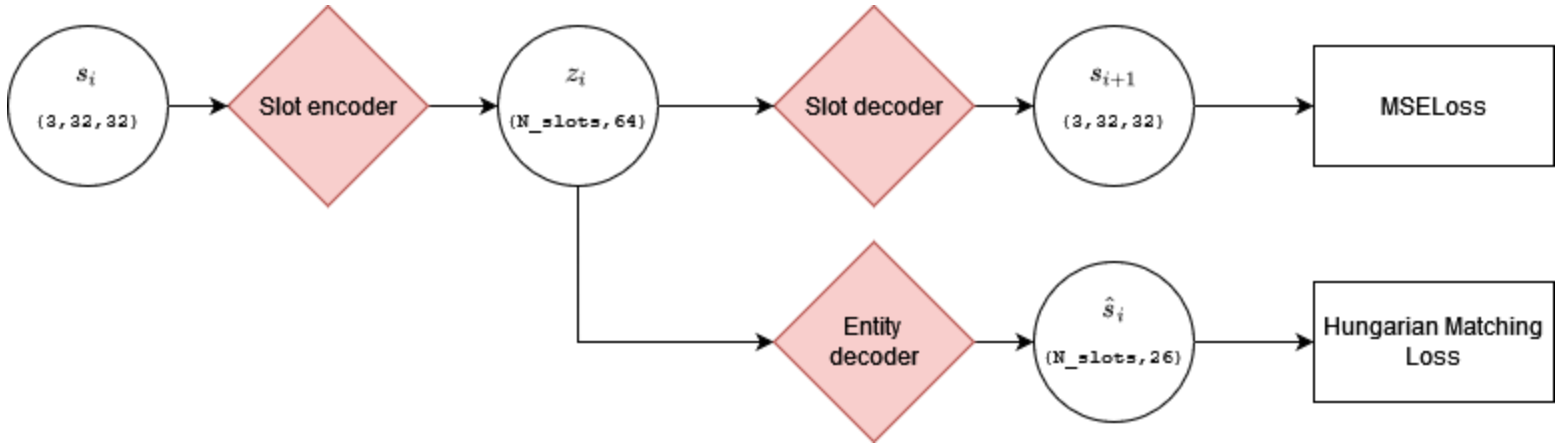
# Slot Attention with rule learning

# Agenda:

- Slot attention decoder
- DSL
- (Extra) Biological fluid dynamics (https://arxiv.org/abs/1904.13013)

# Slot Attn Decoder



# Changes

*[Submitted on 15 Jun 2019 (v1), last revised 24 Apr 2020 (this version, v6)]*

## Deep Set Prediction Networks

Yan Zhang, Jonathon Hare, Adam Prügel-Bennett

Current approaches for predicting sets from feature vectors ignore the unordered nature of sets and suffer from discontinuity issues as a result. We propose a general model for predicting sets that properly respects the structure of sets and avoids this problem. With a single feature vector as input, we show that our model is able to auto-encode point sets, predict the set of bounding boxes of objects in an image, and predict the set of attributes of these objects.

