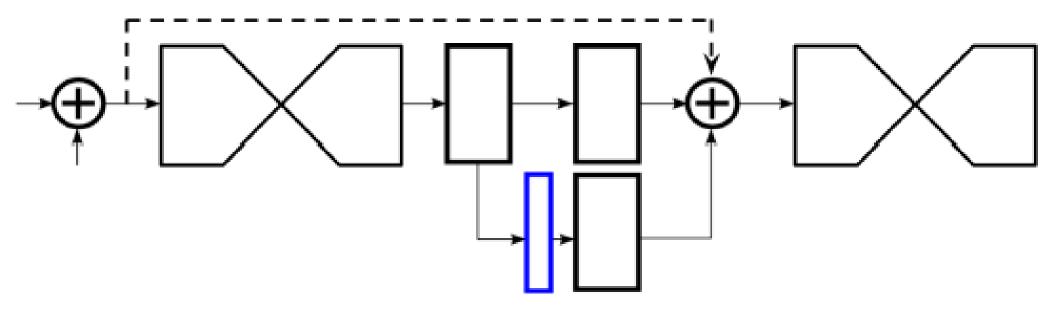
- Activation function is also important
- Mini batch if data is too big

 ROI is very related to problem and dataset. It affects receptive field, spatial subsampling.

Need to make it deeper? How to handle?

- Batch normalization [loffe and Szegedy, 2014]
- Activation function (ReLU, ELU, PRELU...) can solve vanishing gradients problem
- Spatial Dropout (Especially when your model deals with big size data eg: input size of model is: 320x320x3)
- Residual Layers [He and Zhang, 2015]
- Intermediate Supervision [Newell and Yang, 2016]

Intermediate Supervision



Source : Newell, Yang, 2016

Merged_Model = Model(inp,[int_out_1,int_out_2,final_out])
Mrged_Model.compile(optimizer = RMSProp, loss=['mean_squared_error', 'my_loss_func_1', 'mean_squared_error'])

Stacked Hourglass Networks for Human Pose Estimation

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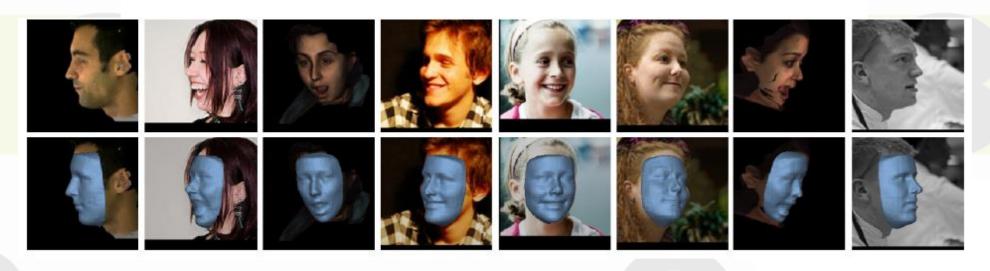


Large Pose 3D Face Reconstruction from a Single Image via Direct Volumetric CNN Regression

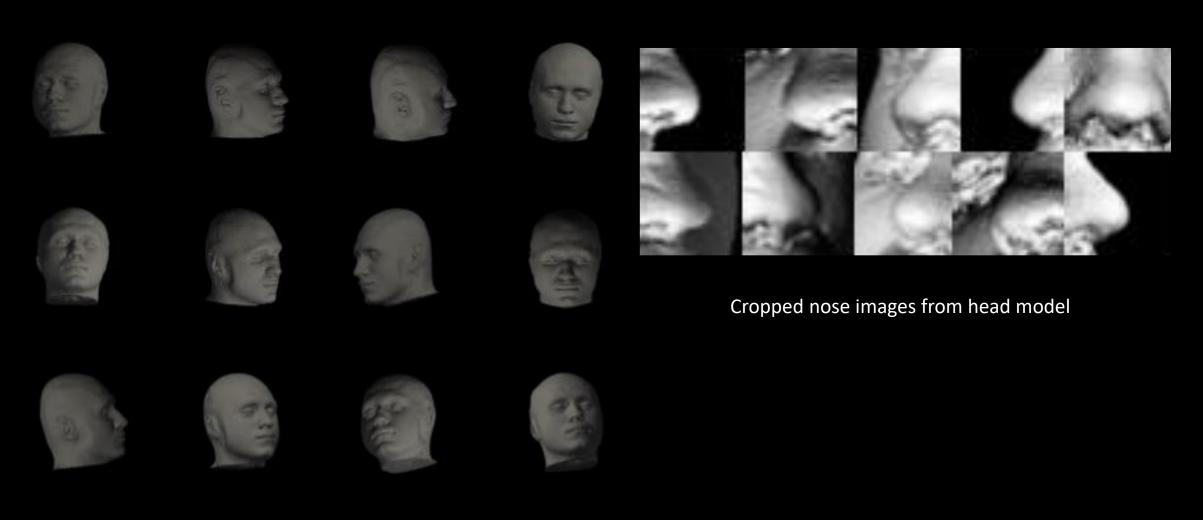
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Dataset



