Multi-StyleGAN: Towards Image-Based Simulation of Time-Lapse Live-Cell Microscopy

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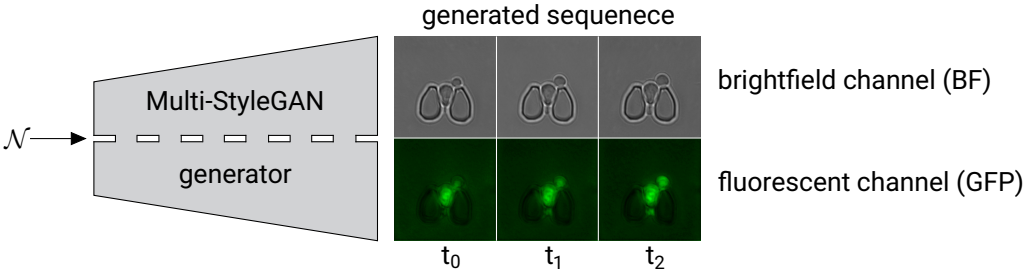
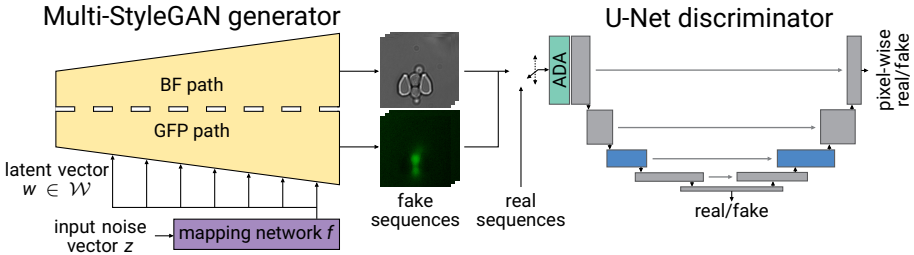
Introduction

Multi-StyleGAN generates multi-domain sequences.



Multi-StyleGAN

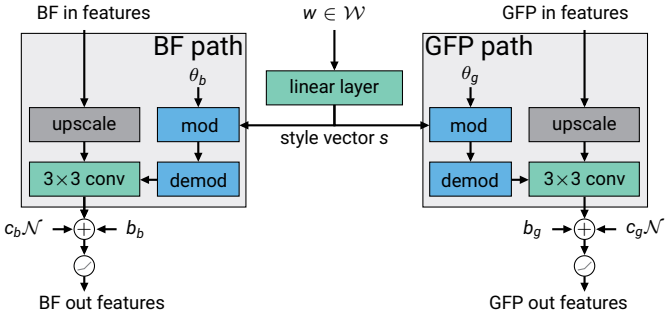
The architecture contains two convolutional paths, one for each domain.



Multi-StyleGAN

Dual-Style-Convolution block is the main component of Multi-StyleGan

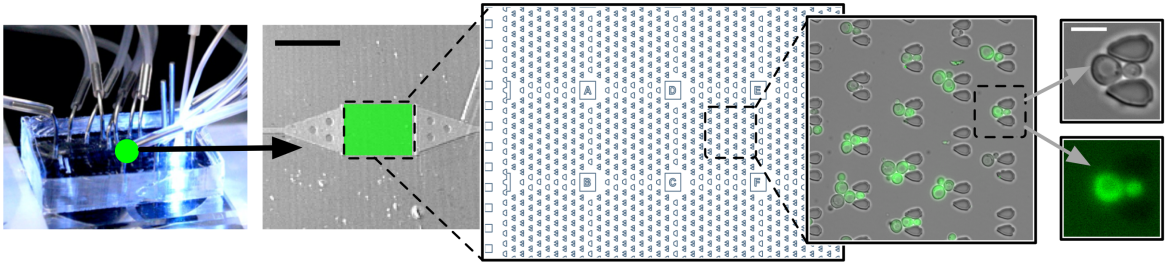
- Single style vector s enforces consistency between domains.



