SR-CACO-2: A Dataset for Confocal Fluorescence Microscopy Image Super-Resolution

Soufiane Belharbi[1], Mara KM Whitford[2,3], Phuong Hoang[2], Shakeeb Murtaza[1], Luke McCaffrey[2,3,4], and Eric Granger[1]

[1] LIVIA, ILLS, Dept. of Systems Engineering, ETS Montreal, Canada
[2] Goodman Cancer Institute, McGill University, Montreal, Canada
[3] Dept. of Biochemistry, McGill University, Montreal, Canada
[4] Gerald Bronfman Dept. of Oncology, McGill University, Montreal, Canada

{soufiane.belharbi,eric.granger}@etsmtl.ca, luke.mccaffrey@mcgill.ca

Why New Dataset?

- There are only **very few** microscopy super-resolution **datasets**
- Existing super resolution microscopy **datasets are private**
- Confocal imaging is widely accessible
- The need to **upscale LR images with less photobleaching and phototoxicity (cell damage)** using machine learning → need of data
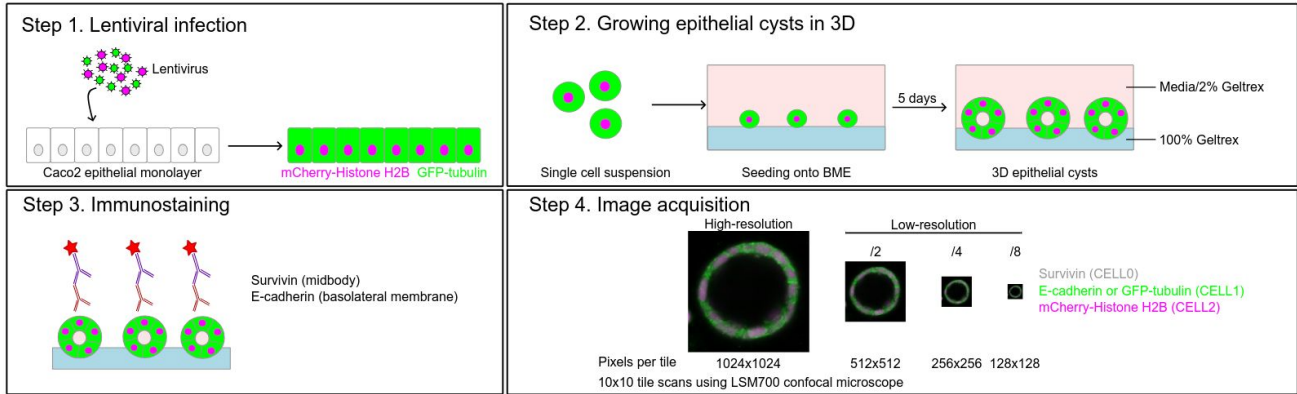
SR-CACO-2 Dataset

- Confocal imaging
- Real pairs: LR, HR
- Diverse: 4 scales: HR, LR (/2, /4, /8),
  3 protein markers, 16, 800 multi-cellular objects
- Per-scale: 22,00 unique images (22 tiles),
  +9k patches (512x512)
- Designed for super-resolution task
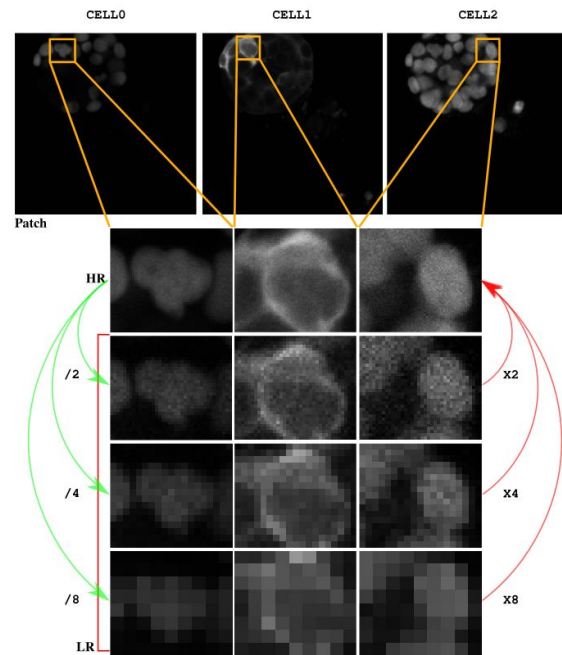
SR-CACO-2: Capture

- Based on human epithelial cell line Caco-2 (ATCC HTB-37)
- Fixed-imaging with simulated live-imaging (3D)

