Coral*Lite*: µCT Reconstruction of Coral Colonies from Individual Corallites

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Natural History Museum

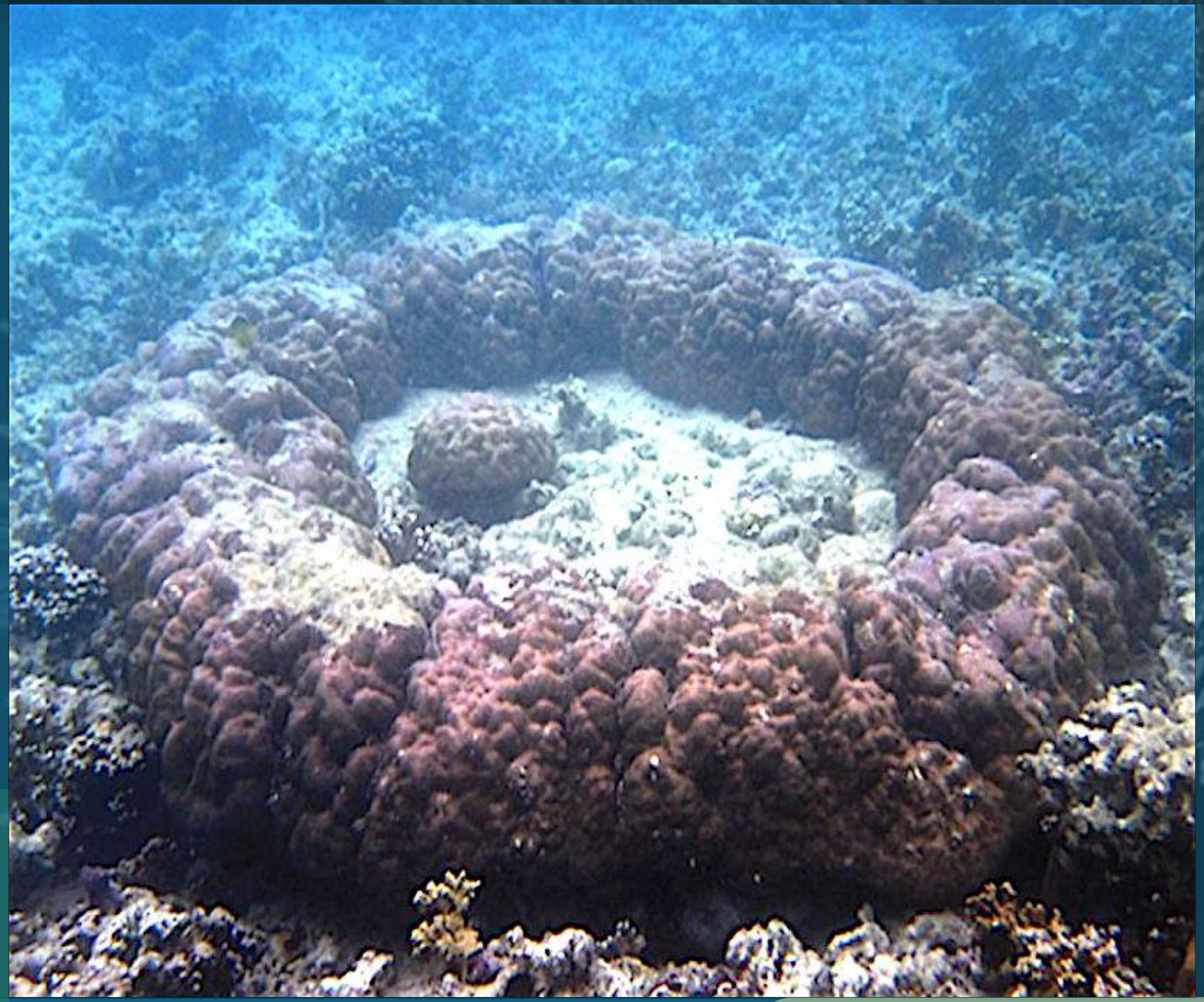
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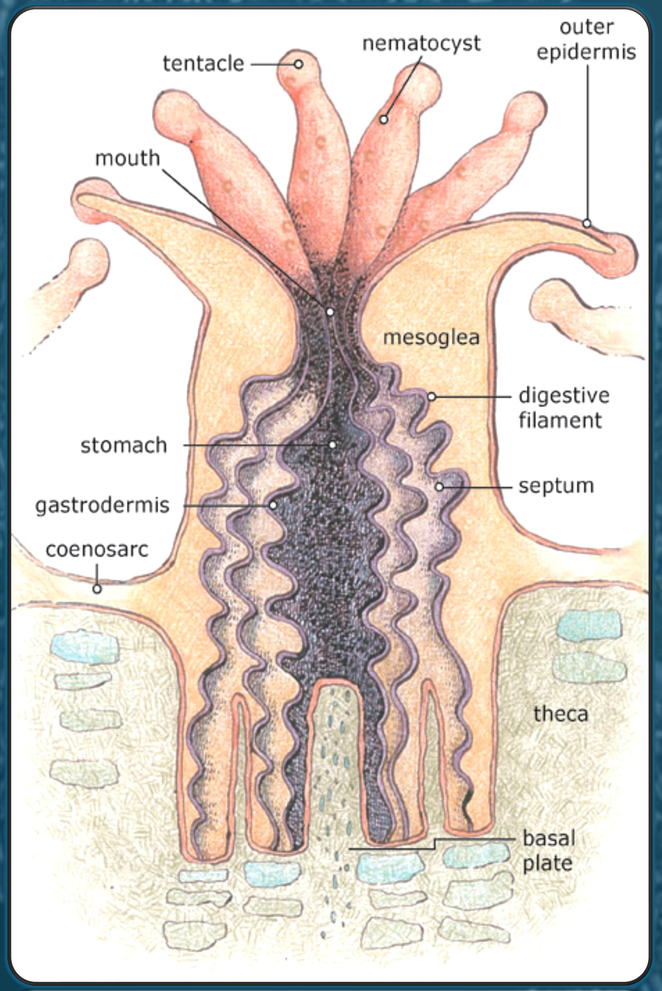


