



# Towards an ultra-high resolution 3D neurotransmitter receptor atlas

BIG BRAIN WORKSHOP 2020 | THOMAS FUNCK, PHD



**McGill**



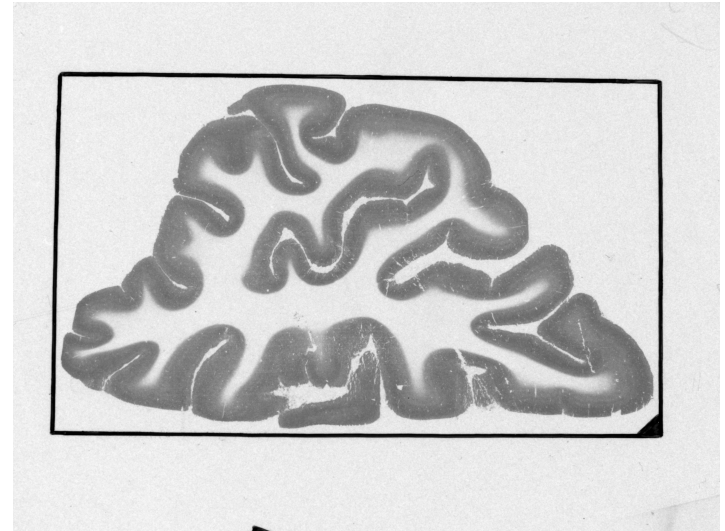
**JÜLICH**  
Forschungszentrum

# Creating neurotransmitter receptor atlases

- Characterize normal + pathologic receptor distributions
  - Chemoarchitecture of information processing

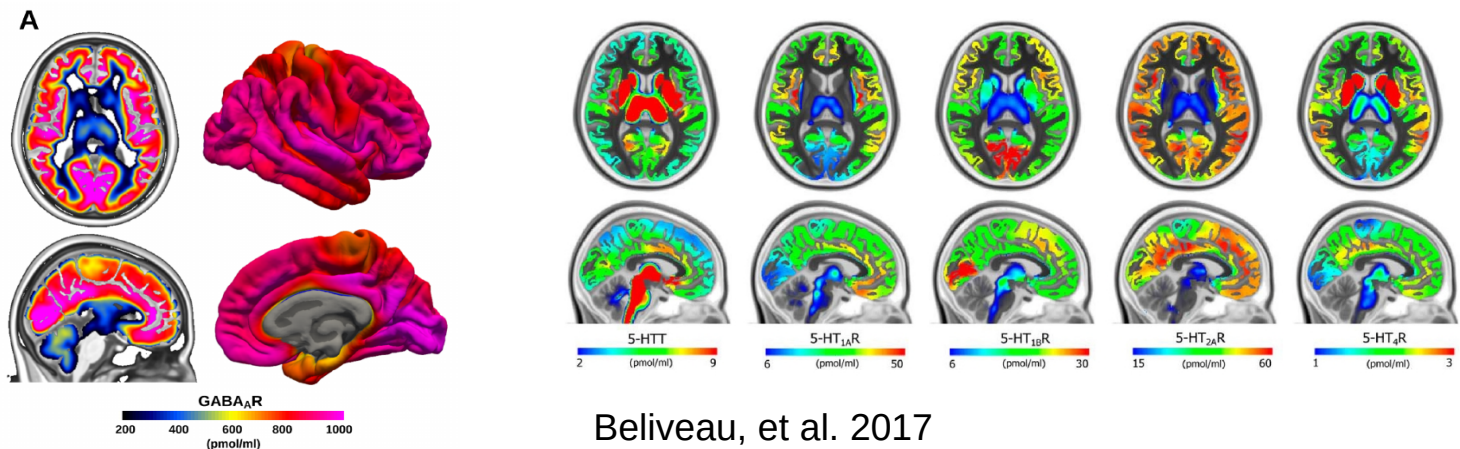
# Creating neurotransmitter receptor atlases

- Characterize normal + pathologic receptor distributions
- Autoradiography
  - + High resolution (0.05mm)
  - + More ligands than PET
  - Extremely expensive
  - Only 2D images
  - Post-mortem



# Creating neurotransmitter receptor atlases

- Characterize normal + pathologic receptor distributions
- Autoradiography
- PET
  - + In vivo
  - + Relatively inexpensive → larger data sets
  - Lower resolution → what is maximum resolution of PET?



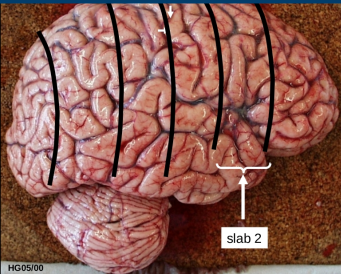
Beliveau, et al. 2017

Norgaard, et al. 2020 (preprint)

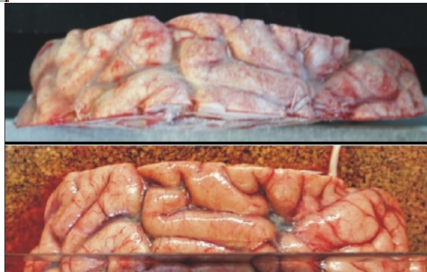
# Reconstructing 3D atlases from 2D autoradiographs

# The data

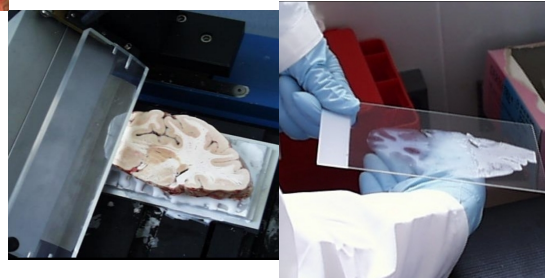
Brain extracted and cut into 2-3cm slabs



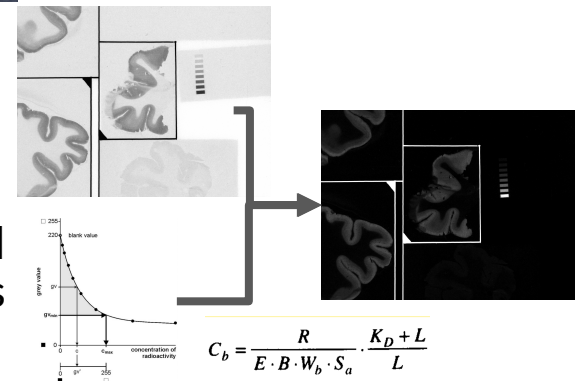
Slabs shock frozen ~-40C



Slabs sectioned and bathed in solution with radioligand



Raw autoradiographs transformed to binding densities

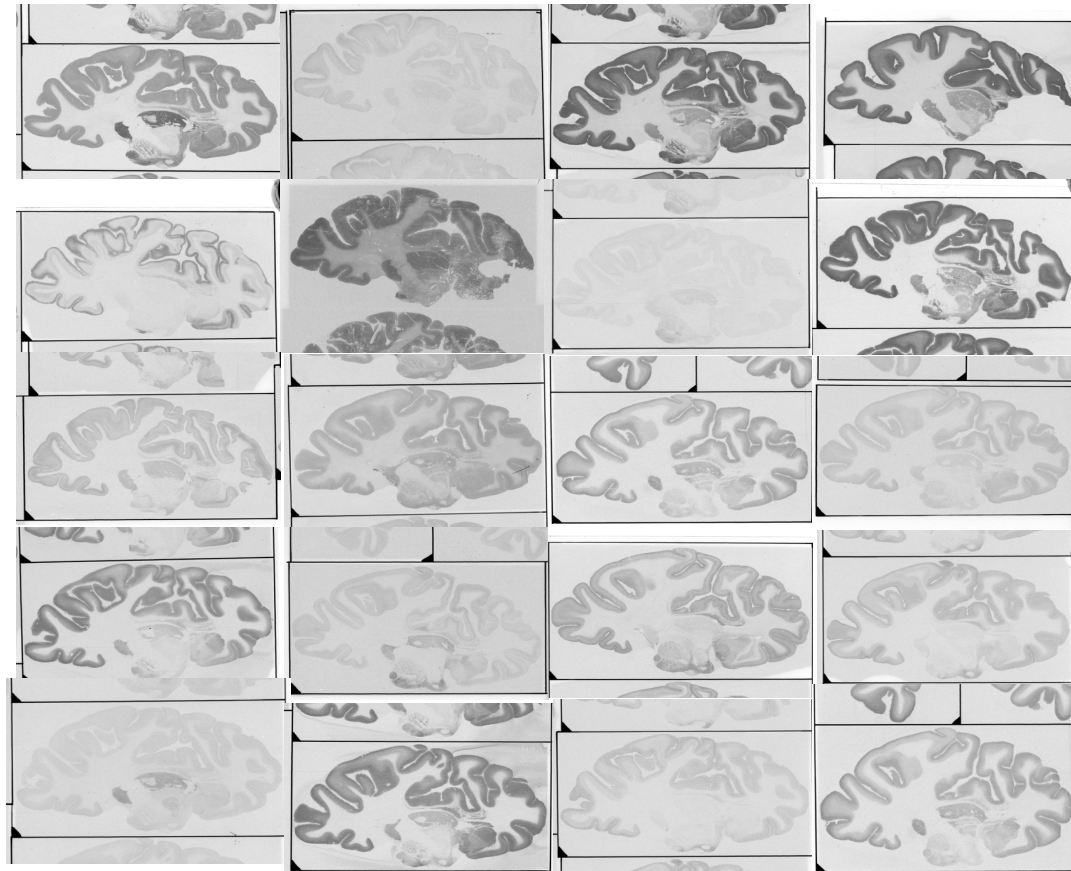


# The data

- 3 post-mortem human brains
- 20 receptor binding sites
  - visualized with quantitative in vitro receptor autoradiography
  - acquired sequentially → ~400 $\mu$ m+ between particular receptor