SR-CACO-2: Access

- Freely accessible under license: CC BY-NC-SA 4.0

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https://github.com/sbelharbi/sr-caco-2

More details

https://arxiv.org/pdf/2406.09168

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+ Benchmarking of 16 SISR methods

More details

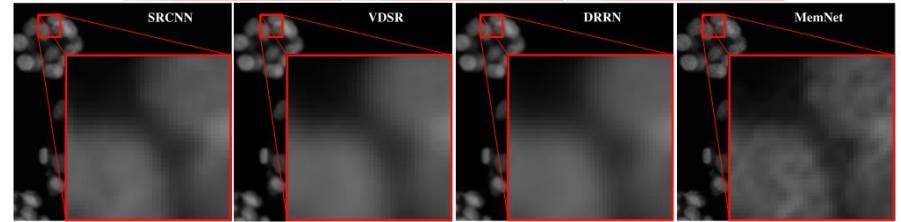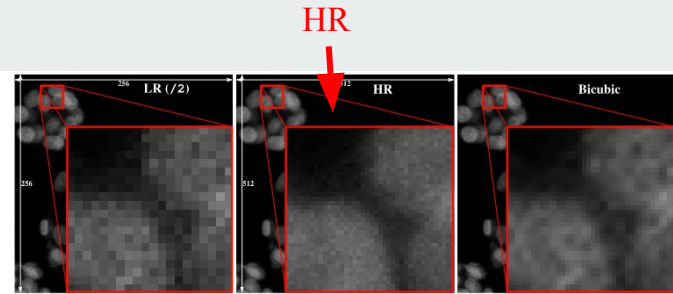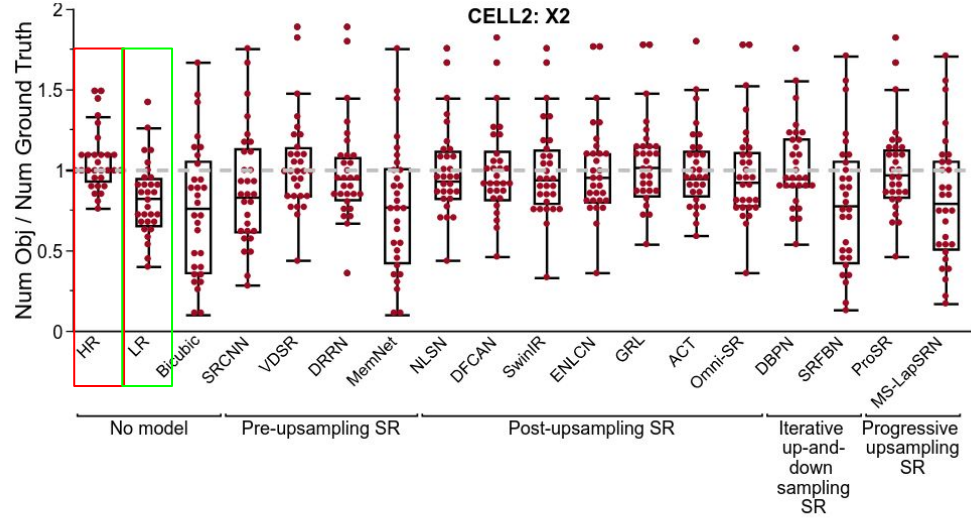https://github.com/sbelharbi/sr-caco-2