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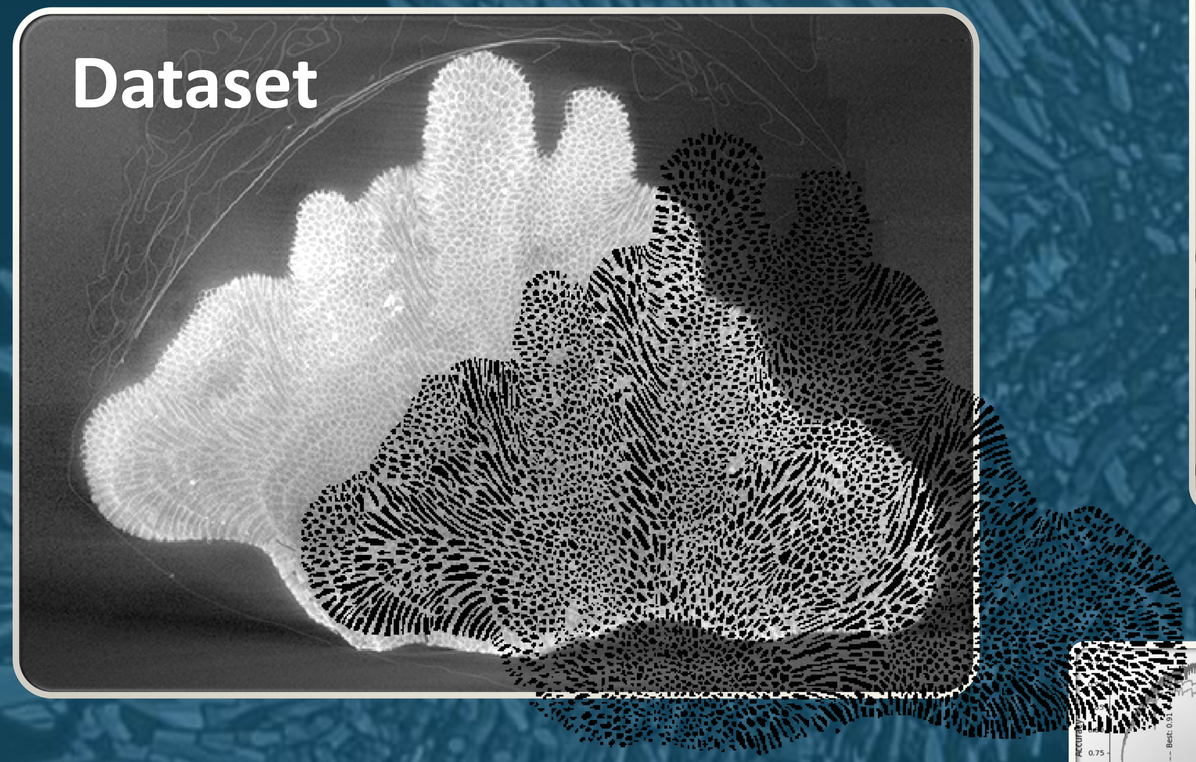
Why? - Importance of Corals and Individual Corallites