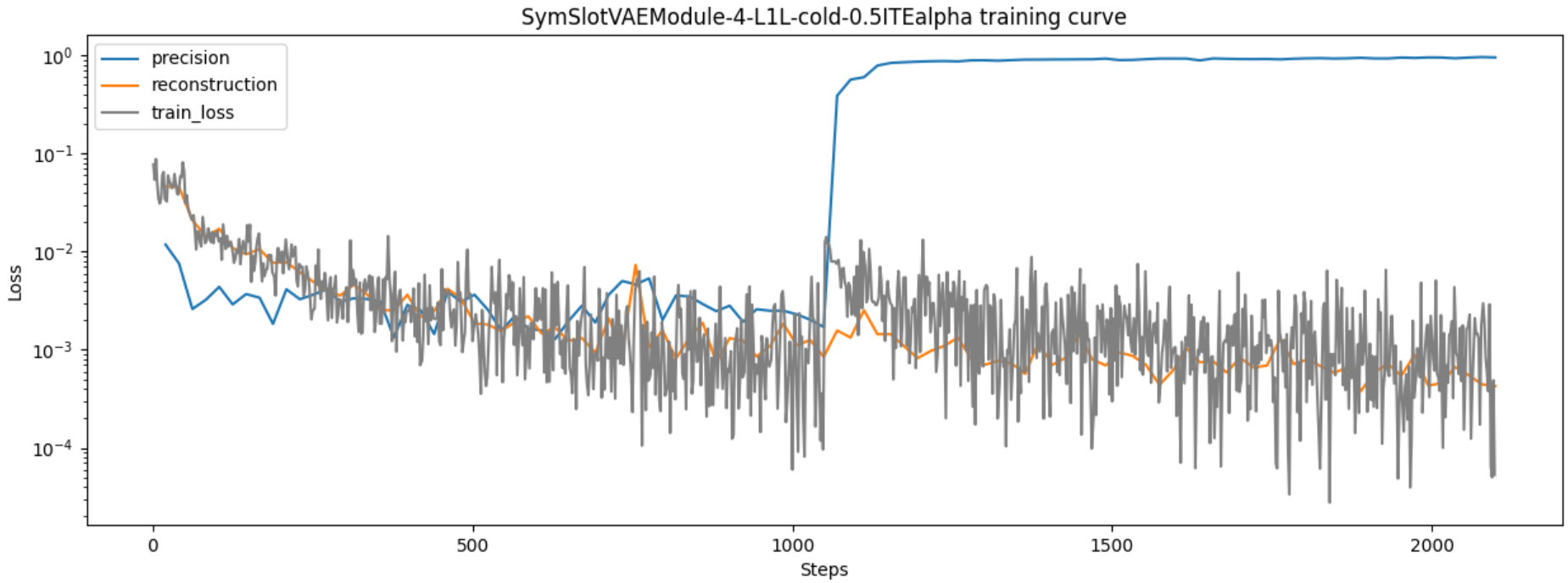
| | |
|---|---|
| Comments: | Appendix C contains an erratum |
| Subjects: | **Machine Learning (cs.LG)**; Machine Learning (stat.ML) |
| Journal reference: | Advances in Neural Information Processing Systems 32 (NeurIPS 2019) |
| Cite as: | arXiv:1906.06565 **[cs.LG]** |
| | (or arXiv:1906.06565v6 **[cs.LG]** for this version) |

