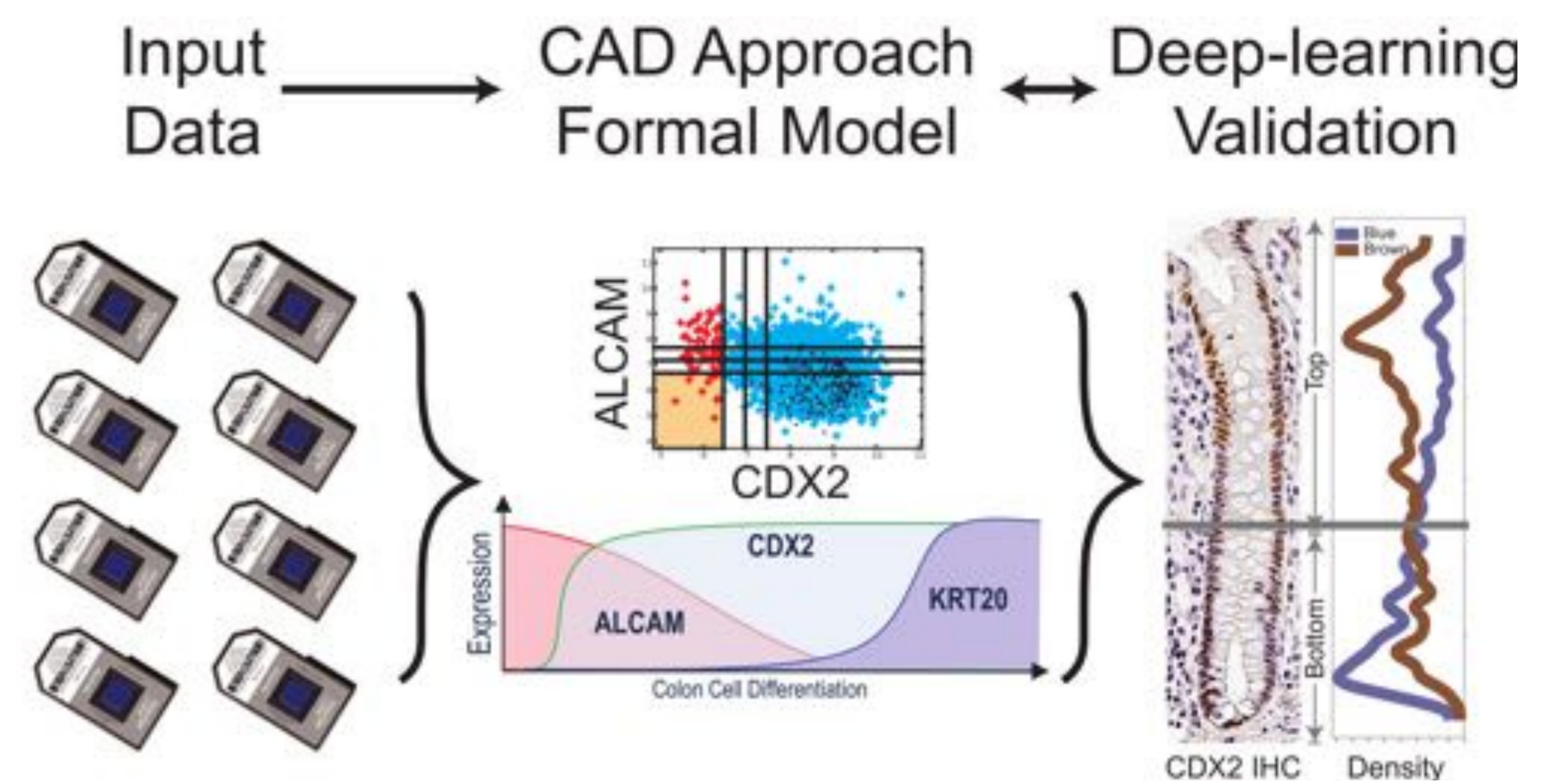