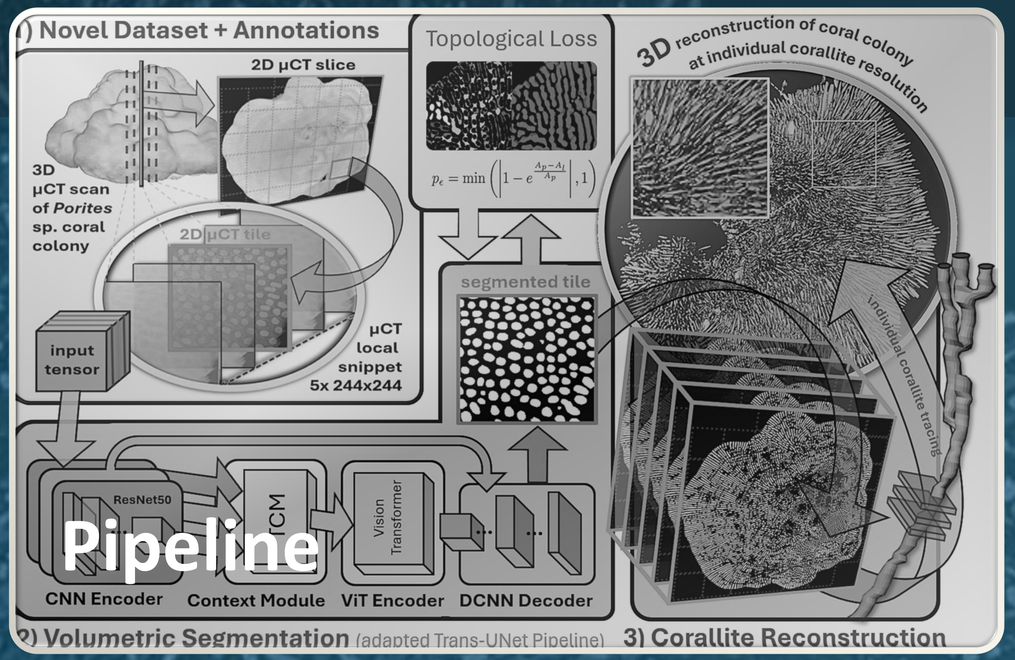


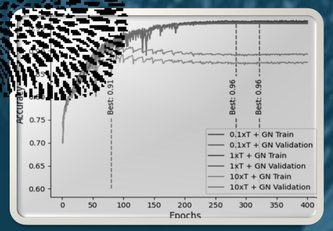


Paper Contributions

Dataset

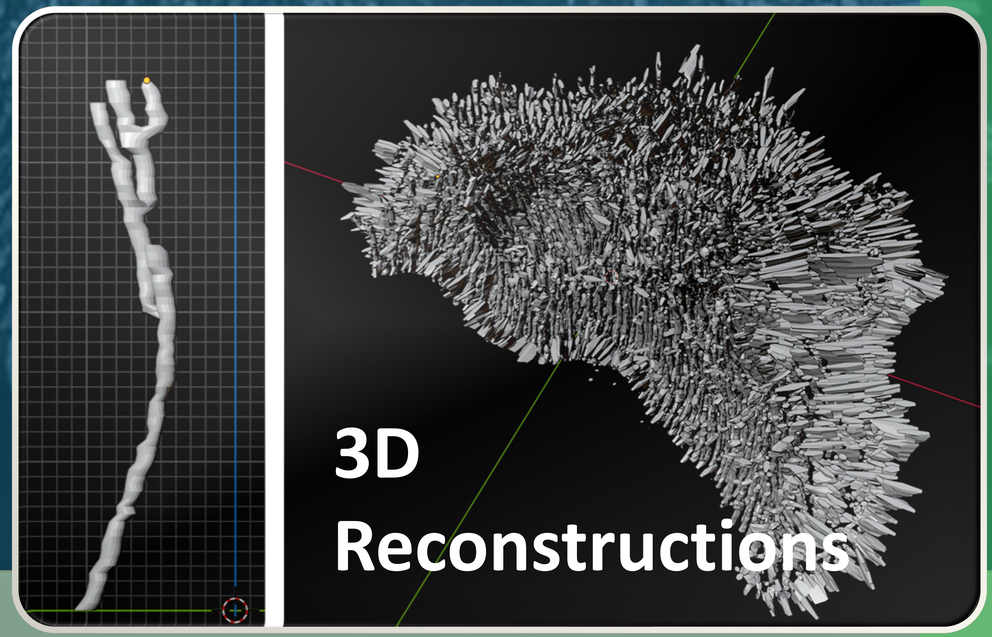




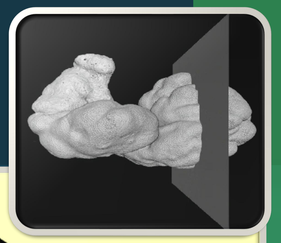


Baselines

Model	Parameters	Task A (same axis) Naturalis 6781 Growth #2499 mDSC	Task A Topo	Task B (same species) Naturalis 6781 Ortho #1003 mDSC	Task B Topo	Task C (diff. species) *Astraeiformis* mDSC	Task C Topo
Pre-training only	n/a	0.008	0.66	0.01	0.75	0.01	0.68
FT *(fine-tuned)*	$k = 224$	0.75	0.93	0.67	0.92	0.61	0.88
FT + $\mathcal{L}_{Topo}$ **max tile overlap** (k = 50) **plus noise augmentation**	$T = 0.01$	0.76	0.94	0.70	0.92	0.61	0.87
	$T = 0.1$	**0.77**	**0.94**	**0.71**	**0.93**	**0.63**	0.87
	$T = 1$	0.77	0.94	0.70	0.93	0.60	0.86
	$T = 10$	0.77	0.94	0.70	0.93	0.63	**0.89**



The Dataset … and associated Evaluation Tasks



697 µCT slices from
3 *Porites* specimens
4 segmented GT slices



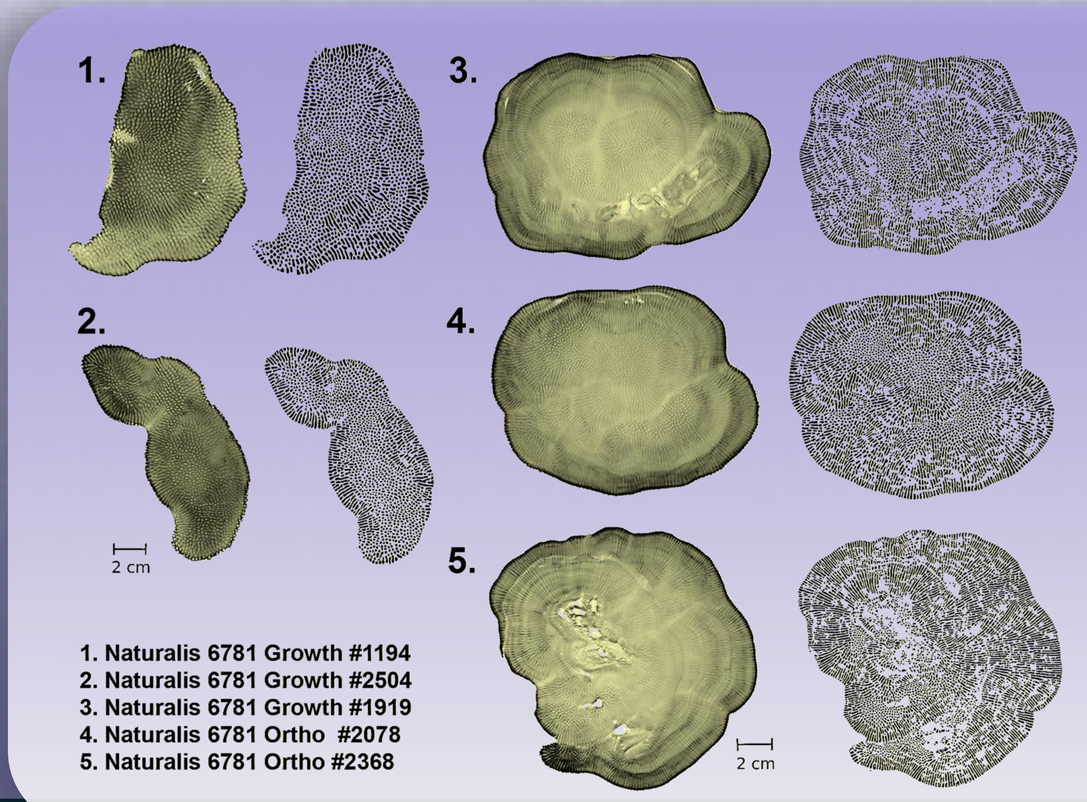
33 weak GT slices
8412 exact corallite annotations