DeepCon'18

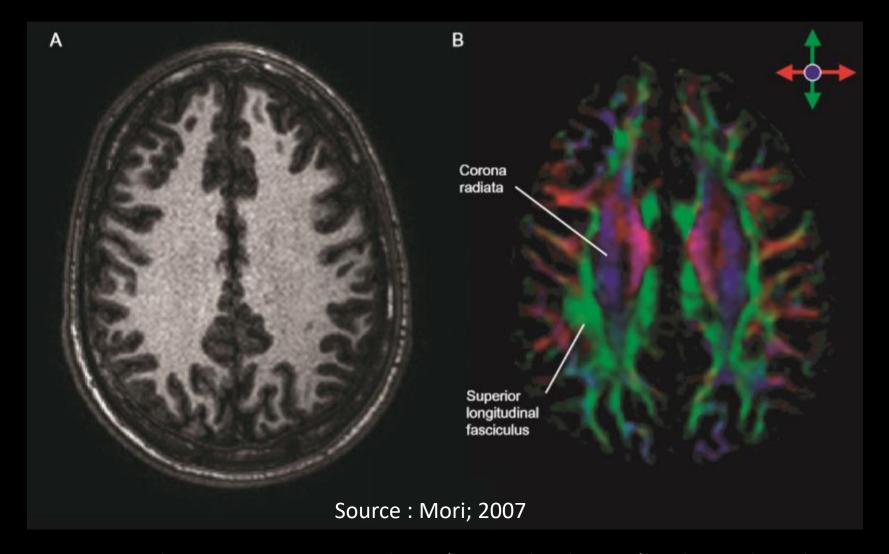
Source: Yetkin, Hamamcı, 2017

What is Diffusion Tensor Imaging?

- Measures molecular motion along an arbitrary, predetermined axis; we can measure water diffusion along right-left, fore-aft, up-down, or any oblique angle.
- If we are measuring freely diffusing water, this unique capability does not mean much, because measurements along any orientation give the same result. This is what we call isotropic diffusion.
- However, the situation changes when we study biological tissues such as muscle and brain, which consist of fibers with coherent orientations. In such systems, water tends to diffuse along the fiber, and diffusion becomes anisotropic. This means that the results of diffusion measurements are not the same if they are measured along different orientations.