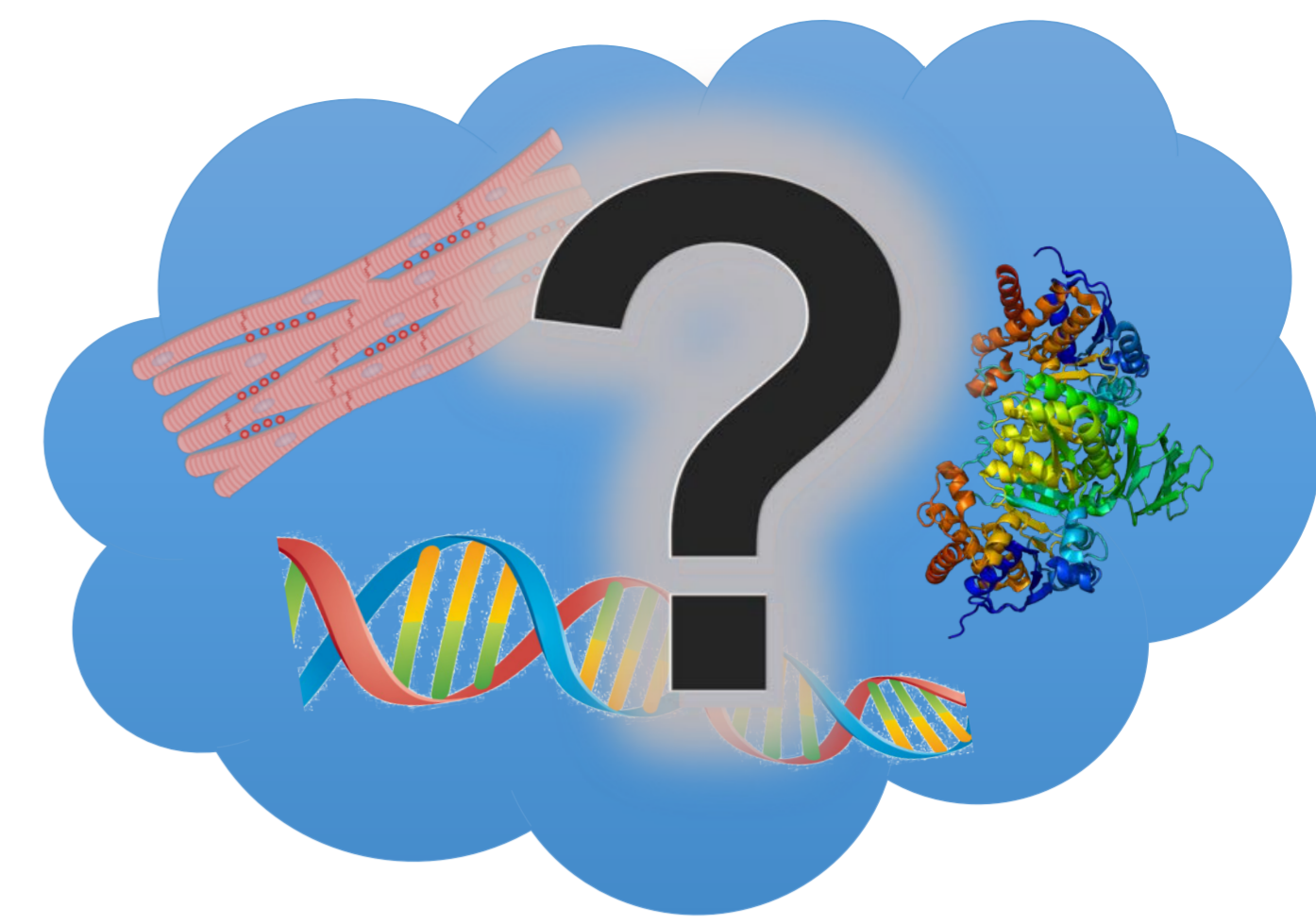