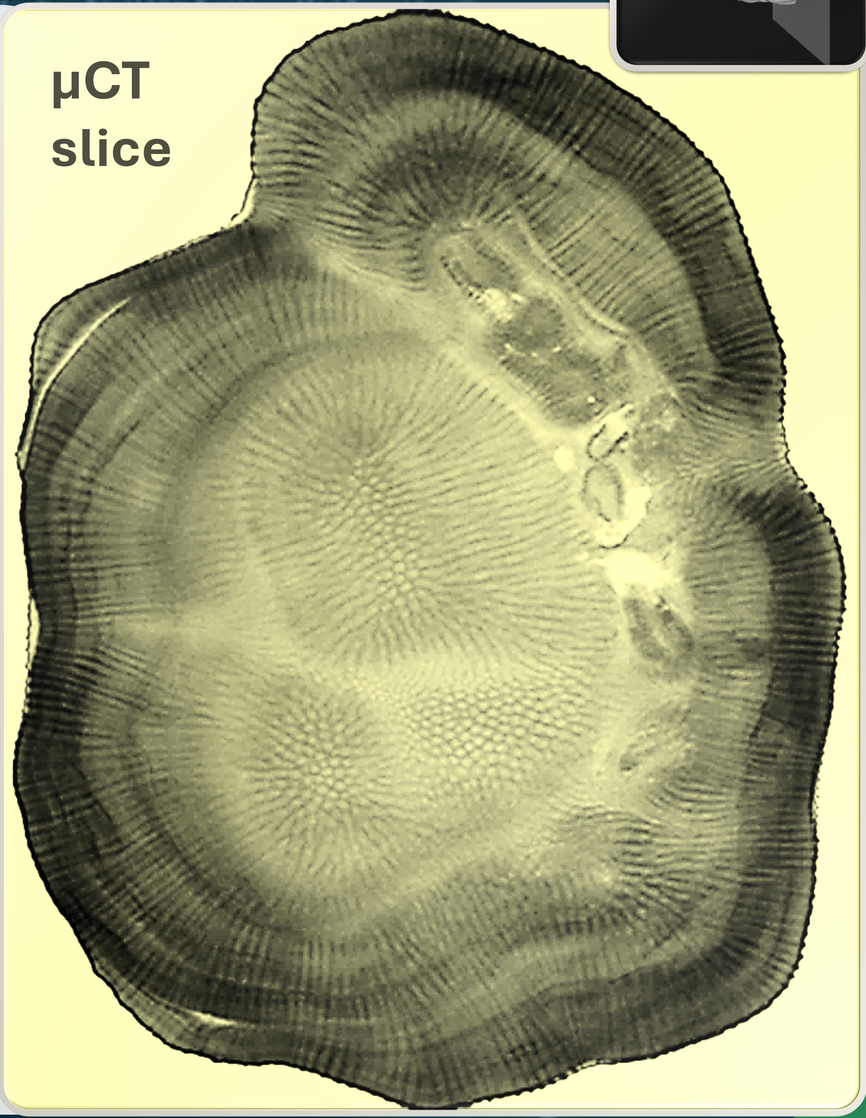
Task A: same colony & axis

Task B: same colony, ortho axis

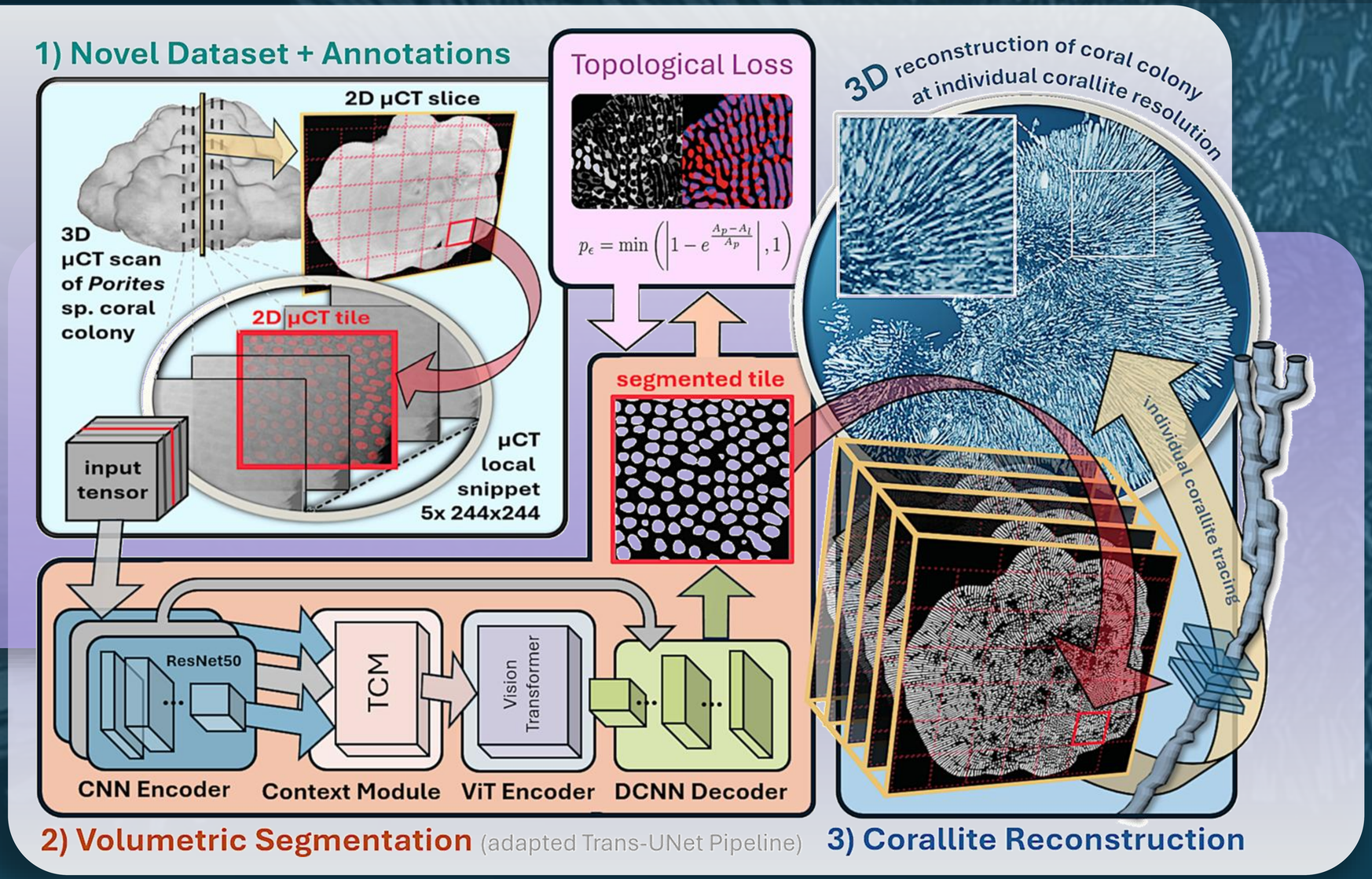
Task C: new specimen.