## Changes:

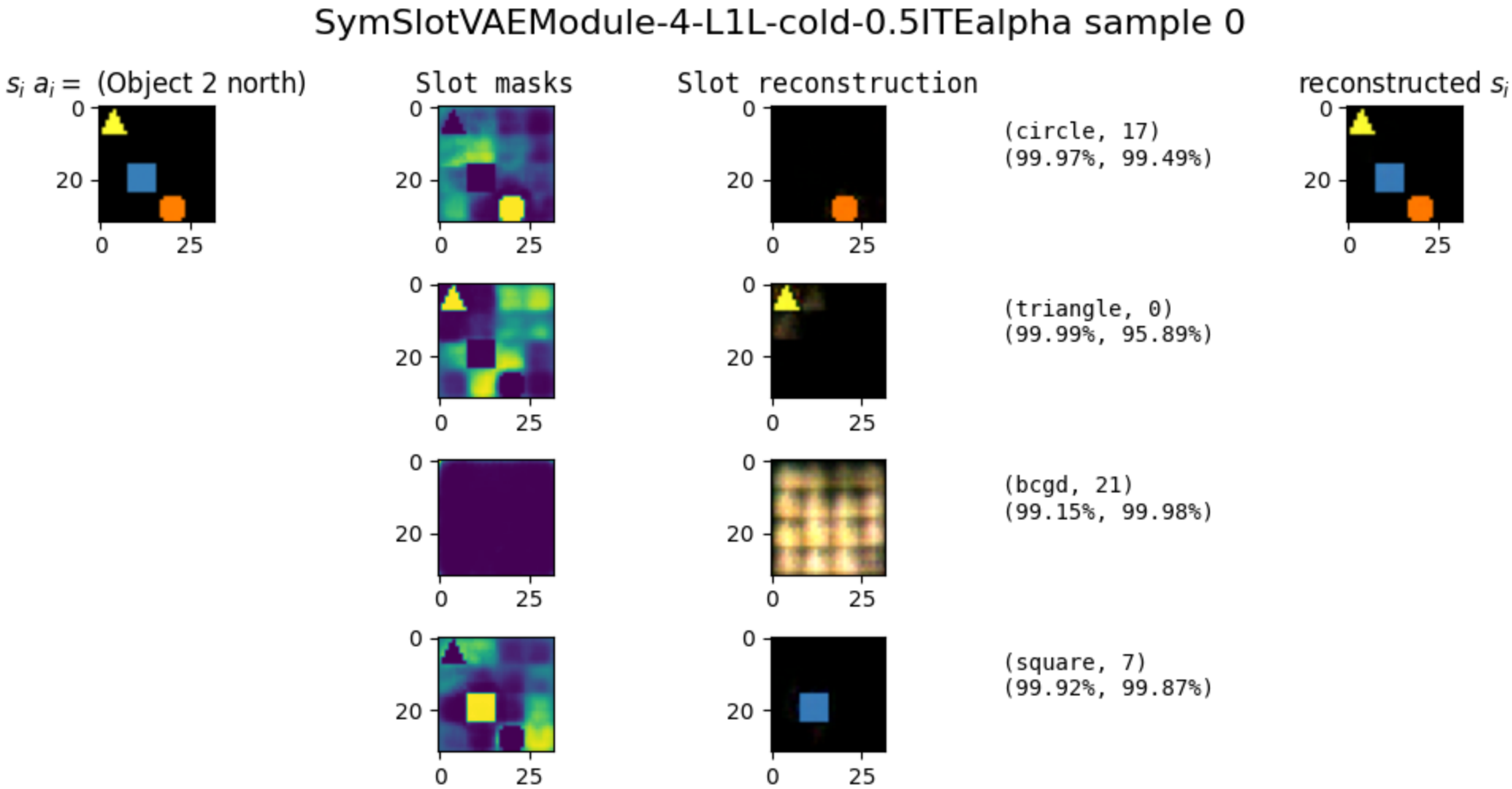
- Instead of using L1 loss, use Smooth
- Use the same loss function for matching and backprop.