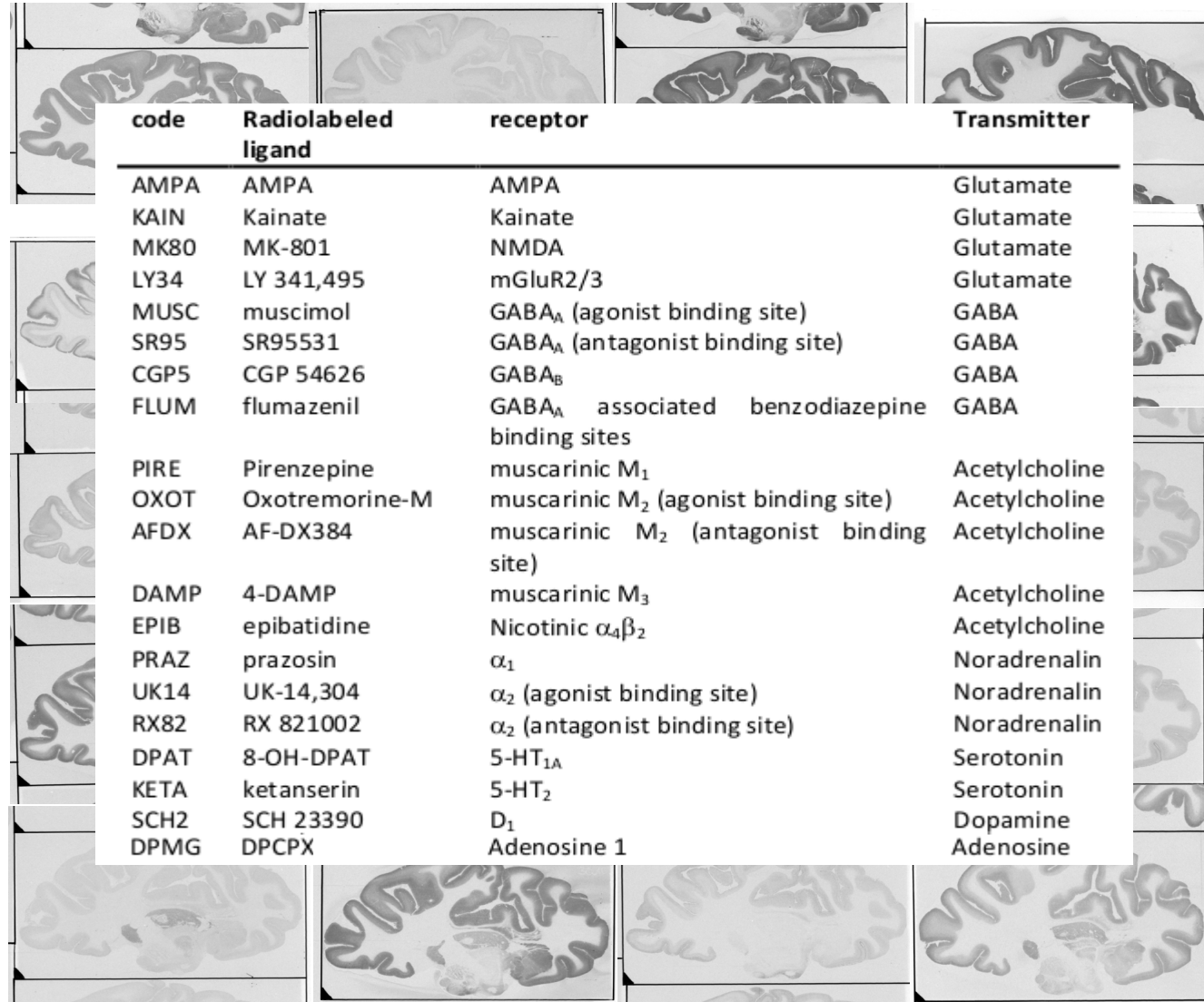
# Autoradiographs

- 3 post-mortem human brains
- 20 receptor binding sites
  - visualized with quantitative in vitro receptor autoradiography
  - acquired sequentially →  $\sim 400\mu\text{m}+$  between particular receptor





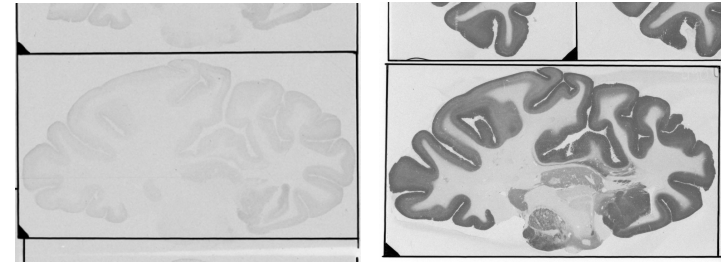
# Autoradiographs



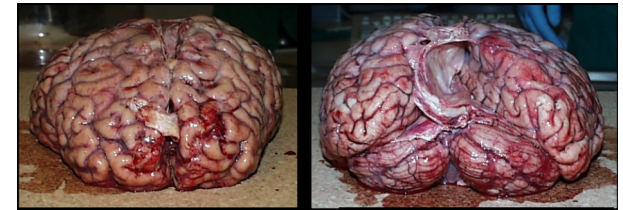
code	Radiolabeled ligand	receptor	Transmitter
AMPA	AMPA	AMPA	Glutamate
KAIN	Kainate	Kainate	Glutamate
MK80	MK-801	NMDA	Glutamate
LY34	LY 341,495	mGluR2/3	Glutamate
MUSC	muscimol	GABA <sub>A</sub> (agonist binding site)	GABA
SR95	SR95531	GABA <sub>A</sub> (antagonist binding site)	GABA
CGP5	CGP 54626	GABA <sub>B</sub>	GABA
FLUM	flumazenil	GABA <sub>A</sub> associated benzodiazepine binding sites	GABA
PIRE	Pirenzepine	muscarinic M <sub>1</sub>	Acetylcholine
OXOT	Oxotremorine-M	muscarinic M <sub>2</sub> (agonist binding site)	Acetylcholine
AFDX	AF-DX384	muscarinic M <sub>2</sub> (antagonist binding site)	Acetylcholine
DAMP	4-DAMP	muscarinic M <sub>3</sub>	Acetylcholine
EPIB	epibatidine	Nicotinic $\alpha_4\beta_2$	Acetylcholine
PRAZ	prazosin	$\alpha_1$	Noradrenalin
UK14	UK-14,304	$\alpha_2$ (agonist binding site)	Noradrenalin
RX82	RX 821002	$\alpha_2$ (antagonist binding site)	Noradrenalin
DPAT	8-OH-DPAT	5-HT <sub>1A</sub>	Serotonin
KETA	ketanserin	5-HT <sub>2</sub>	Serotonin
SCH2	SCH 23390	D <sub>1</sub>	Dopamine
DPMG	DPCPX	Adenosine 1	Adenosine