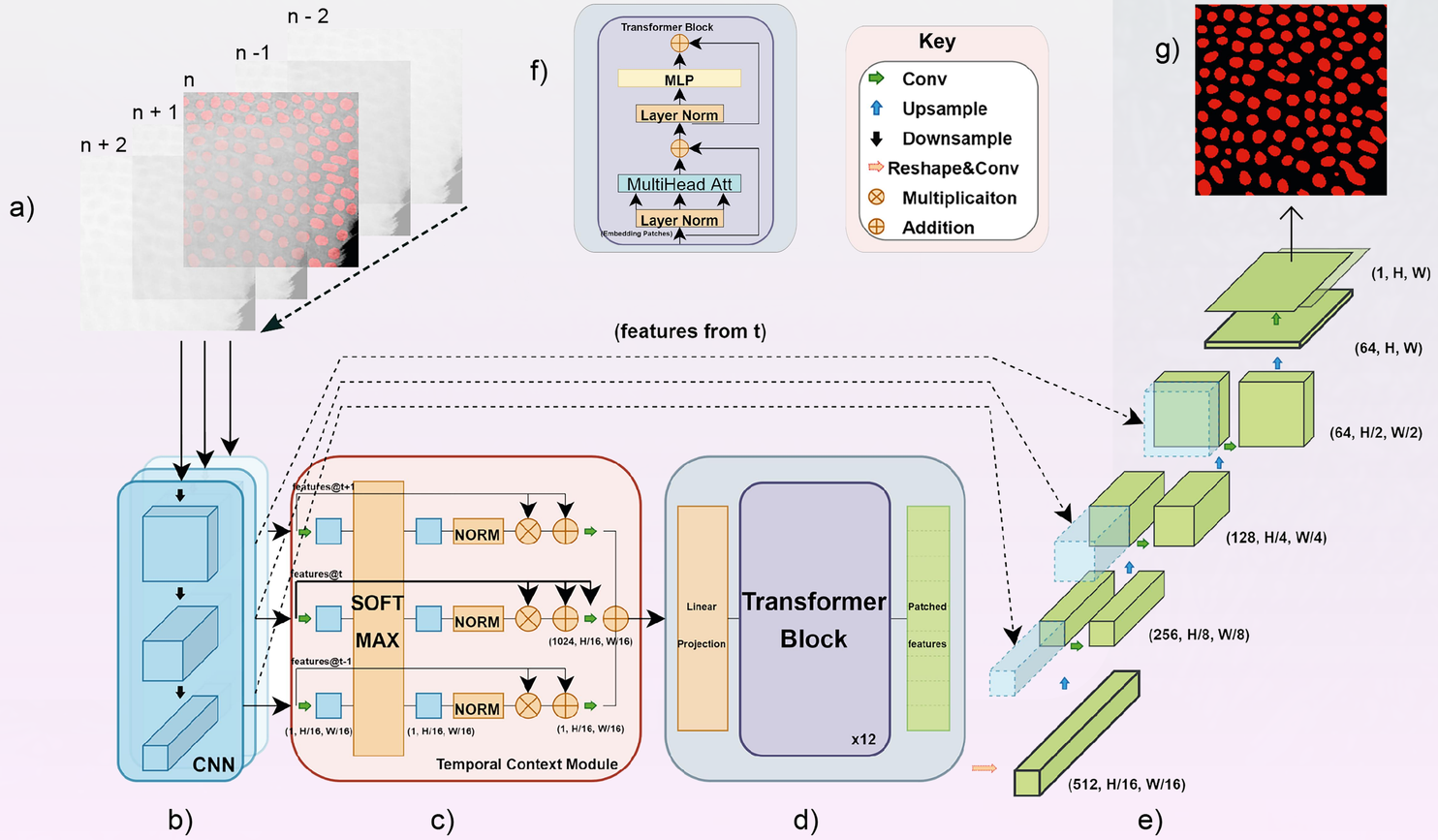
µCT slice



Pipeline Overview



V-Trans-UNet Architecture



5×224×224 tiled snippets · ResNet-50 encoder · Temporal Context Module · 12-layer ViT · UNet decoder (centre-slice output)

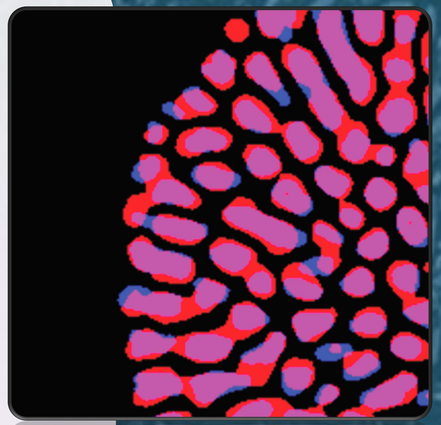
Topology-aware Loss

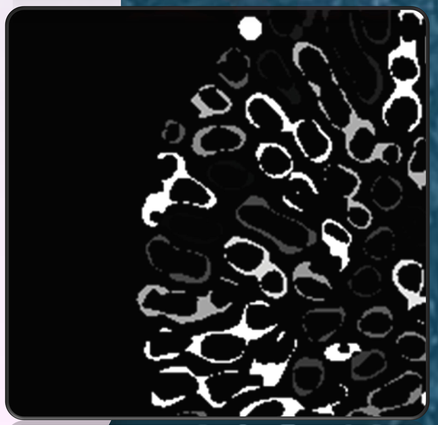
Component Penalty Formulation. Using basic connected-component analysis on binary annotation and prediction maps via `skimage.measure`, we obtain the set of predicted regions P and labelled regions L. For each predicted connected component $p \in P$ with area A_p, we identify its nearest labelled region $l \in L$ with area A_l and define the component penalty:

$$p_\epsilon = \min\left(\left|1 - e^{\frac{A_p - A_l}{A_p}}\right|, 1\right). \tag{1}$$