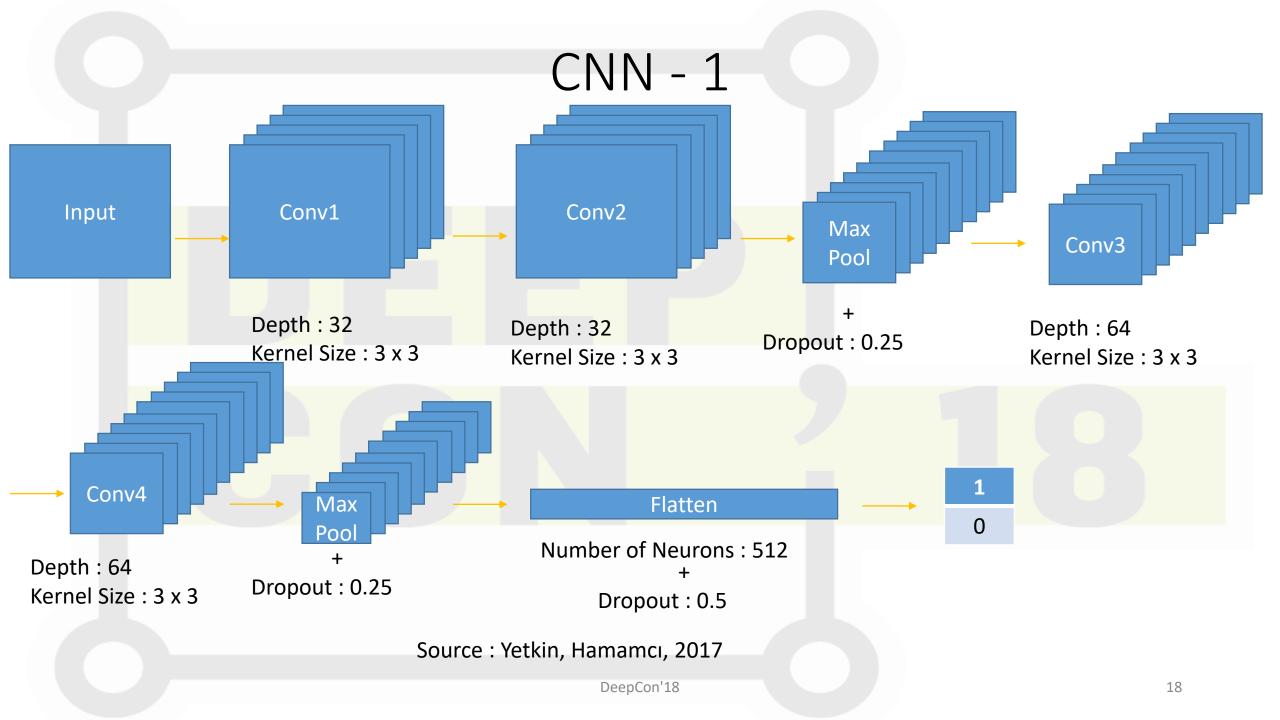
T1/T2 MRI vs DTI

- Conventional MRI based on relaxation time relies on differences in chemical composition for their contrasts. For T1- and T2-weighted images, the amount of myelin plays a major role in differentiating the gray and white matter.
- However, the white matter looks quite homogeneous because it is homogeneous in terms of the chemical composition.
- In contrast, DTI can generate contrasts that are sensitive to fiber orientations

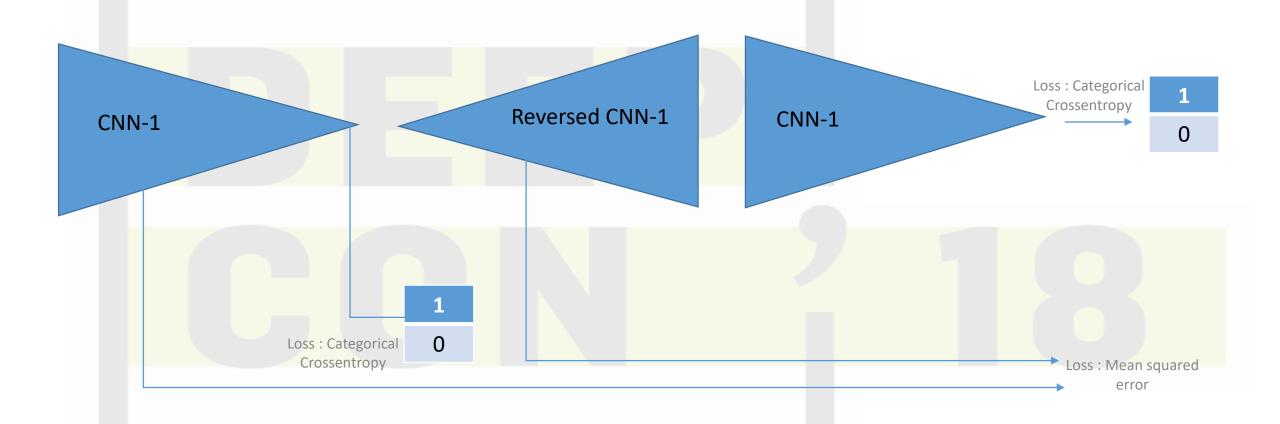


Comparison between a conventional MRI (T1-weighted image) and a DTI-based map (color map). In the color map, color represents fiber orientations; red, green, and blue represent fibers running along the right-left, anterior-posterior, and superior-inferior orientations. DeepCon'18

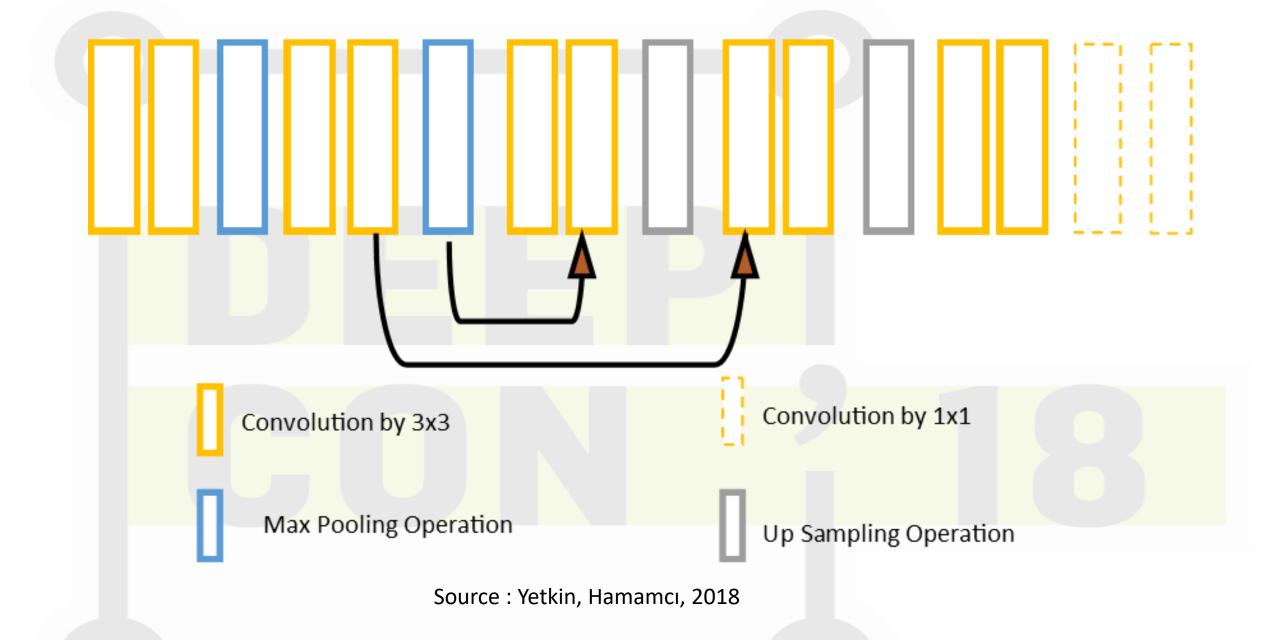
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CNN - 2