# Challenges to 3D Reconstruction

(I) Autoradiograph intensities

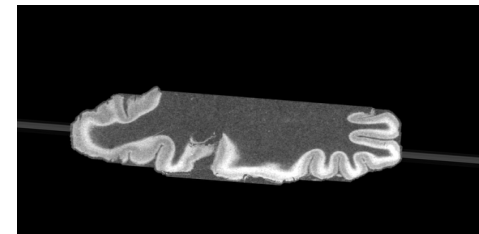


(II) Morphological deformation

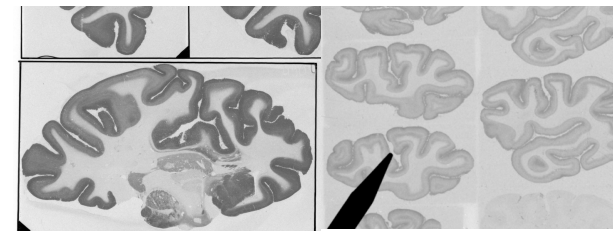


(III) Non-parallel slabs

(IV) Missing / incomplete slices

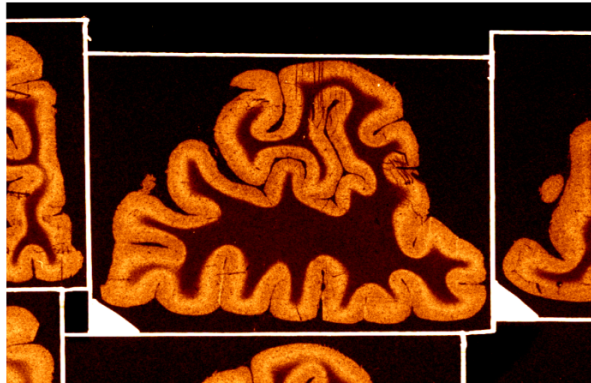


(IV) Autoradiograph slice acquisition



# Preprocessing

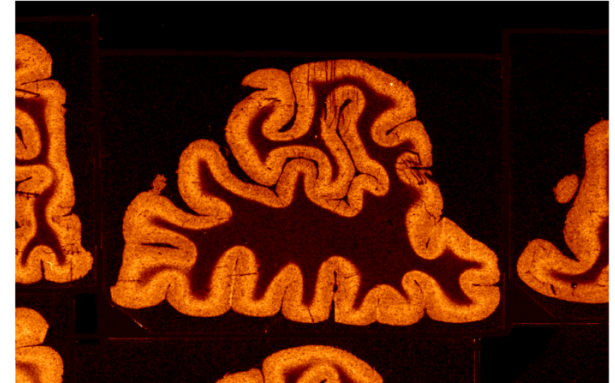
*Initial Image*



*Line Detection*



*Lines Removed*



*Target Tissue Mask*

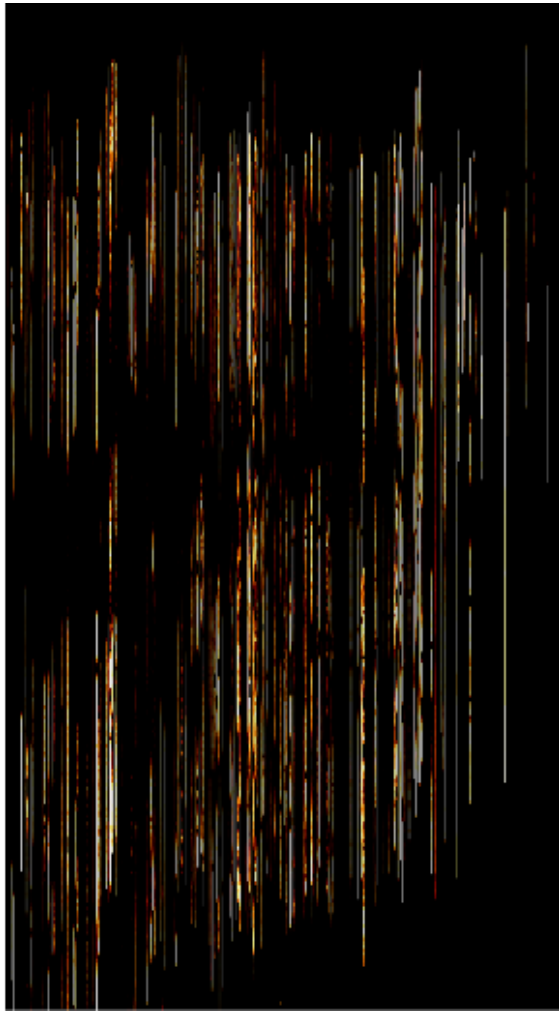


*Cropped Image*

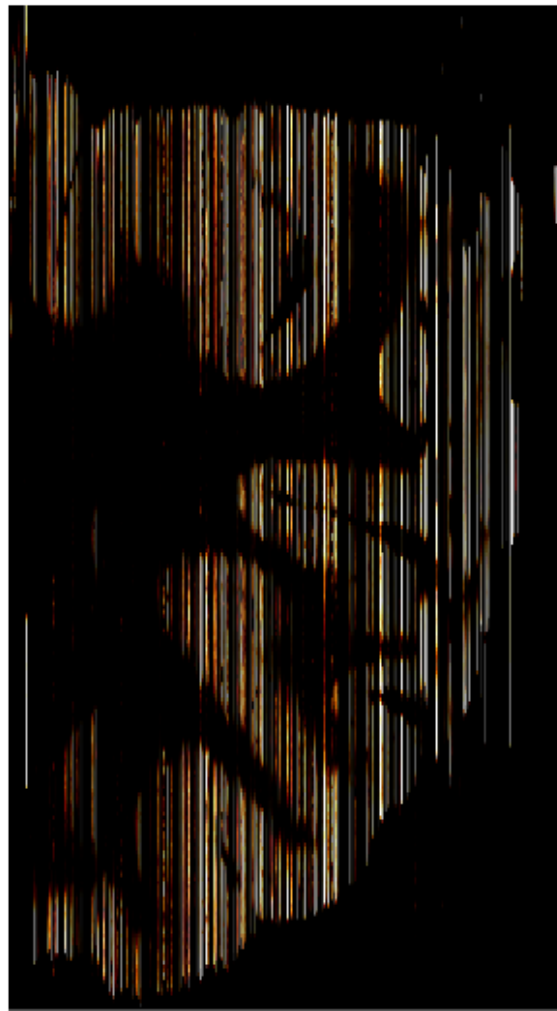


# Rigid 2D Autoradiograph Alignment

Iteration 0



Iteration 1



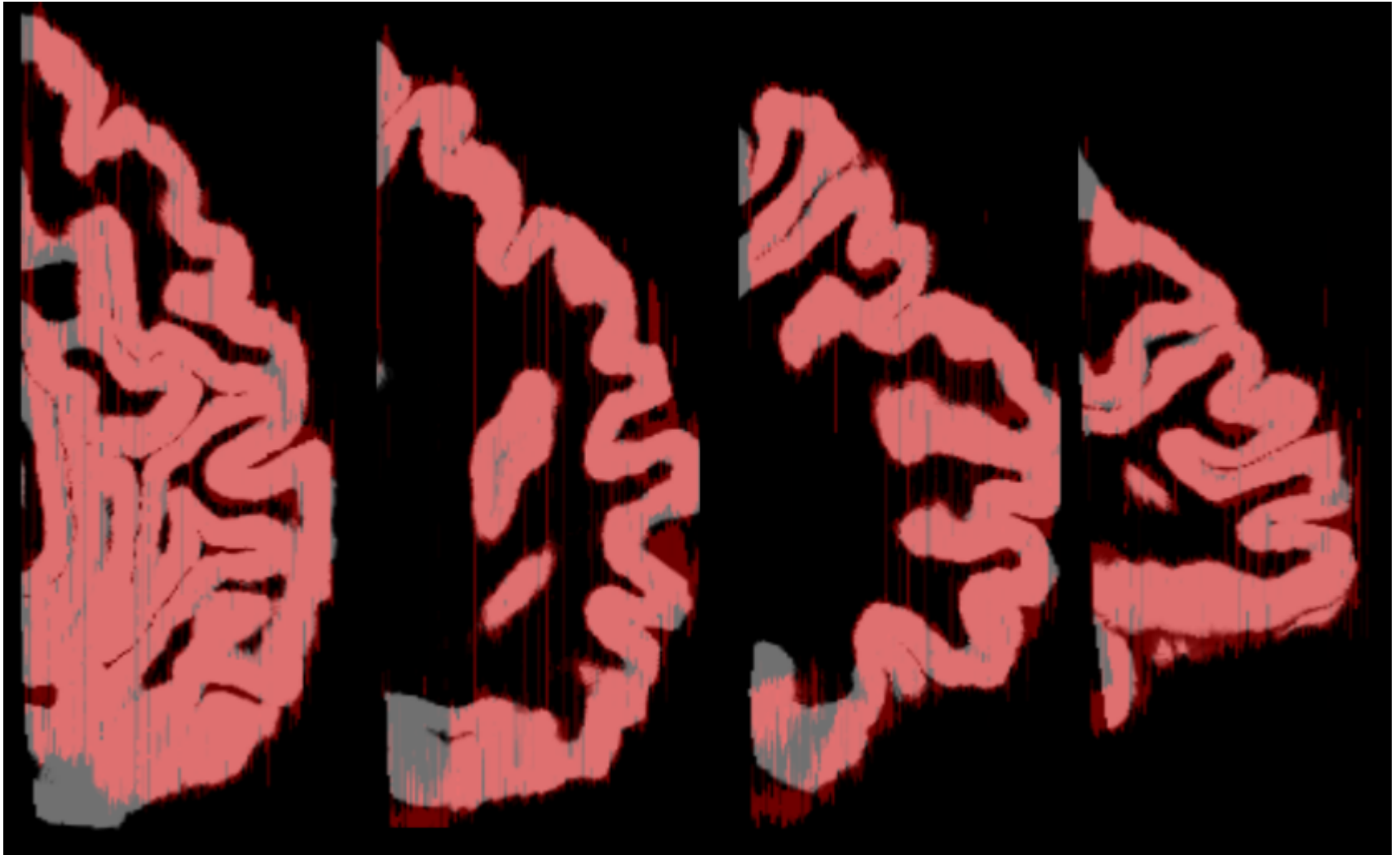
...

Iteration 9



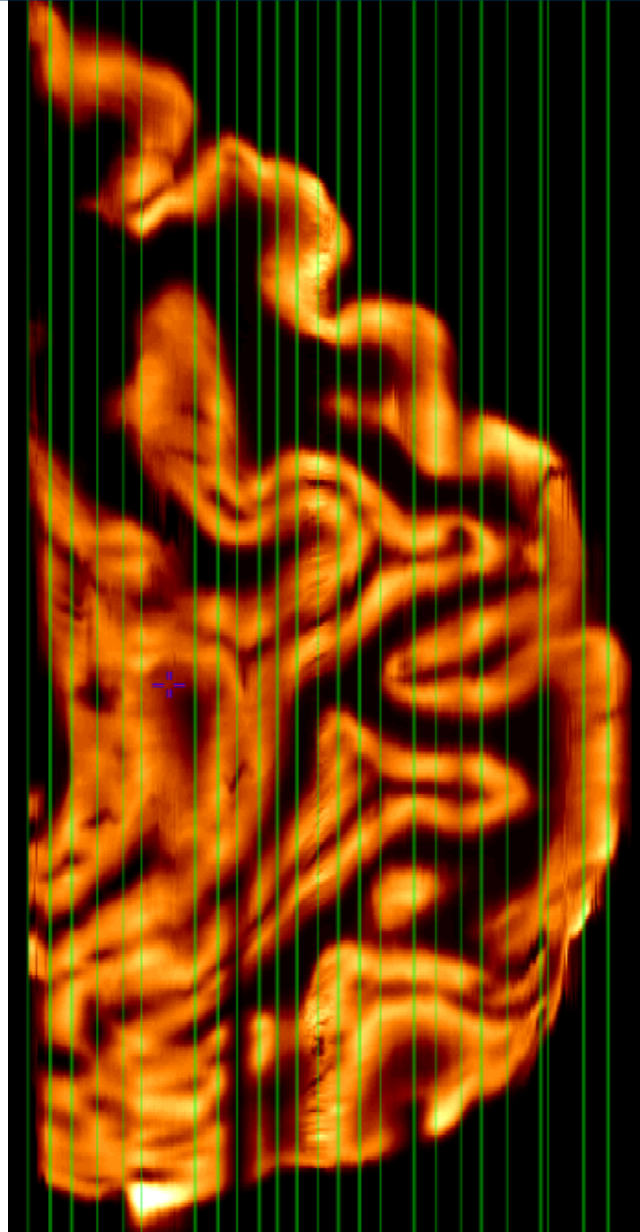
# MRI to Autoradiograph Volume Alignment

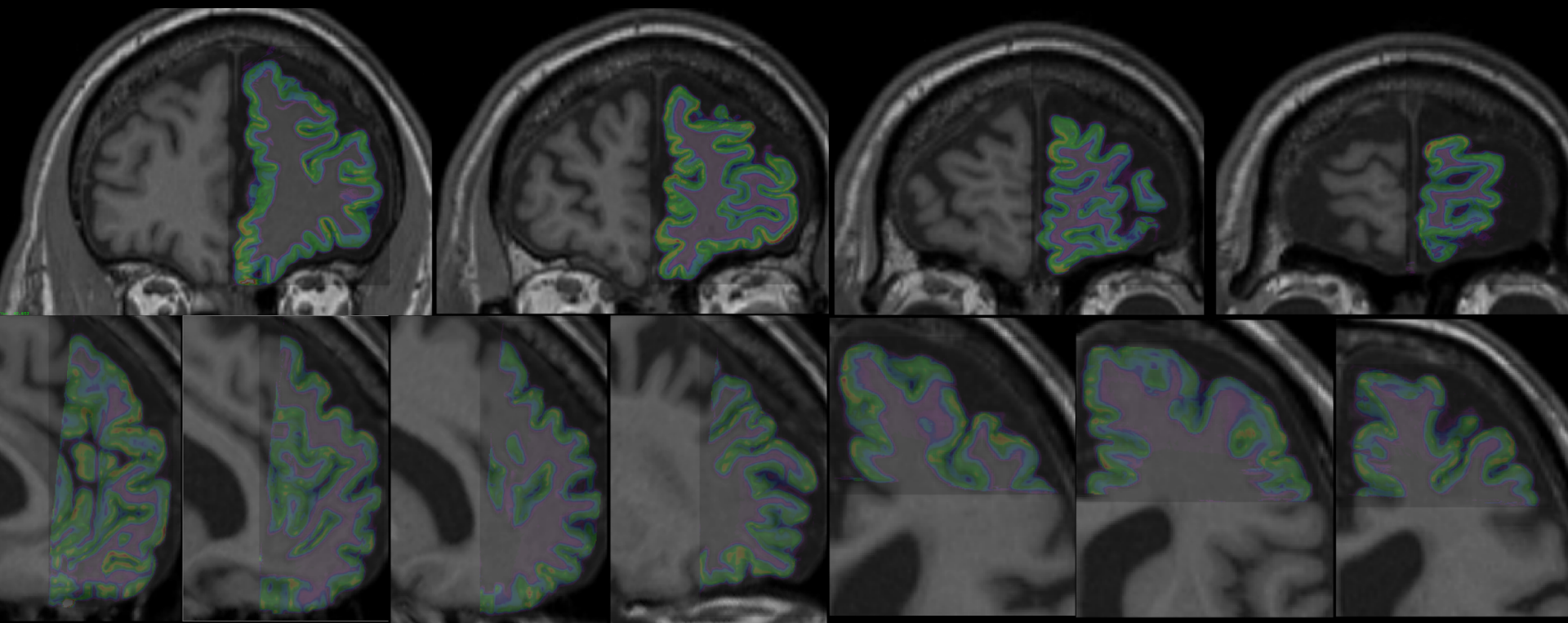
- Grey : Warped MRI GM mask
- Red : Receptor volume GM mask