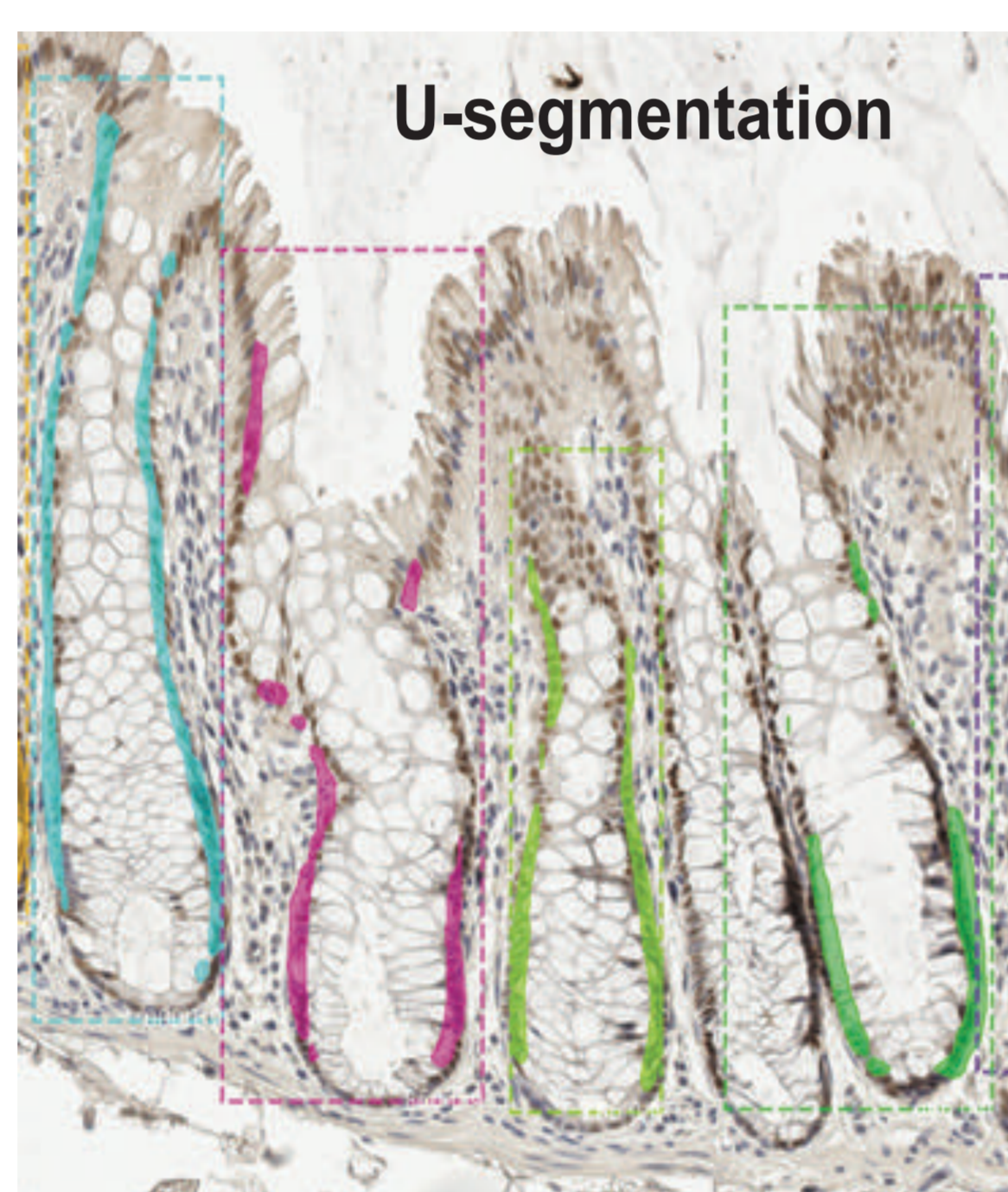