# Slot Attn Decoder

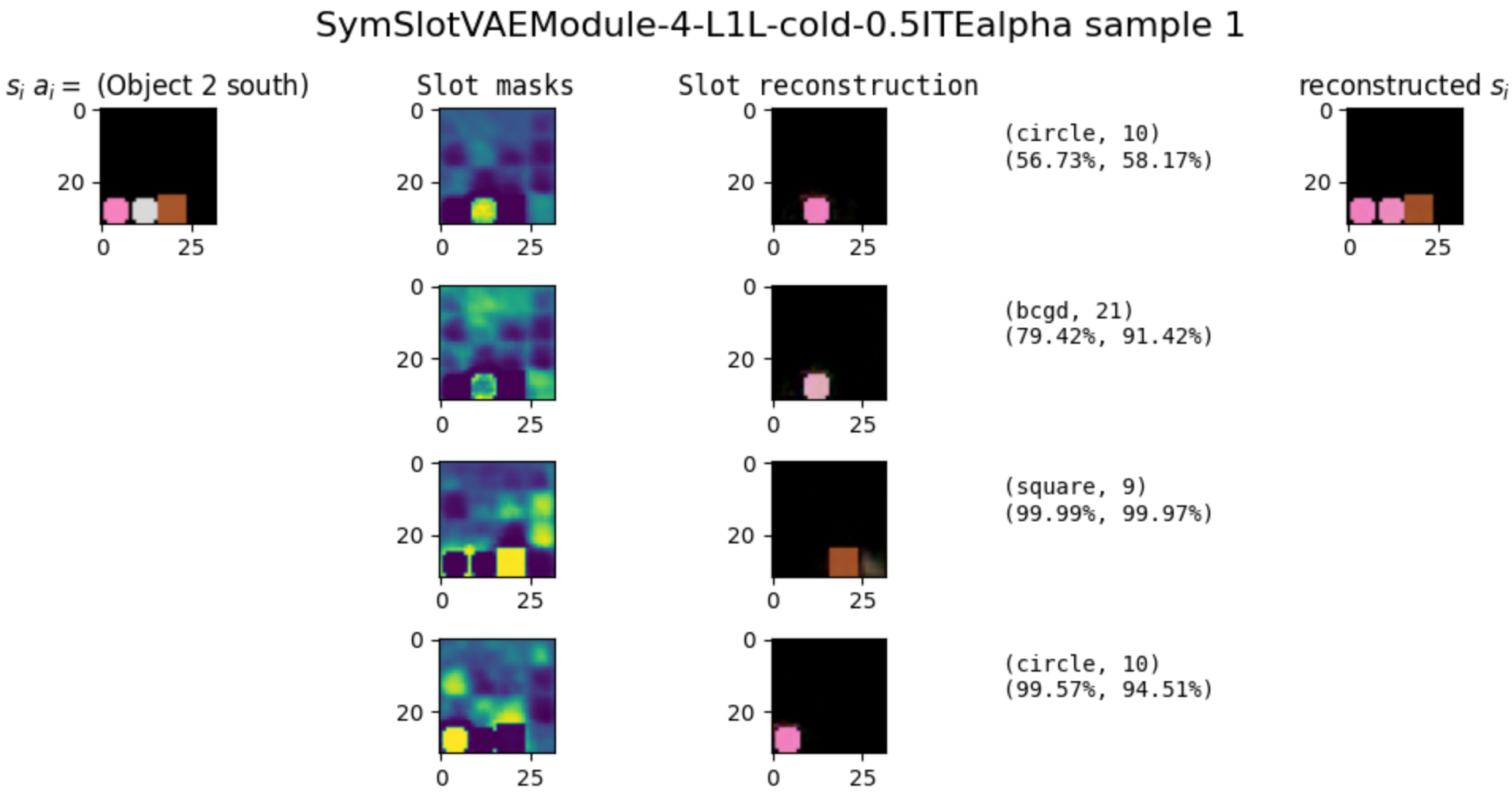
Training Curve



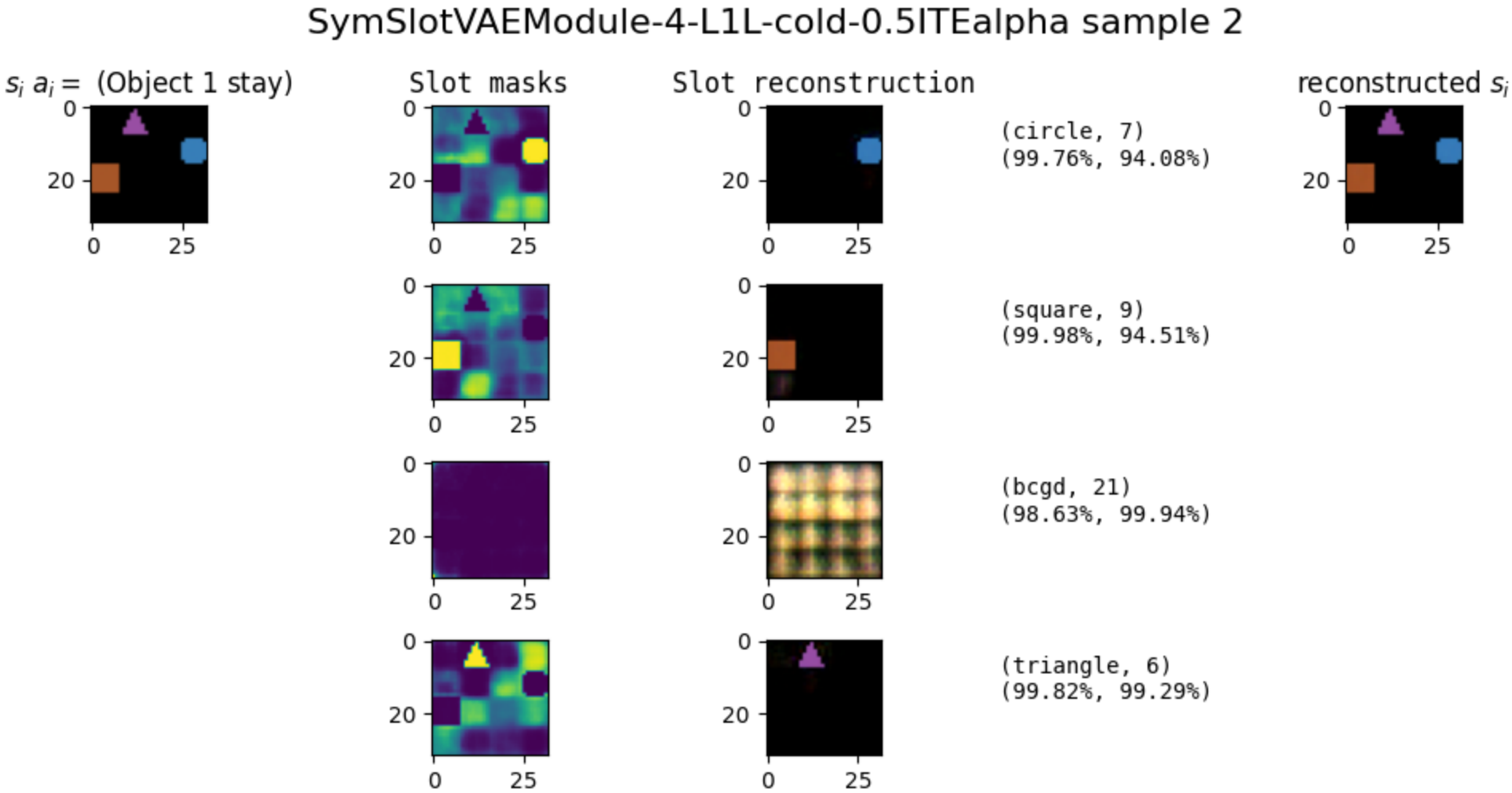
# Sample 0


SymSlotVAEModule-4-L1L-cold-0.5ITEalpha sample 0
$s_i$ $a_i$ = (Object 2 north)
Slot masks
Slot reconstruction
reconstructed $s_i$
(circle, 17)
(99.97%, 99.49%)
(triangle, 0)
(99.99%, 95.89%)
(bcgd, 21)
(99.15%, 99.98%)
(square, 7)
(99.92%, 99.87%)
0
20
0
25

# Sample 1


SymSlotVAEModule-4-L1L-cold-0.5ITEalpha sample 1
$s_i$ $a_i$ = (Object 2 south)
Slot masks
Slot reconstruction
reconstructed $s_i$
(circle, 10)
(56.73%, 58.17%)
(bcgd, 21)
(79.42%, 91.42%)
(square, 9)
(99.99%, 99.97%)
(circle, 10)
(99.57%, 94.51%)

# Sample 2


SymSlotVAEModule-4-L1L-cold-0.5ITEalpha sample 2
$s_i$ $a_i$ = (Object 1 stay)
Slot masks
Slot reconstruction
reconstructed $s_i$
(circle, 7)
(99.76%, 94.08%)
(square, 9)
(99.98%, 94.51%)
(bcgd, 21)
(98.63%, 99.94%)
(triangle, 6)
(99.82%, 99.29%)

# DSL

Inputs:

```
pos :: [int, int]
color :: int
shape :: {circ, sq, tri}
slot :: [color, shape, pos]
```

# (Extra) Fluid Dynamics

https://arxiv.org/abs/1904.13013

*[Submitted on 30 Apr 2019 (v1), last revised 10 Jul 2019 (this version, v2)]*

## Landmarks and Frontiers in Biological Fluid Dynamics

John O. Dabiri

Biological systems are influenced by fluid mechanics at nearly all spatiotemporal scales. This broad relevance of fluid mechanics to biology has been increasingly appreciated by engineers and biologists alike, leading to continued expansion of research in the field of biological fluid dynamics. While this growth is exciting, it can present a barrier to researchers seeking a concise introduction to key challenges and opportunities for progress in the field. Rather than attempt a comprehensive review of the literature, this article highlights a limited selection of classic and recent work. In addition to motivating the study of biological fluid dynamics in general, the goal is to identify both longstanding and emerging conceptual questions that can guide future research. Answers to these fluid mechanics questions can lead to breakthroughs in our ability to predict, diagnose, and correct biological dysfunction, while also inspiring a host of new engineering technologies.