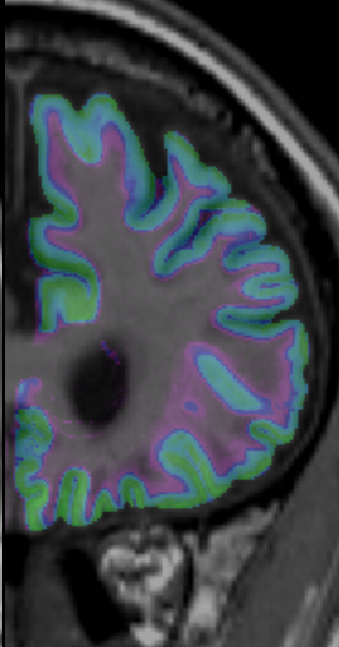
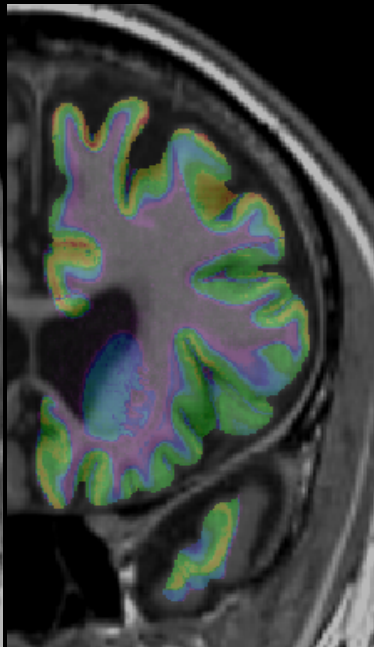
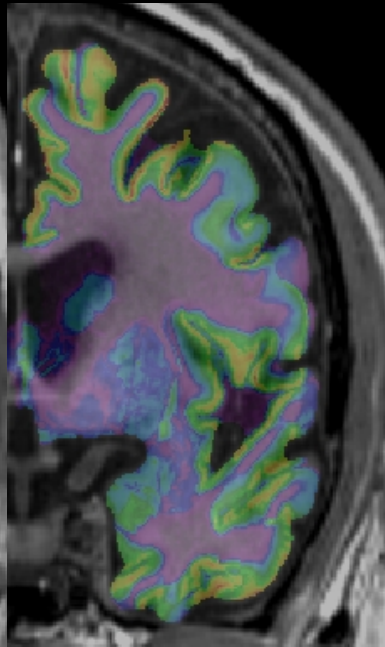
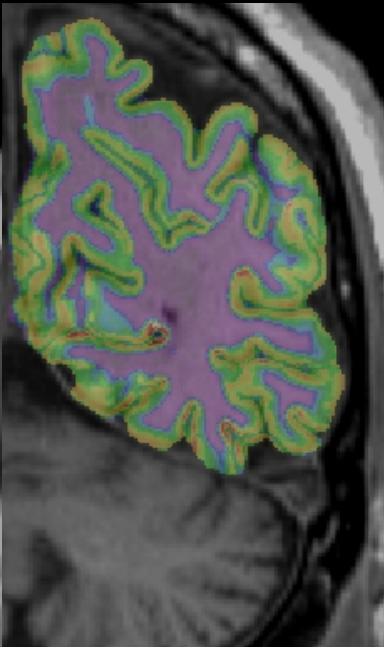
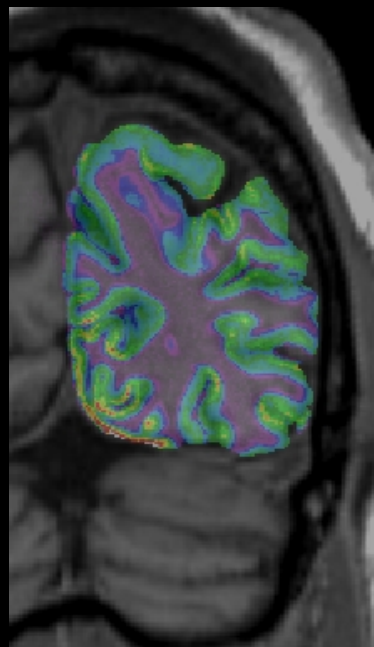
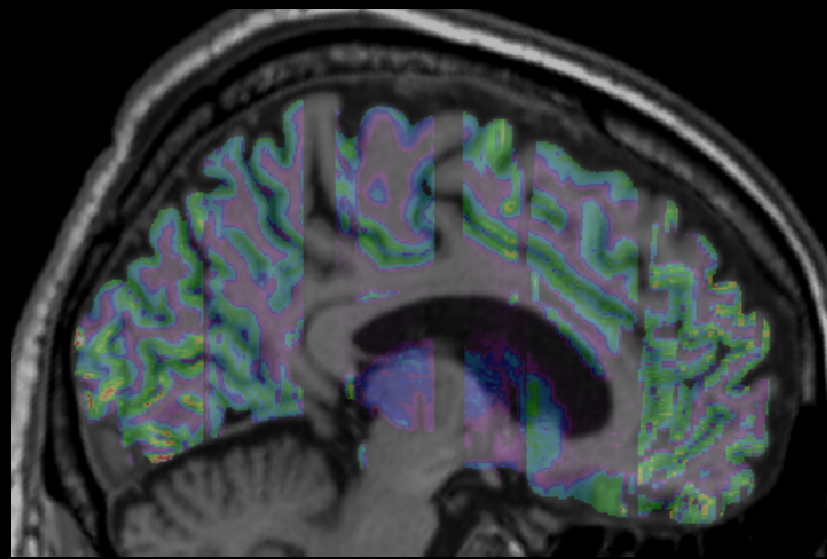


# Interpolating missing autoradiographs

- Morphologically adaptive, distance-weighted interpolation
- Reconstructed GABA-A<sub>Benz</sub> volume
  - Ligand = Flumazenil
  - Green = acquired autoradiographs

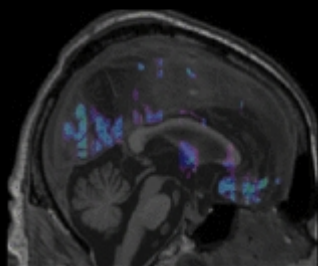




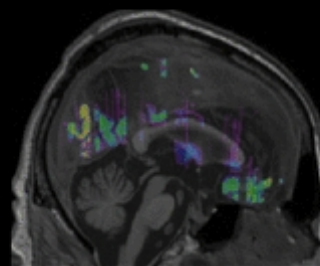




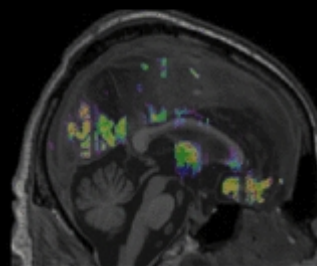
GABAA.Benz.



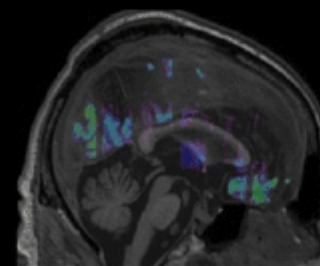
GABAA.Ag.



GABAB

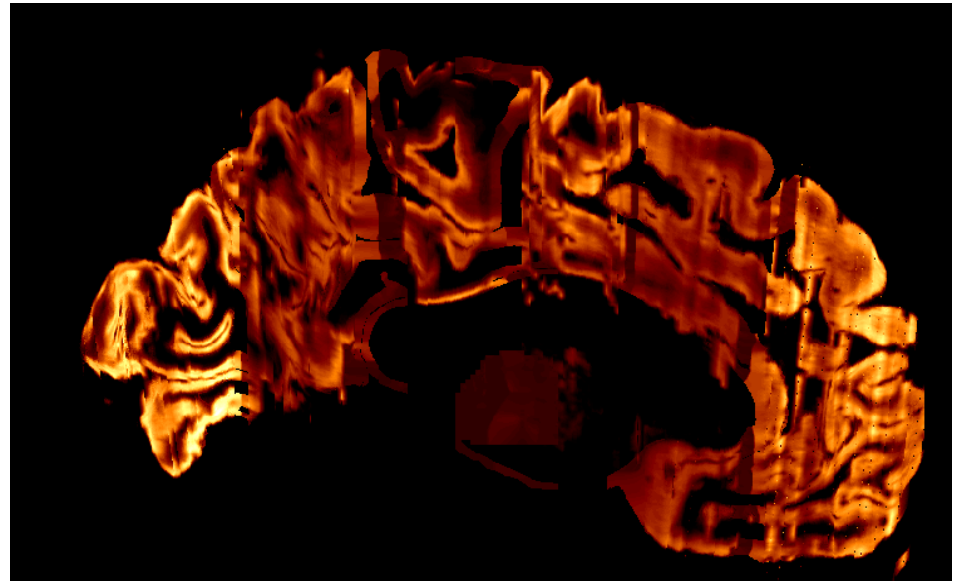
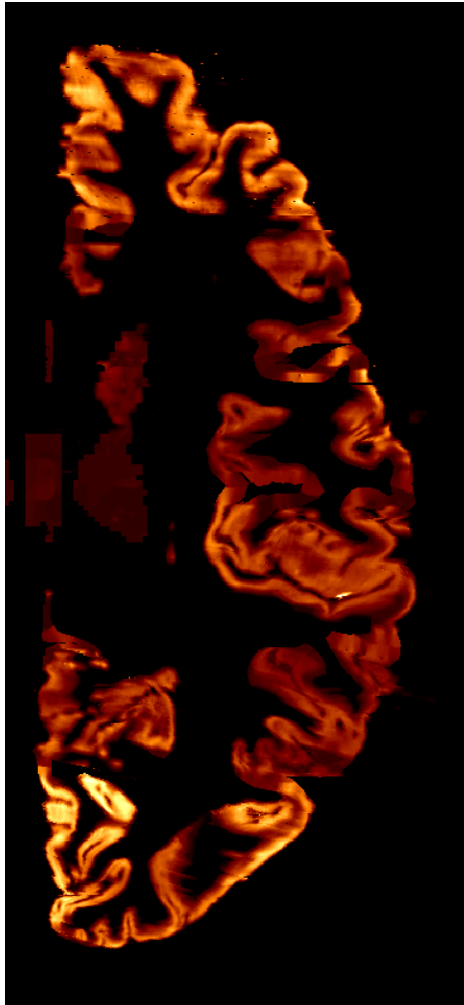


GABAA.Ant.



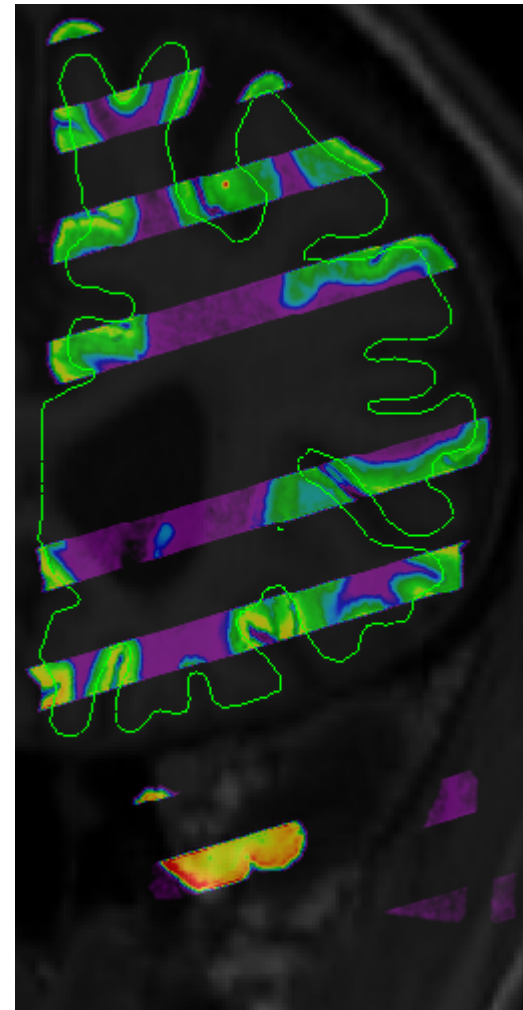
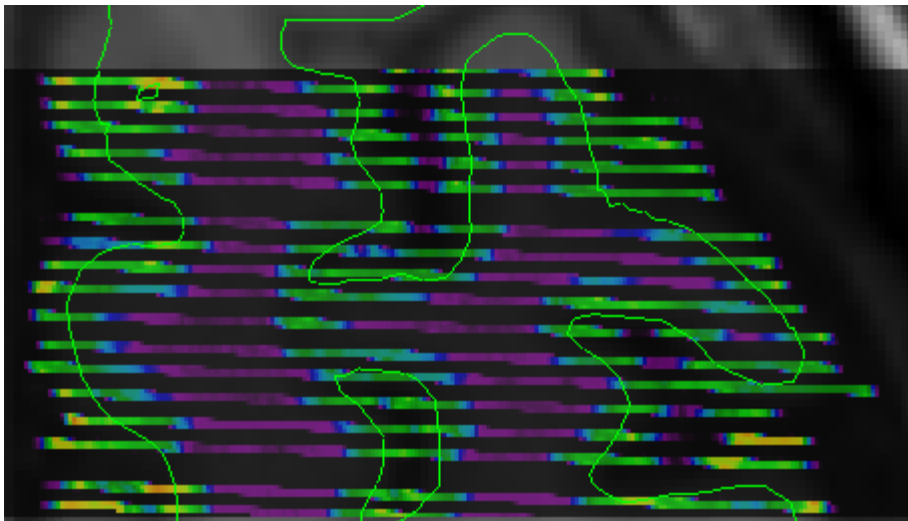
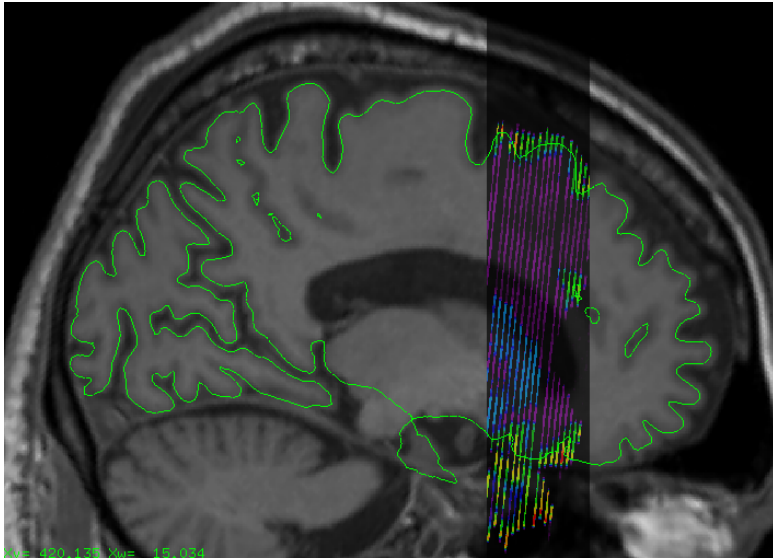
# Interslab Interpolation