Error Map and Topological Loss Stipulation. Each pixel belonging to a region p is assigned the corresponding penalty if it does not belong to the matched ground-truth region l. This yields an error map $\mathcal{E}(n)$ that highlights for each pixel n its contribution towards incorrect corallite connections, false positive corallites and over-expanded regions (see Figure 5). This map is used to calculate a topological loss by averaging evidence over all N pixels of a tile during training as:

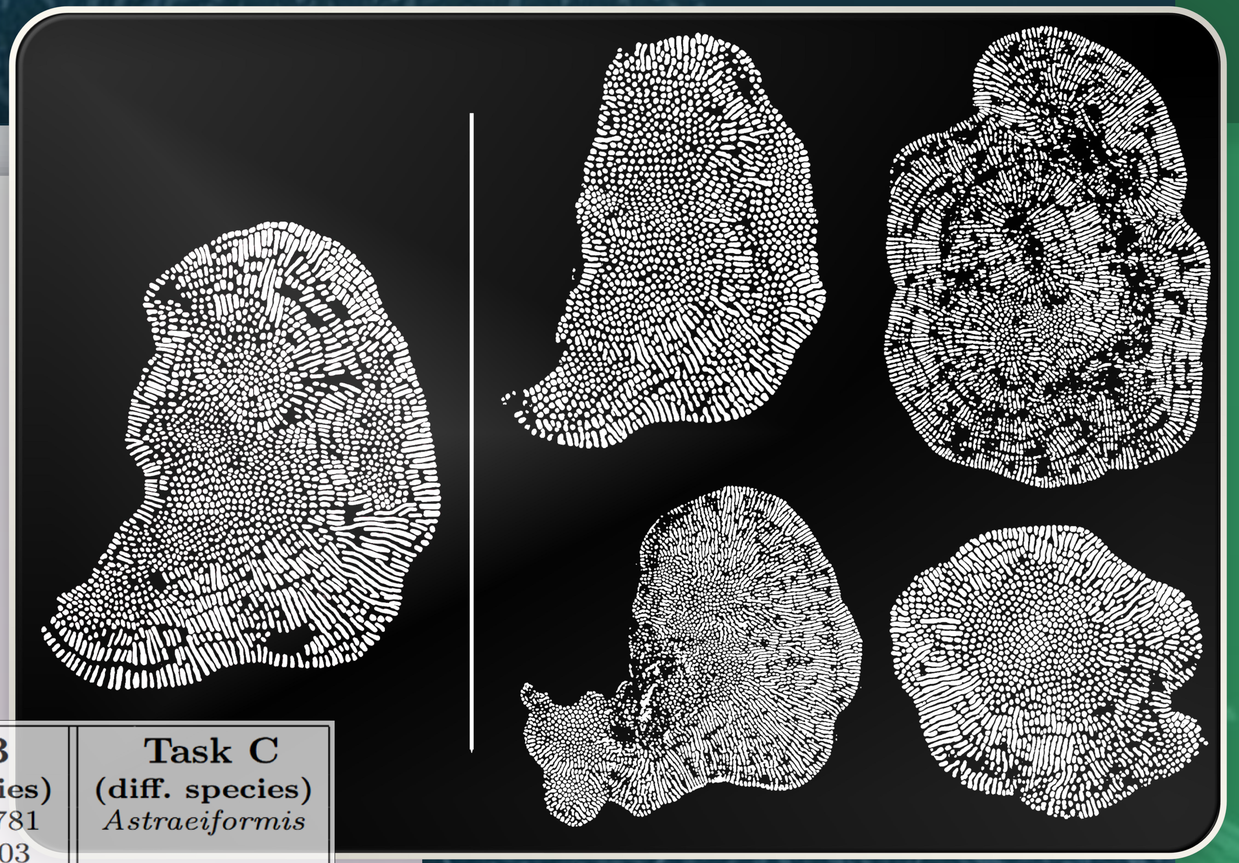
$$\mathcal{L}_{\text{Topo}} = \frac{1}{2N} \sum_{n=1}^{N} \sigma\left(\mathcal{E}(n)\right) - 0.5. \tag{2}$$