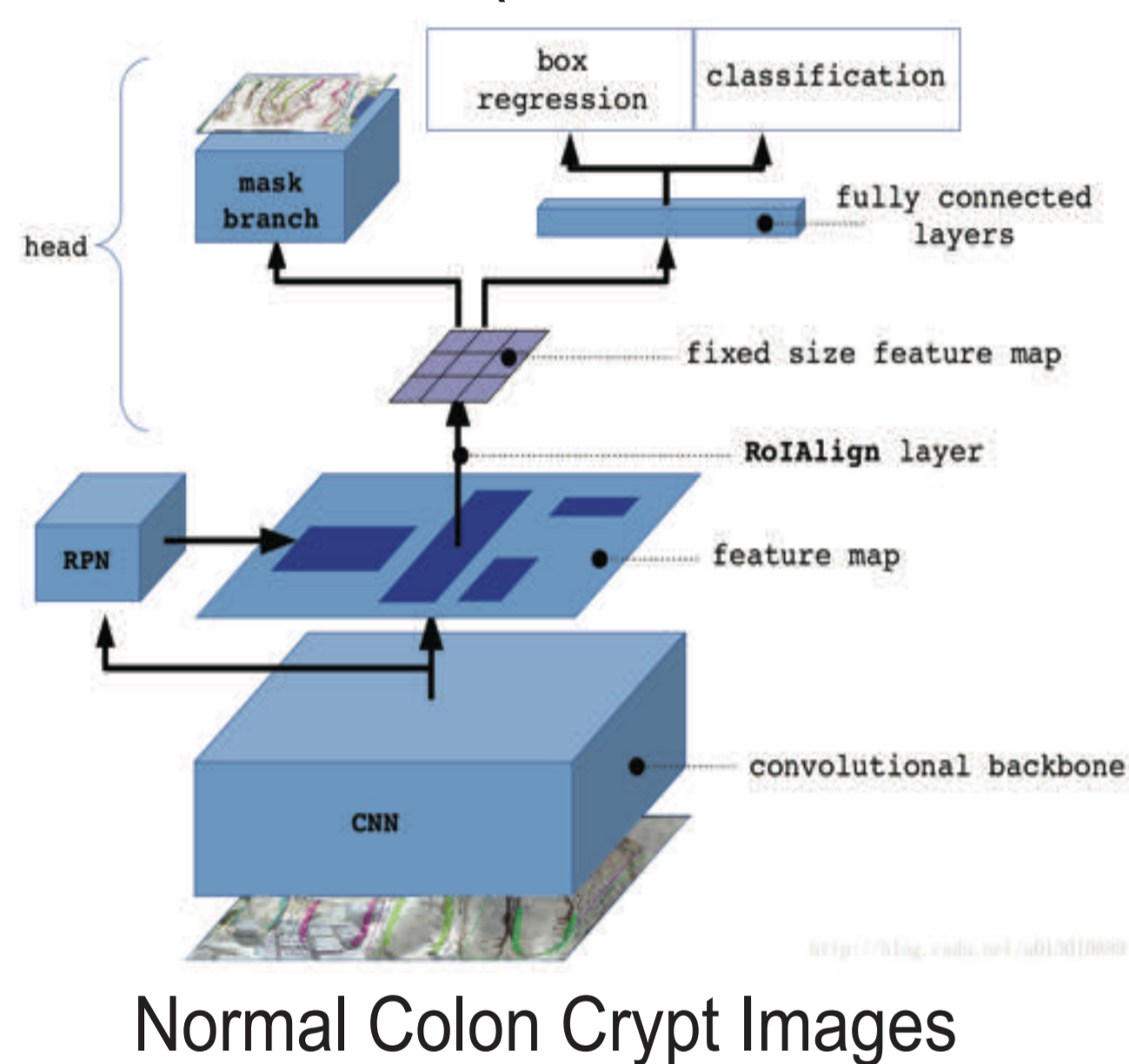
## Motivation