Dataset

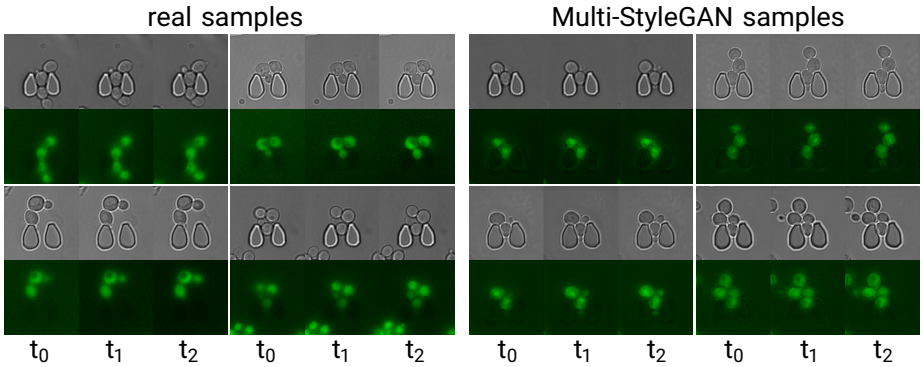
Live yeast in microsctructured environment dataset recorded in our lab

- Microfluidics based microscopy of multi-domain (BF+GFP) temporal sequences.
- Training dataset comprised of:
  - 8148 training sequences
  - 9696 multi-domain images (256 $\times$ 256 pix.)
  - training sequences length 3
  - timestep Δt=10min



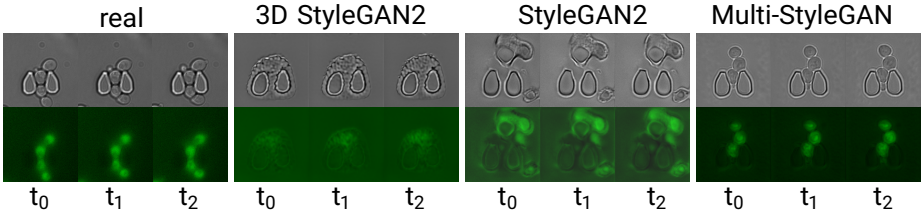
Results

Multi-StyleGAN captures biophysical factors and time dependencies realistically



Results

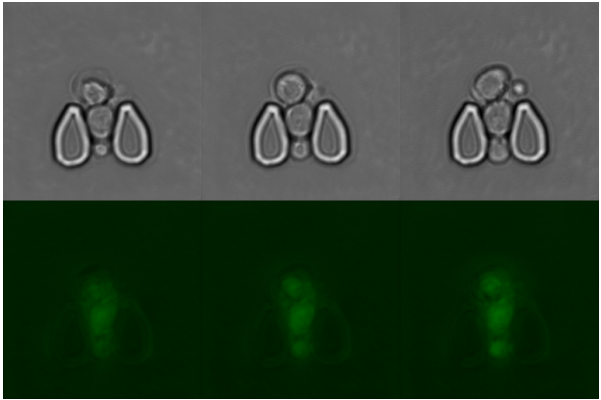
Multi-StyleGAN significantly outperforms biophysically unrealistic baselines



	FID ↓		FVD ↓	
Method	BF	GFP	BF	GFP
Multi-StyleGAN (ours)	**33.3687**	**207.8409**	**4.4632**	**30.1650**
StyleGAN2 + ADA + U-Net dis.	200.5408	224.7860	45.6296	35.2169
StyleGAN2 3D + ADA + U-Net dis.	76.0344	298.7545	14.7509	31.4771

Results

Multi-StyleGAN transitions smoothly through interpolation of latent space



Conclusion

- Mult-StyleGAN synthesises multi-domain image sequences.
- Novel Dual-styled-convolutional block enforces domain consistency with a single style vector.
- Multi-StyleGAN showcased on time-lapse fluorescent microscopy sequences of yeast.
- The simulations realistically capture spatio-temporal organisation of multiple living yeast cells, as well as other biophysical factors, cell fluorescence and time-dependencies.
- Code and dataset are available online (see paper and poster).

Questions and corresondance:

- Poster Session 3, Pathable or SpatialChat (Tim Prangemeier)
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