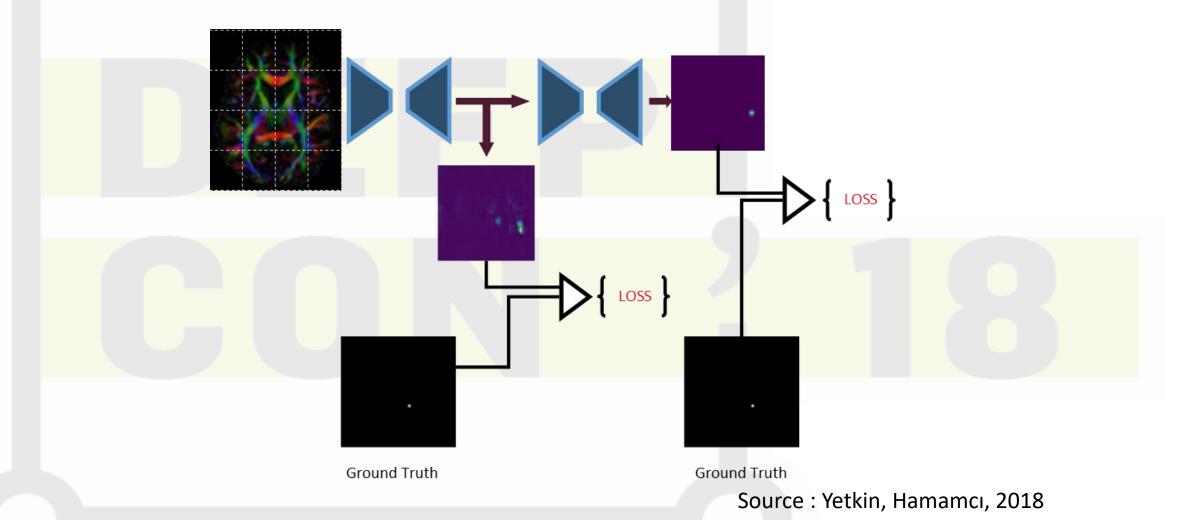


Source: Yetkin, Hamamcı, 2017





Intermediate Supervision Implementation



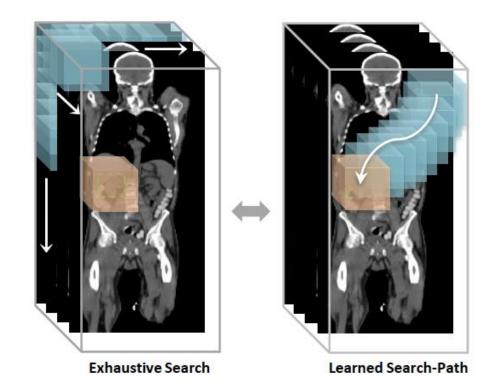
Mini Suggestion about debugging the Net

- Keep log about everything you can.
- Visualize kernels.
- Test the model during training.
- (ex: every 500 iteration, save results, compare results)
- It's an easy way to know that model converges. Saves time.

Read Suggestion

Multi-Scale Deep Reinforcement Learning for Real-Time 3D-Landmark Detection in CT Scans

Florin C. Ghesu, Bogdan Georgescu, *Member, IEEE*, Yefeng Zheng, *Senior Member, IEEE*, Sasa Grbic, Andreas Maier, Joachim Hornegger, and Dorin Comaniciu, *Fellow, IEEE*



Thank you for listening. Any questions?