- It is hard to create a formal model of biological systems because the working principles are often unknown.
- Availability of high-throughput sequencing, generated massive data in the context of biological systems
- We developed a computational framework where we can start to build abstract formal model of a biological system between gene expressions
- In this poster, we demonstrate a deep-learning based validation strategy for the formal models of biological systems
- Successful validation will have big impacts in the field of biology & medicine
- This study will encourage development of novel algorithms in formal methods that can create next generation multi-disciplinary research idea.



## Method

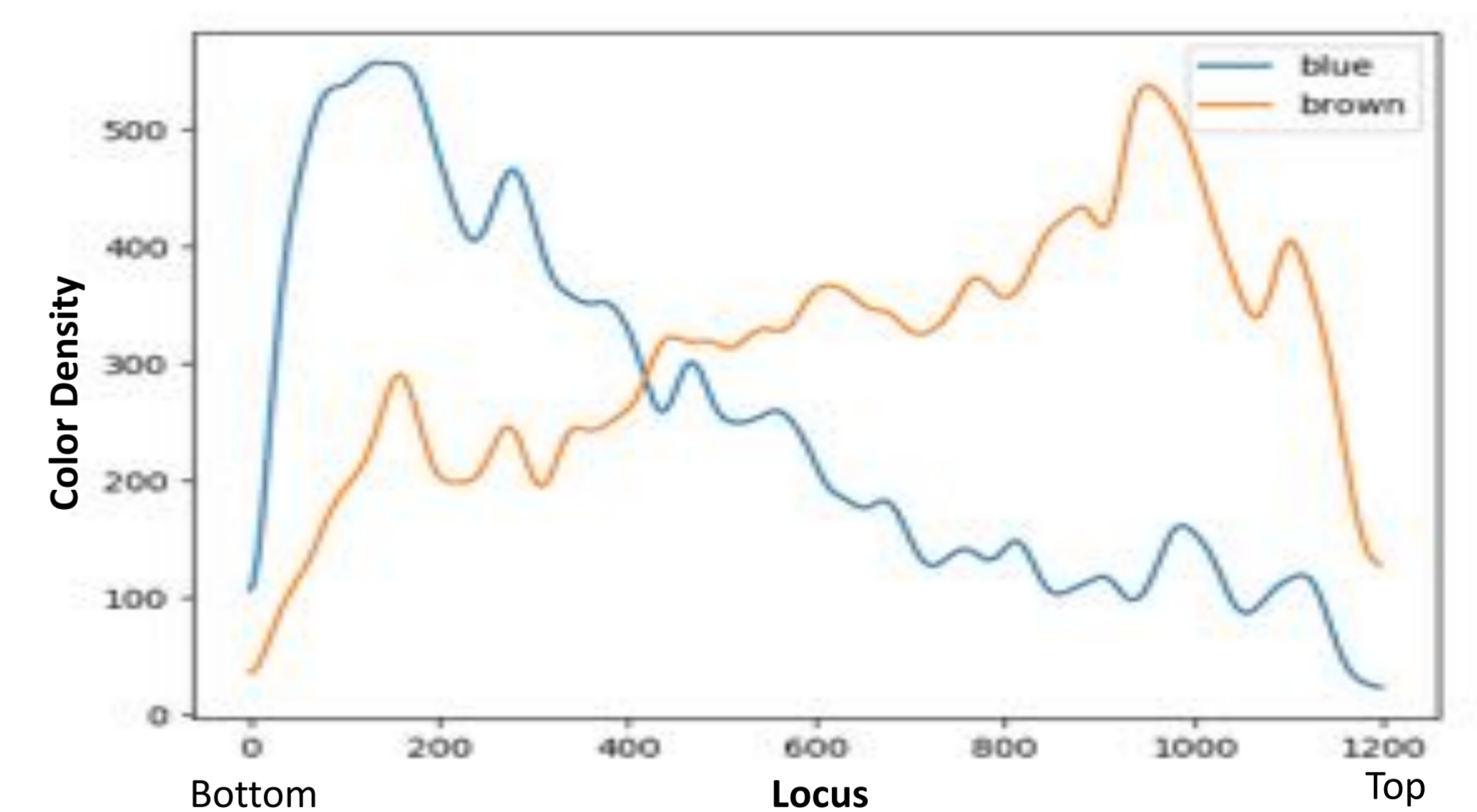
### Mask-R-CNN (ResNet-101-FPN)