- Volumetric interpolation



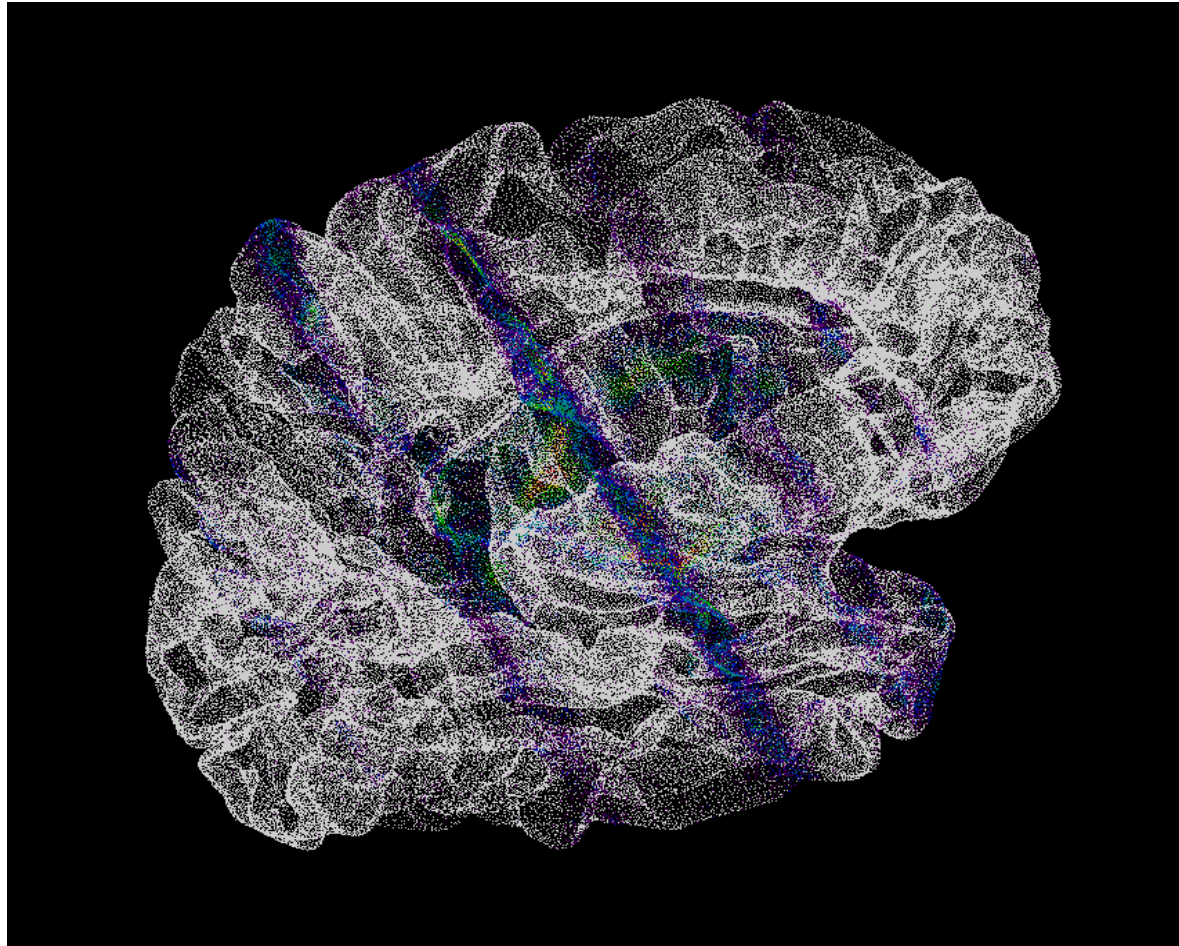
# Inter/intra-slab Interpolation

- Surface-based interpolation



# Inter/intra-slab Interpolation

- Surface-based interpolation



# Preprocessing of all autoradiographs

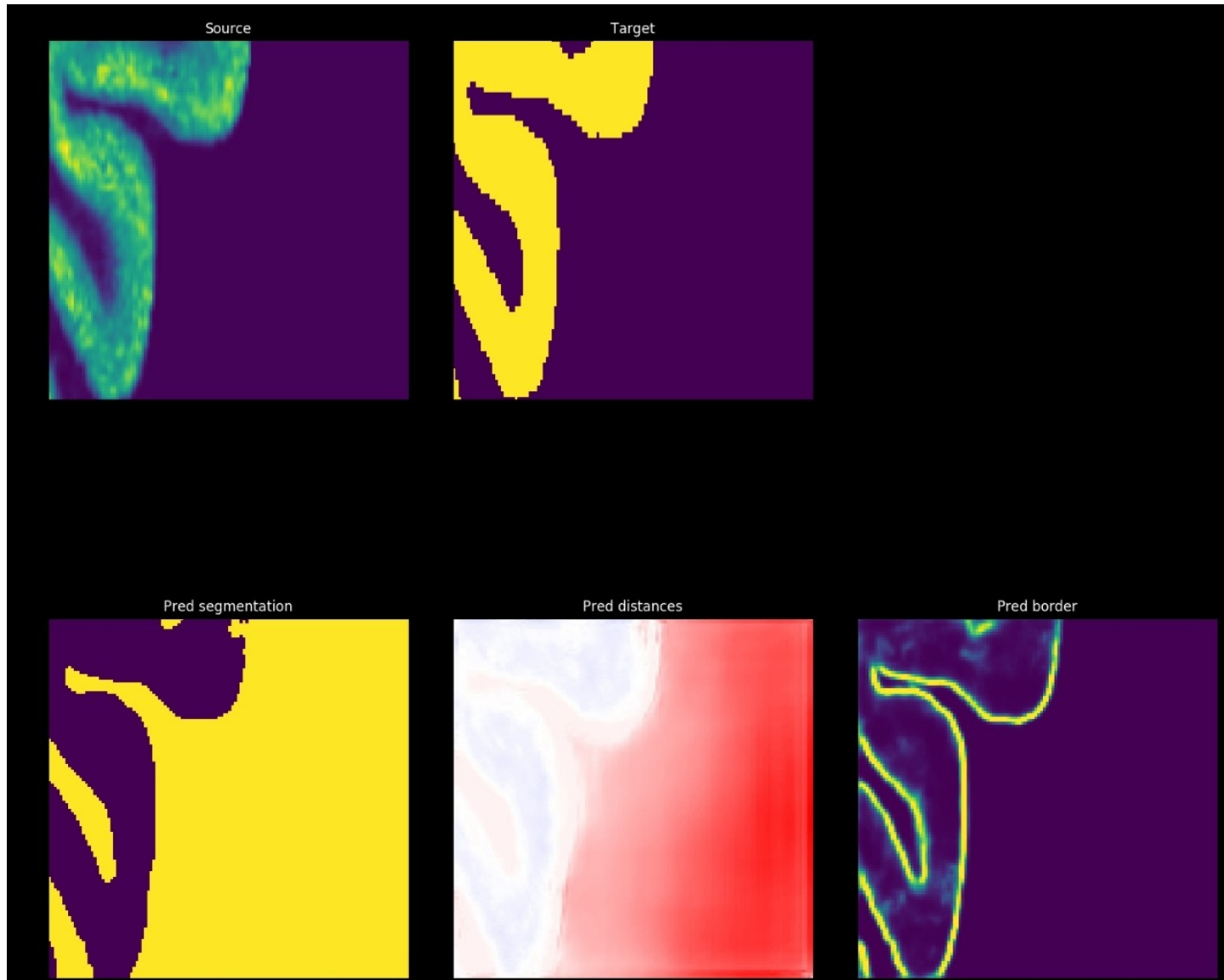
- Semi-automated and manual cropping
- ~18,000 autoradiographs
- 3 brains x 2 hemispheres → ready for reconstruction



# GM Segmentation

- Segmentation with deep neural nets
  - Network learns intensity thresholds instead of shapes
- Solution: make learning task harder
  - → nudge network away from simple intensity thresholding
- Learning targets :
  - Prior cortical segmentation
  - Distance map from cortex
  - Cortical border

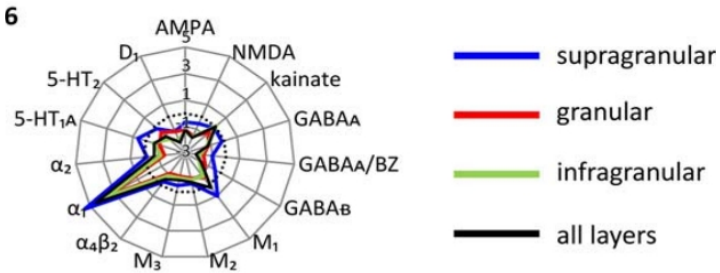
# GM Segmentation



# Future Perspectives

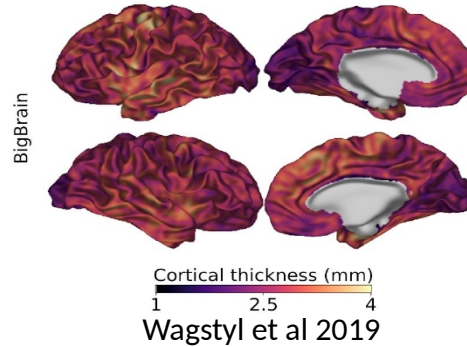
- Multi-modal receptor mapping → novel atlases