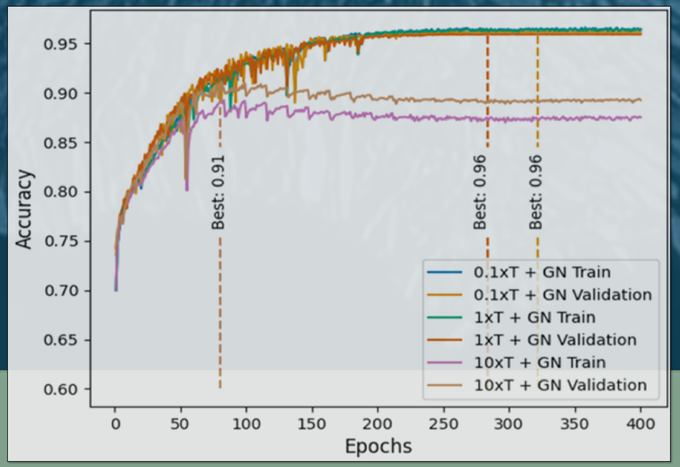


Training, Segments, Baselines

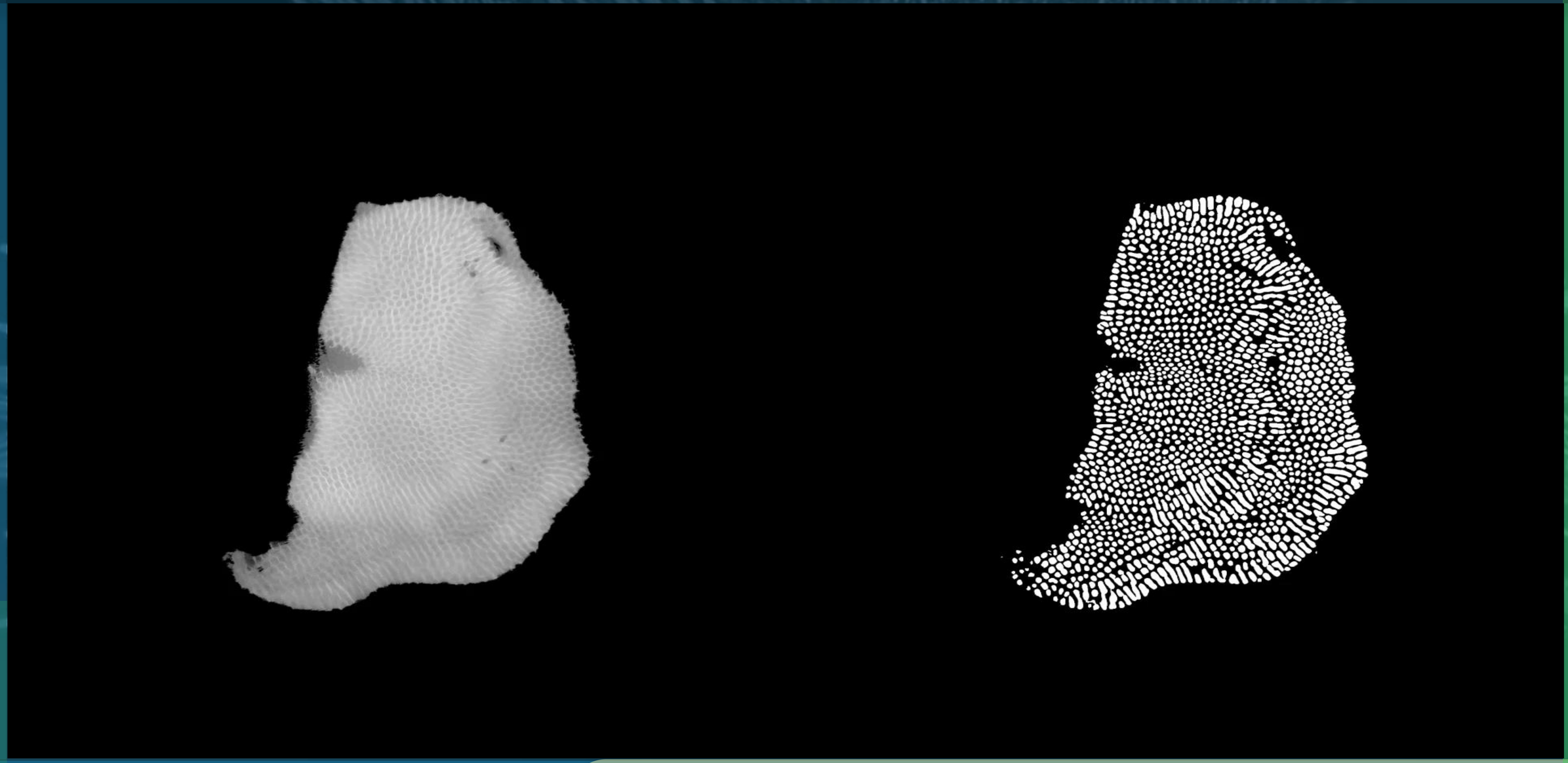
- **Stage 1 —** Pre-train on Naturalis 6785 weak point annotations (ImageNet-init ResNet + ViT).
- **Stage 2 —** Fine-tune on one fully annotated slice (Naturalis 6781 Growth #1279).
- **Dense sliding-window tiles** (k=50 overlap) · snippet depth D=5 · Adam lr 5×10^{-4}.
- **Augmentation:** rotation, flips, additive Gaussian noise (best cross-species config).
- **Metrics:** mean Dice (mDSC) and topology score TS = 1 − L_Topo.



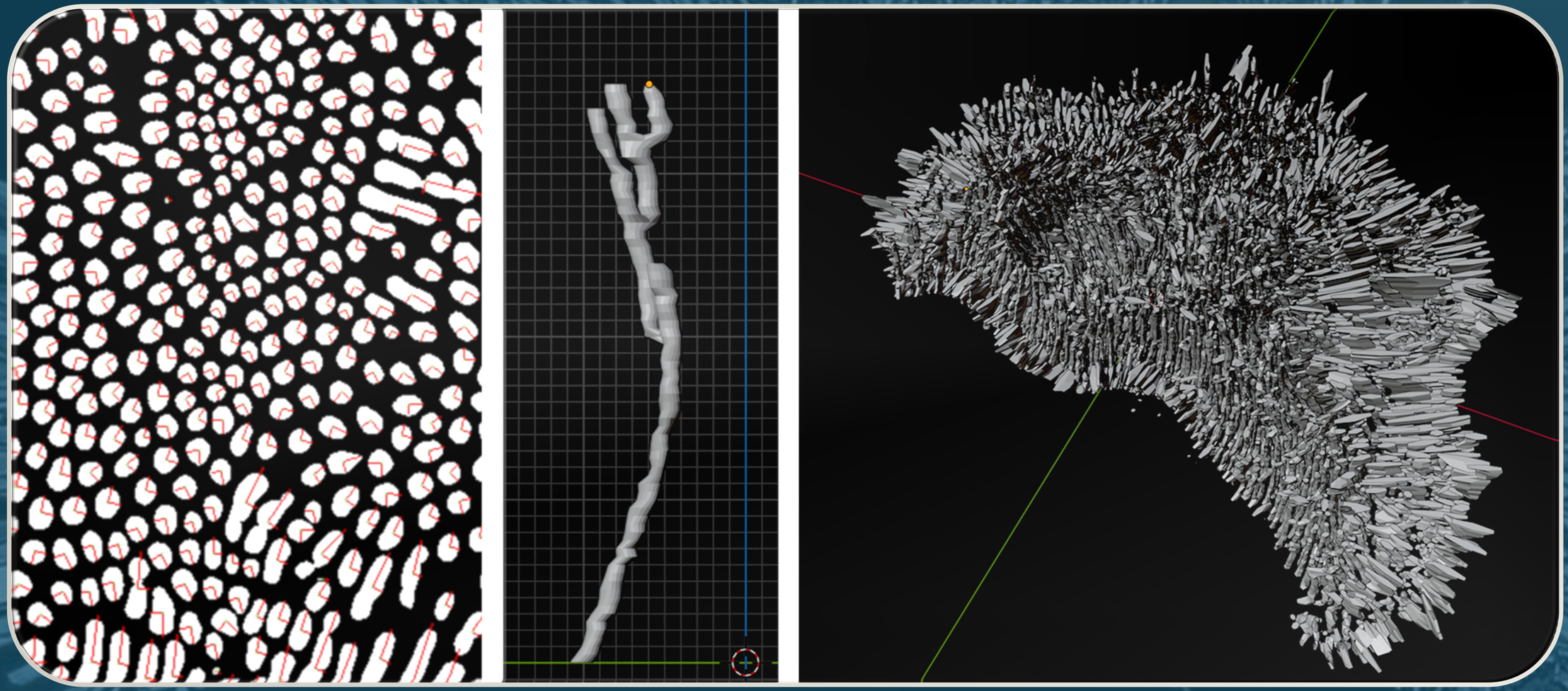
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		mDSC	Topo	mDSC	Topo	mDSC	Topo
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Segmentation of Full Colony *(fly-through-slices)*