- We inferred candidate Boolean invariant properties of biological system by mining large publicly available gene expression dataset such as Microarray and RNA-Seq.
- **CDX2 low => ALCAM high** is candidate invariant in the context of normal colon and colorectal cancer tissue.
- This Invariant was verified extensively in colorectal cancer by using data-derived from RNA and protein.
- To validate this invariant in a normal colon tissue we developed a deep learning strategy that used MaskRCNN and U-Net architecture.
- Using deep learning method we identified normal colon crypts and distribution of CDX2 staining pattern along the crypt differentiation axis

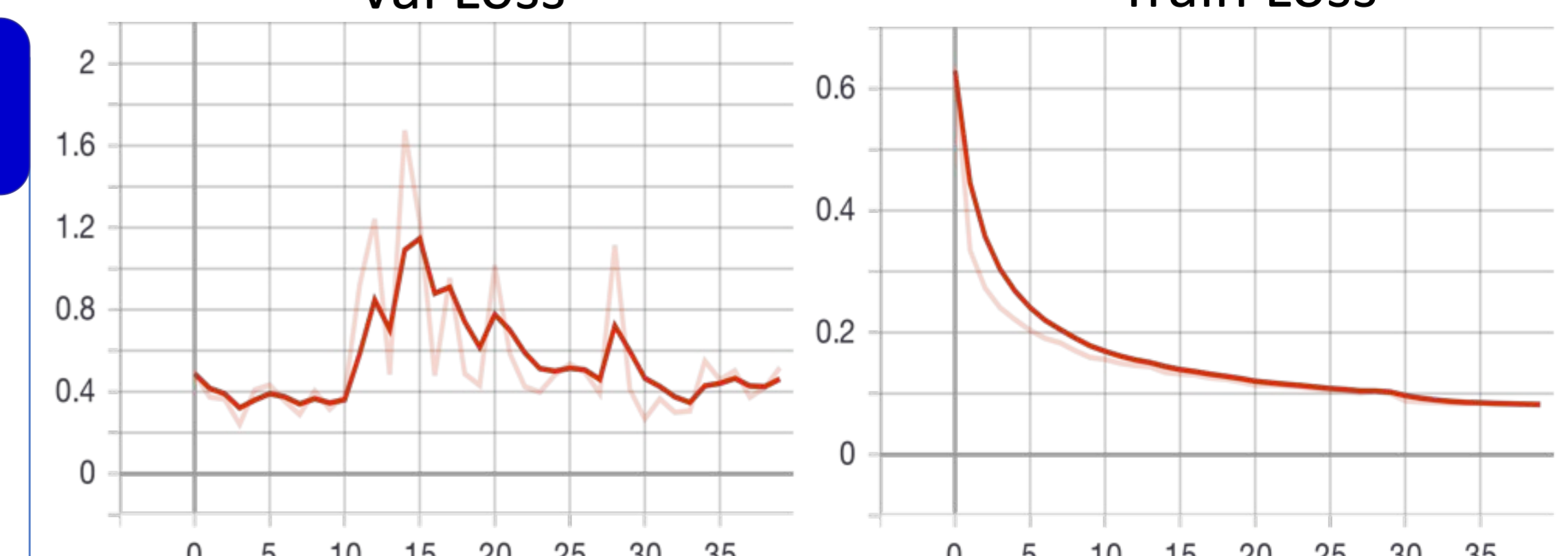
## Result

- **Dataset:** 257 Annotation 1024\*1024, Training: 1000 Images
- **System:** Model has been ran 12H on 4 Nvidia GeForce GTX 1080 Ti
- Strong correlation between color density and locus on the crypts supported our hypothesis about low-level CDX2 at bottom of crypt



Val Loss

Train Loss



## Conclusion

- Boolean invariants have a great potential to model biological system
- Deep learning based technique can further verify the results.
- Stem cells have CDX2 low expression

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