https://arxiv.org/pdf/2406.09168

SR-CACO-2: Usage

Super-resolution task

Limited results

SISR Methods	Scale	PSNR ↑				NRMSE ↓				SSIM ↑			
		CELL0	CELL1	CELL2	Mean	CELL0	CELL1	CELL2	Mean	CELL0	CELL1	CELL2	Mean
Bicubic	X2	35.02	32.15	30.38	32.52	0.1085	0.0601	0.0724	0.0803	0.7618	0.7658	0.6891	0.7389
	X4	35.46	32.03	31.10	32.86	0.0985	0.0586	0.0660	0.0744	0.8206	0.8002	0.7673	0.7960
	X8	31.88	27.50	26.10	28.49	0.1655	0.1139	0.1349	0.1381	0.6683	0.6266	0.6511	0.6487
Pre-upsampling SR													
SRCNN [19] *(eccv,2014)*	X2	37.54	34.27	33.42	35.08	0.0710	0.0450	0.0500	0.0553	0.8517	0.8524	0.8210	0.8417
	X4	36.14	32.73	32.25	33.71	0.0817	0.0528	0.0572	0.0639	0.8522	0.8216	0.8079	0.8272
	X8	33.05	28.04	26.49	**29.19**	0.1265	0.0967	0.1220	**0.1151**	0.7711	0.7085	0.7092	**0.7296**
Post-upsampling SR													
Omni-SR [85] *(cvpr,2023)*	X2	37.70	34.11	33.51	35.11	0.0759	0.0461	0.0496	0.0572	0.8744	0.8539	0.8313	0.8532
	X4	36.44	32.59	32.34	33.79	0.0849	0.0536	0.0563	0.0649	0.8592	0.8203	0.8111	0.8302
	X8	30.75	27.16	25.30	27.74	0.1713	0.1098	0.1352	0.1387	0.6715	0.6419	0.6591	0.6575
Iterative up-and-down sampling SR													
SRFBN [54] *(cvpr,2019)*	X2	36.13	33.15	31.61	33.63	0.0955	0.0531	0.0625	0.0704	0.8078	0.8091	0.7470	0.7880
	X4	36.08	32.52	31.79	33.46	0.0911	0.0545	0.0605	0.0687	0.8405	0.8147	0.7889	0.8147
	X8	32.27	27.78	26.47	28.84	0.1560	0.1091	0.1278	0.1310	0.7022	0.6549	0.6904	0.6825
Progressive upsampling SR													
MS-LapSRN [44] *(tpami,2019)*	X2	33.88	32.36	29.34	31.86	0.1130	0.0535	0.0791	0.0819	0.7652	0.8164	0.7695	0.7837
	X4	30.80	30.99	31.08	30.96	0.1192	0.0615	0.0626	0.0811	0.7885	0.7837	0.7806	0.7843
	X8	31.83	27.14	25.06	28.01	0.1404	0.0982	0.1323	0.1236	0.7478	0.6933	0.6640	0.7017

SR-CACO-2: Usage
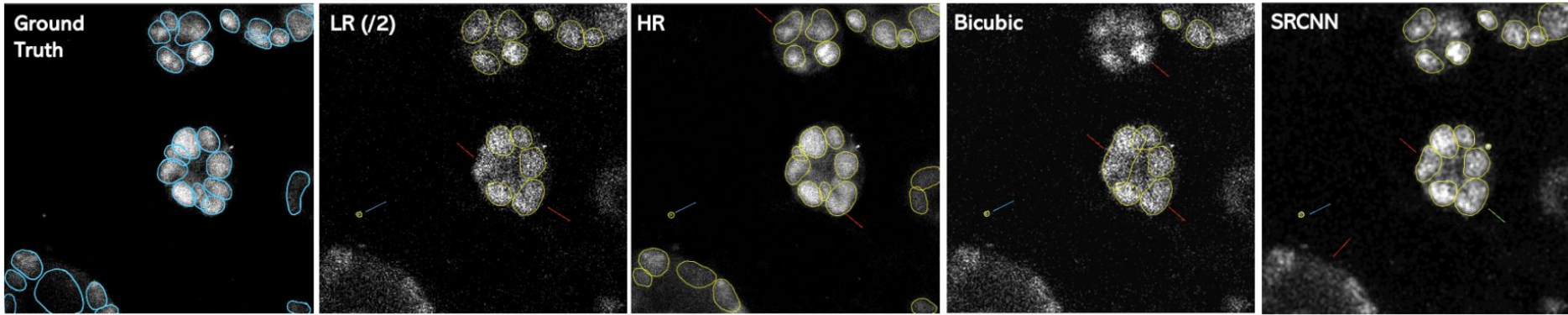
Microscopy
downstream
tasks over cells

Figure 6: Analysis of cell detection performance for CELL2, X2 over 30 random test samples (red dots). More results can be found in the supplementary materials.

Model versus HR		
Level	Score Mean Diff	p-Value
LR	-18	0.001
Bicubic	-21.3667	<.0001
SRCNN	-16.5667	0.0034
VDSR	7.0333	0.6868
DRRN	2.3333	1
MemNet	-18.7667	0.0005
NLSN	-4.1333	0.992
DFCAN	-3.3667	0.9992
SwinIR	-29.9667	<.0001
ENLCN	-3.7	0.9975
GRL	-14.7667	0.014
ACT	-7.7	0.5677
Omni-SR	-4.0667	0.9932
DBPN	-0.6333	1
SRFBN	-19.3667	0.0003
ProSR	-0.8333	1
MS-LapSRN	-17.8333	0.0011

SR-CACO-2: Usage

Microscopy downstream tasks over cells

SR-CACO-2

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See you at the poster!