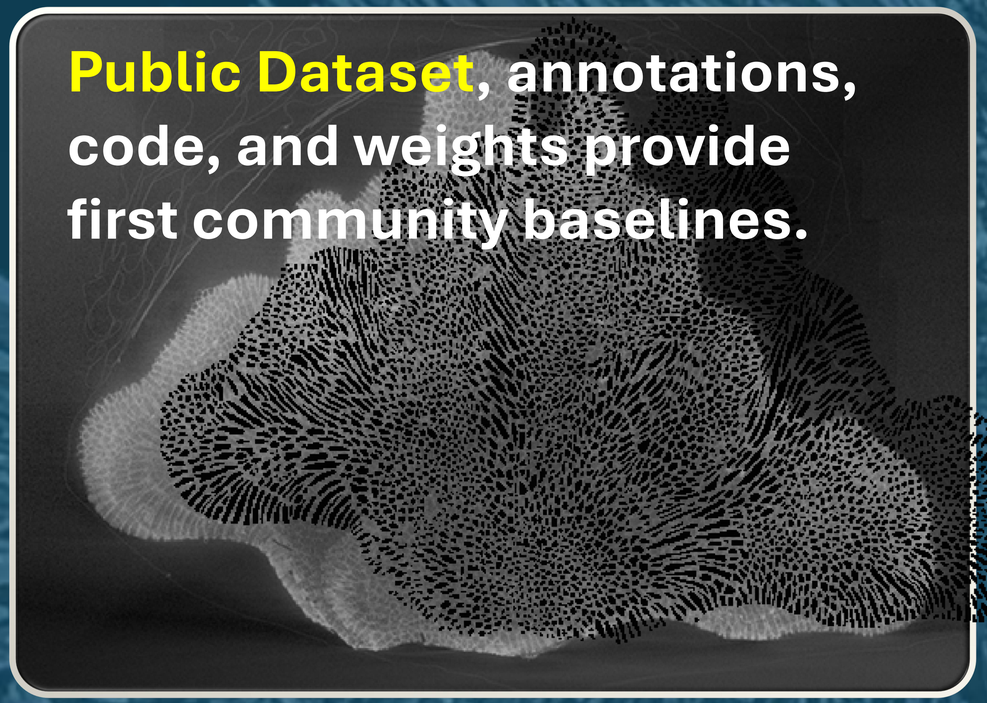
3D Reconstruction from Individual Corallites

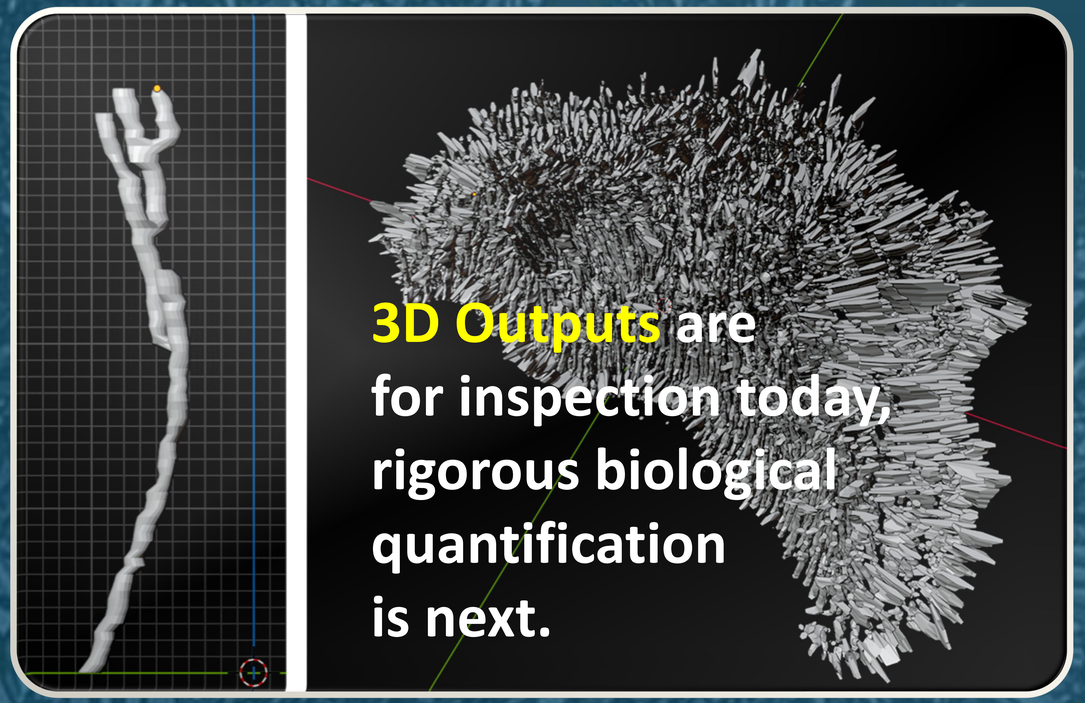


Cross-slice linking (centroid + IoU) → individual 3D tubes → first colony-scale visualisation

Summary … corallite-level auto-reconstruction from µCT is feasible at colony scale

Public Dataset, annotations, code, and weights provide first community baselines.





3D Outputs are for inspection today, rigorous biological quantification is next.

Towards Imageomics … linking polyp division rates to skeletal growth and environmental change.

paper
dataset
code

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