## 3D Receptor Fingerprints



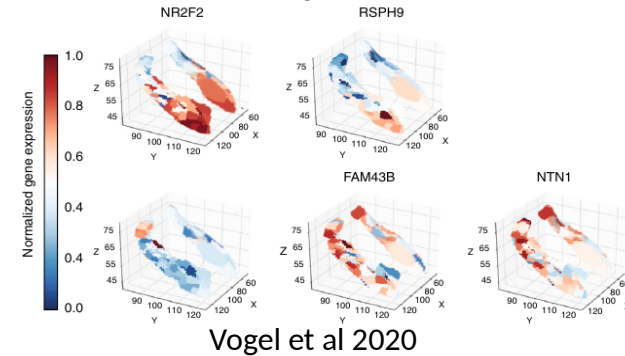
Zilles & Palomero-Gallagher 2017

## Gradients



Wagstyl et al 2019

## Gene Expression



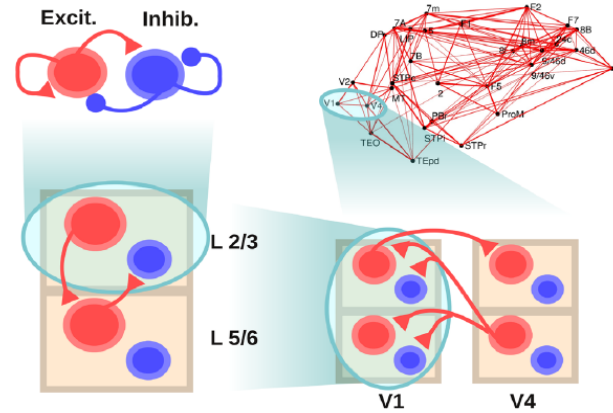
Vogel et al 2020

- Receptor Targets of DBS

- Acetylcholine and dopamine (Udapa & Chen, 2015)

- Computational Modeling

- HIBALL

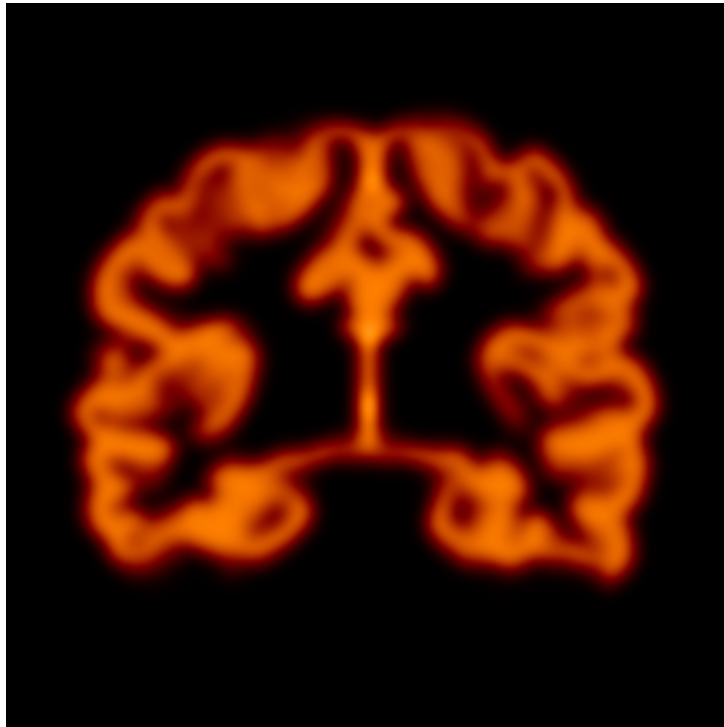


Mejias et al 2016



# Application: PET simulation and resolution

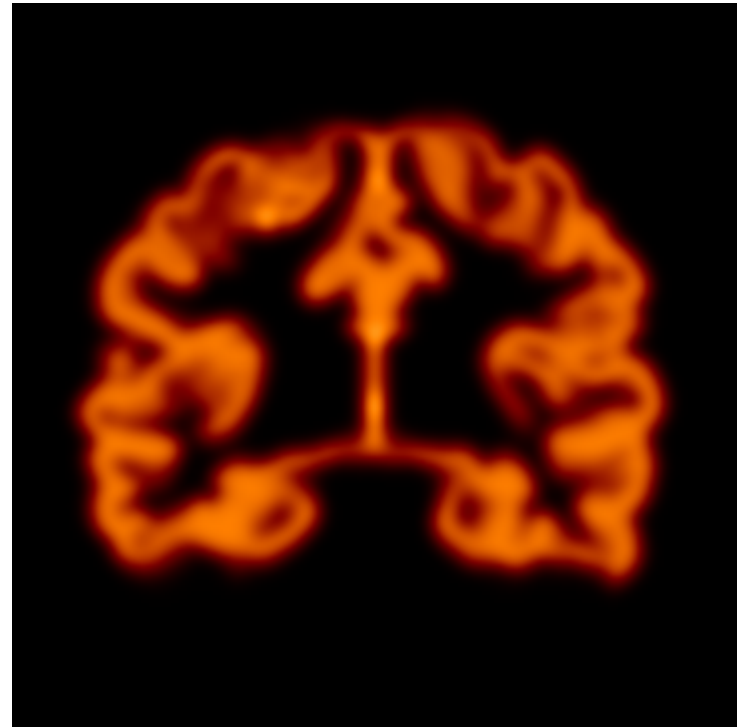
# PET resolution



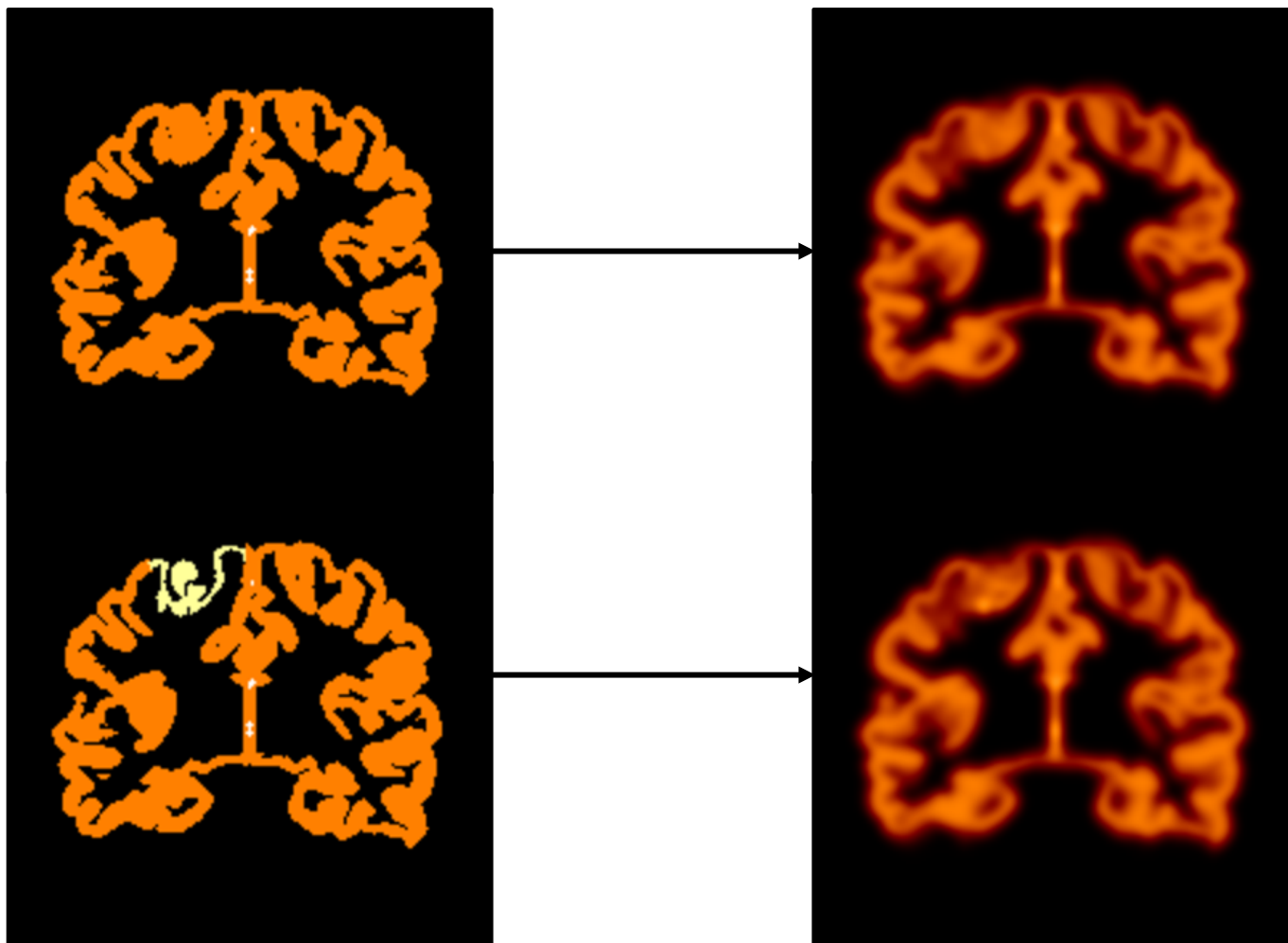
?

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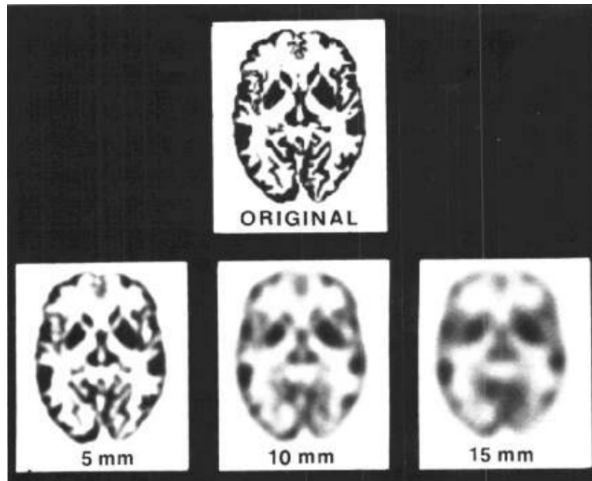


# PET resolution

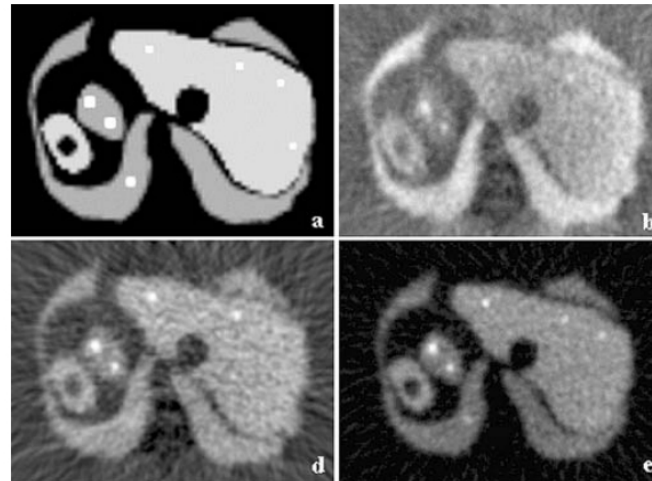


# Receptor volumes for PET simulation

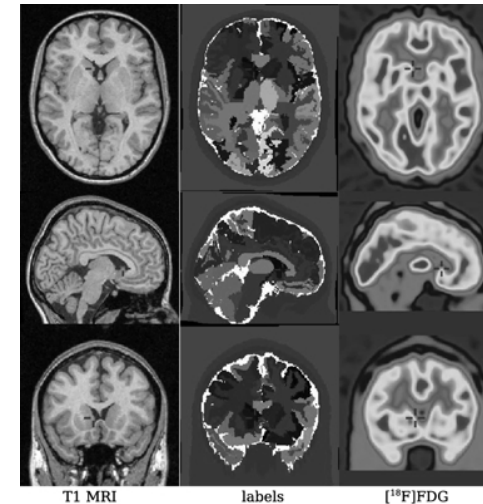
- Previous simulations used large, uniform regions



(Mazziotta, et al 1981)



(Castiglioni, et al 2005)



(Reilhac et al, 2005)

# Receptor volumes for PET simulation

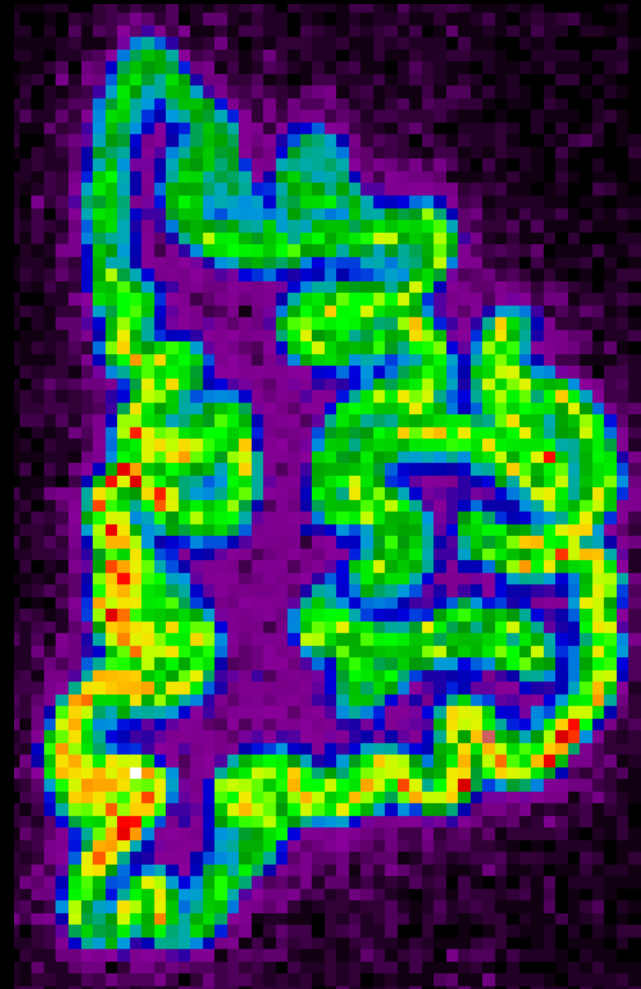
- Previous simulations used large, uniform regions
- 3D GABA-A<sub>Benz</sub> atlas → Ground truth for PET simulation
- PET simulation performed with Gate
  - Digital PET scan simulates most of the physics of acquisition
  - Scanner : Siemens ECAT HRRT (Bataille, et al. 2004)

# Example Application : PET Simulation

GABA-A<sub>Benz.</sub> receptor volume

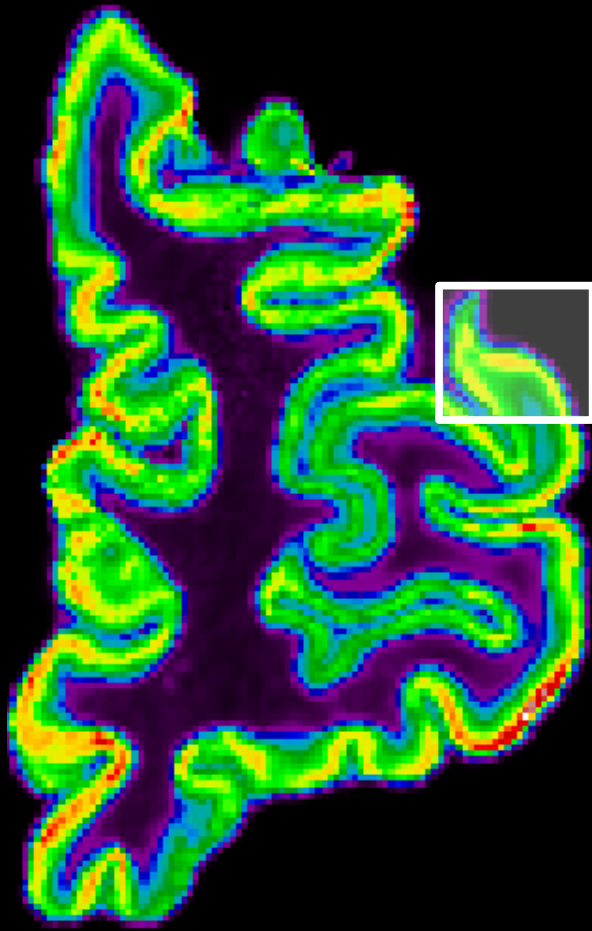


Theoretical Maximum PET Resolution

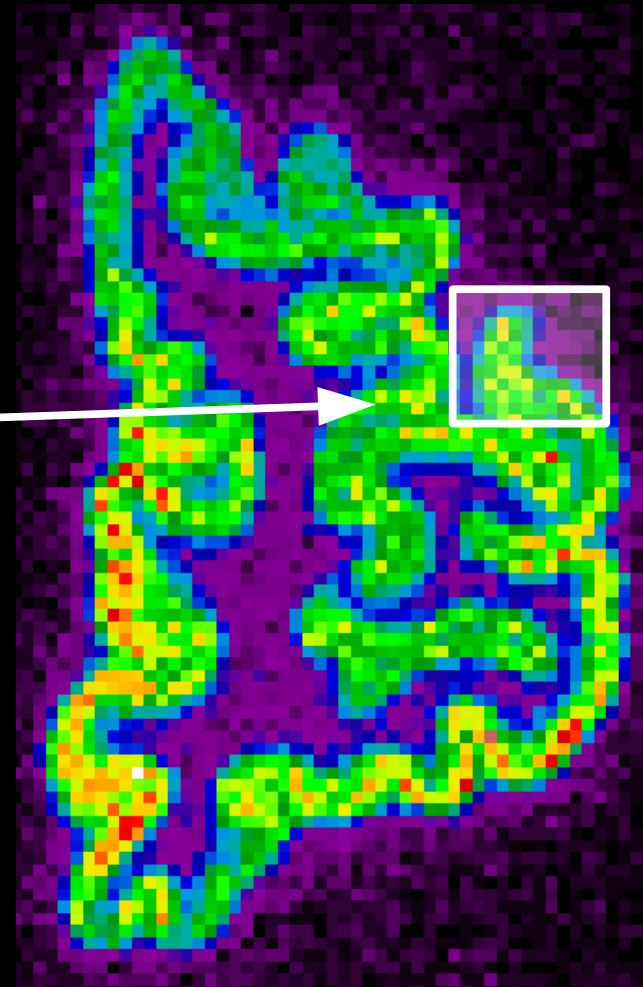


# Evaluating PET Resolution

GABA-A<sub>Benz.</sub> receptor volume

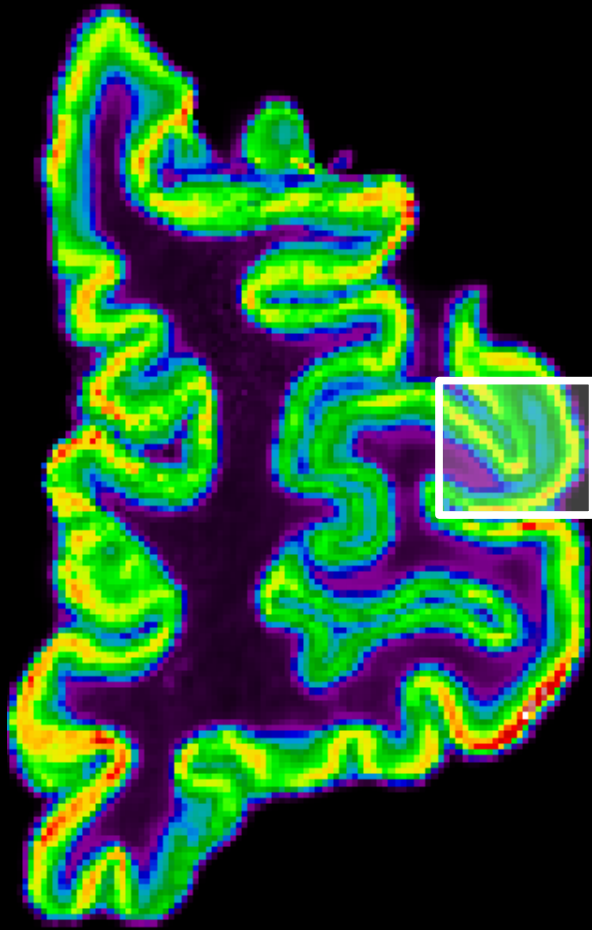


Theoretical Maximum PET Resolution

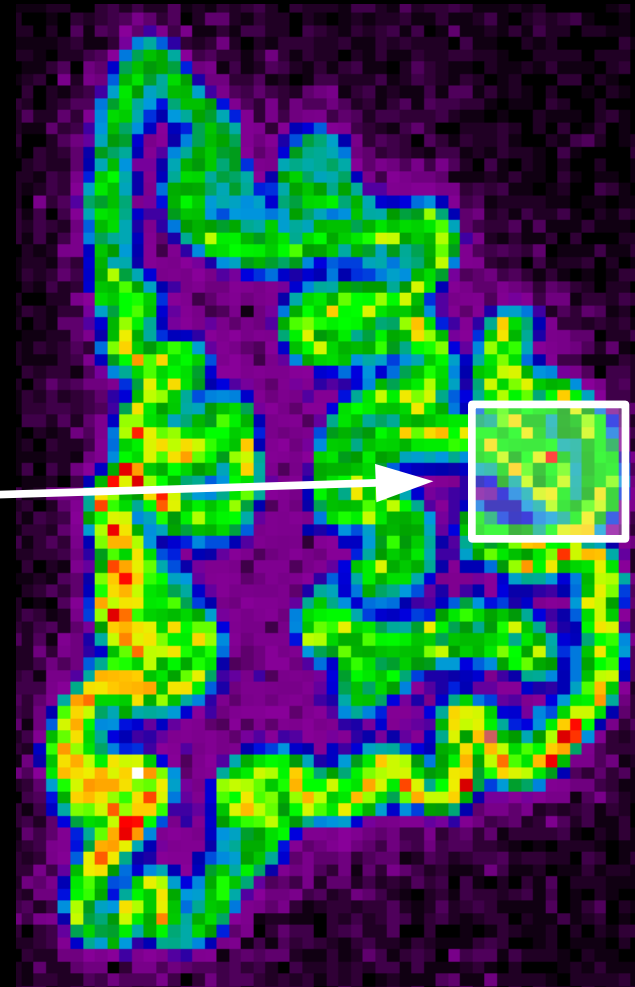


# Evaluating PET Resolution

GABA-A<sub>Benz.</sub> receptor volume



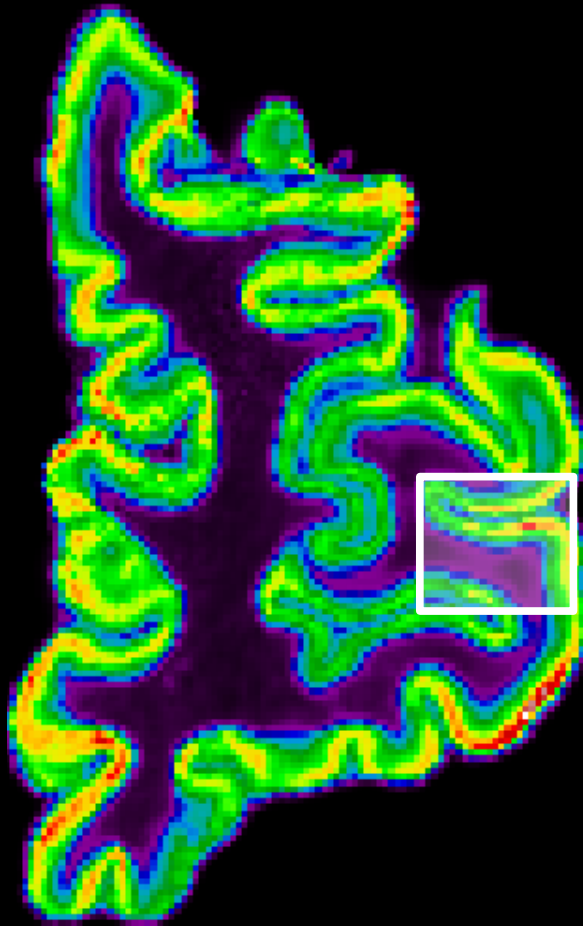
Theoretical Maximum PET Resolution



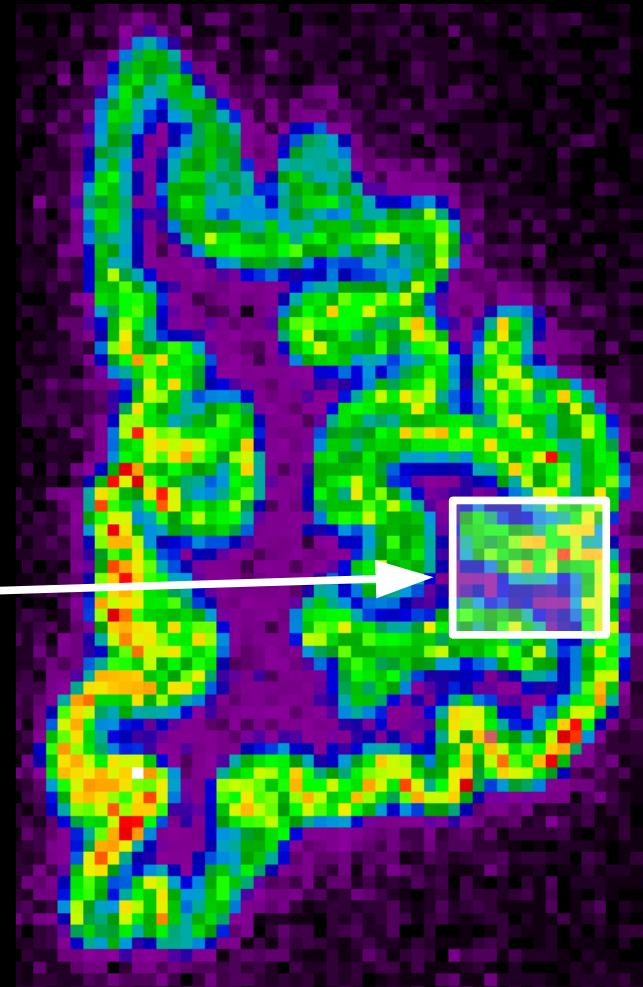


# Evaluating PET Resolution

GABA-A<sub>Benz.</sub> receptor volume

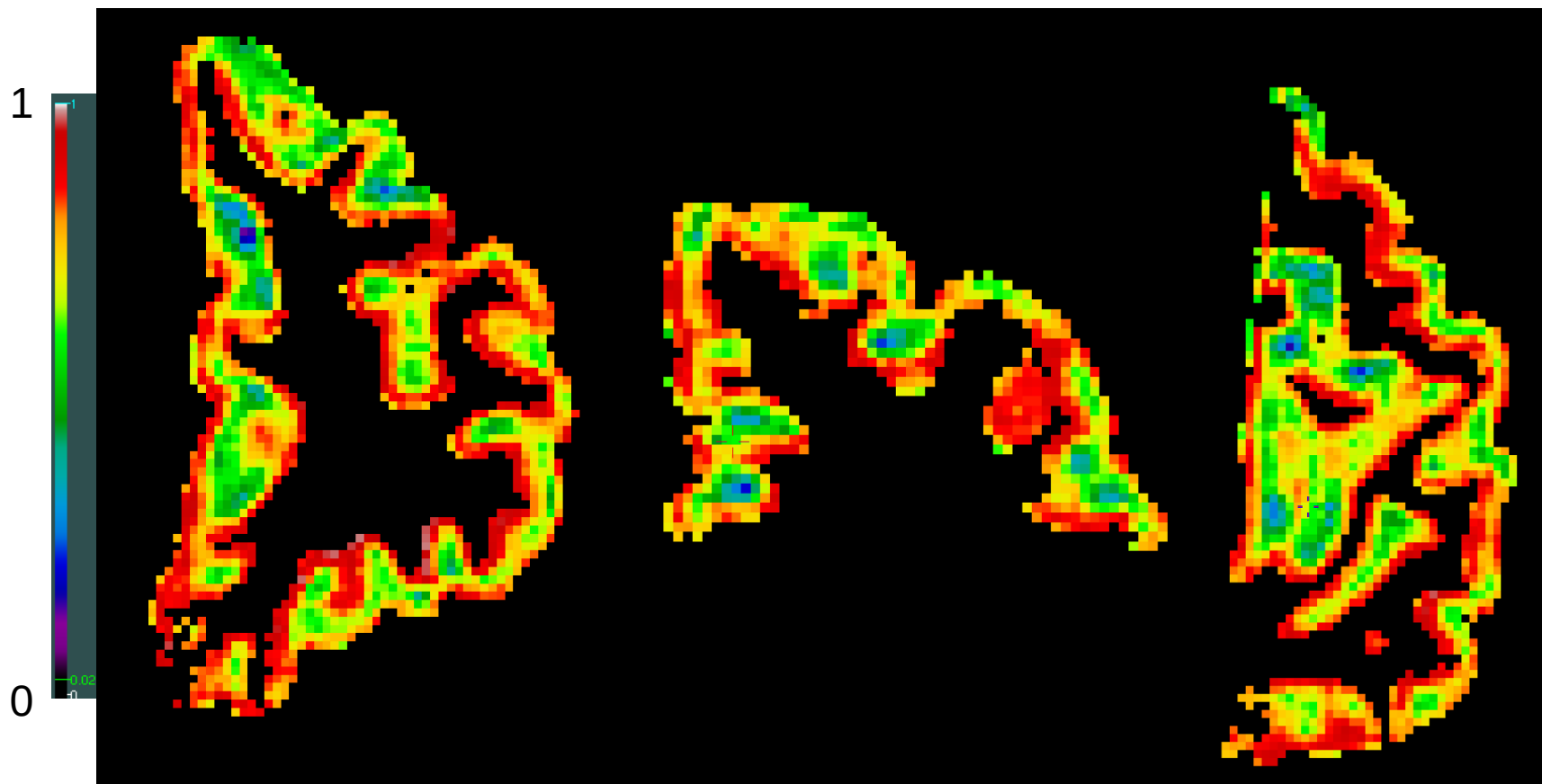


Theoretical Maximum PET Resolution



# Evaluating PET Resolution

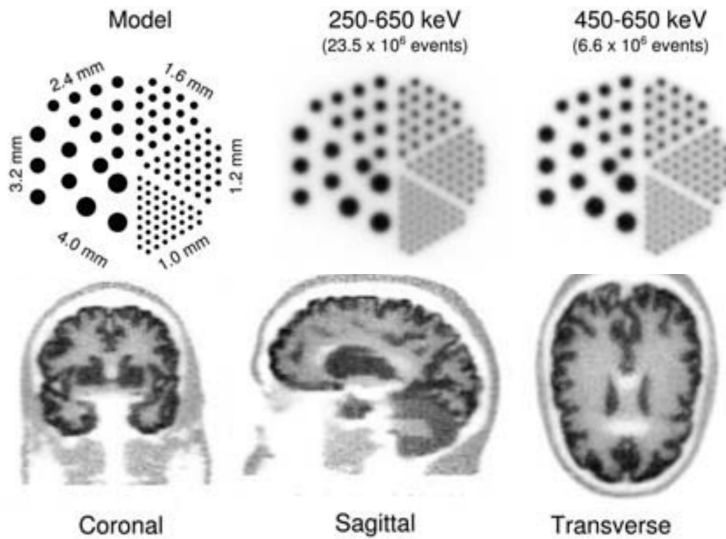
- Local correlation  $5\text{mm}^3$ :  $0.71 \pm 0.09$ 
  - Kendall's Tau



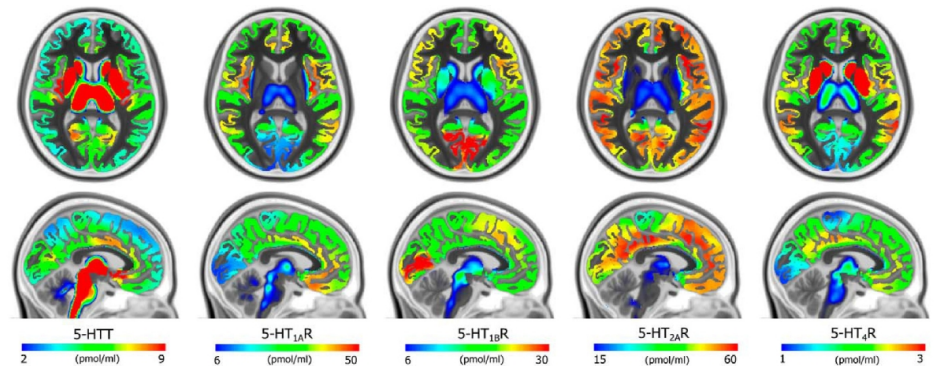
# Future Perspectives

- Sub-millimeter PET Receptor Atlases

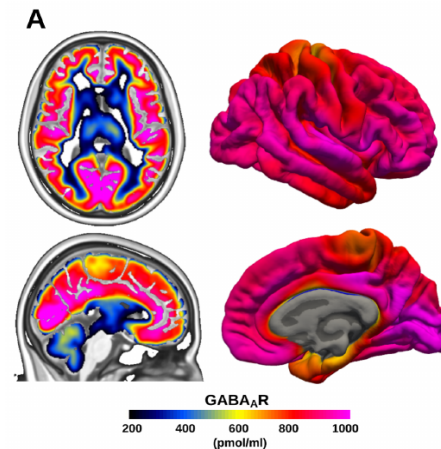
- 1.2mm FWHM PET scanners + PVC (<1mm?) → Laminar PET?



Lecompte, et al. 2019



Beliveau, et al 2017



Norgaard, et al. 2020 (preprint)

# Conclusions

- Reconstruction of 3D receptor atlases
  - Proof-of-principle for pipeline → up to 50um
  - 3 brains x 2 hemispheres x 20 receptors
- Realistic PET simulation
  - Simulated PET from gold-standard receptor distribution
  - Evaluate maximum effective PET spatial resolution
  - Validate resolution-enhancement & quantification algorithms

Questions, comments, suggestions : [thomas.funck@mail.mcgill.ca](mailto:thomas.funck@mail.mcgill.ca)

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Jewish General Hospital  
Lady Davis Institute for Medical Research

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Claude Lepage, PhD

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Mona Omid, PhD



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Konrad Wagstyl



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- Canadian Institutes for Health Research (CIHR)
- The Healthy Brains for Healthy Lives initiative

# Interslab Interpolation

- Volumetric interpolation
  - 1) Dilate mask of receptor slabs
  - 2) Find border voxels inside MRI GM mask
  - 3) For each voxel calculate average within 3x3x3 kernel
  - 4) Add interpolated voxels to receptor slab mask
  - 5) Step 1

