

Learning-based image coding for DNA storage

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15.06.2023

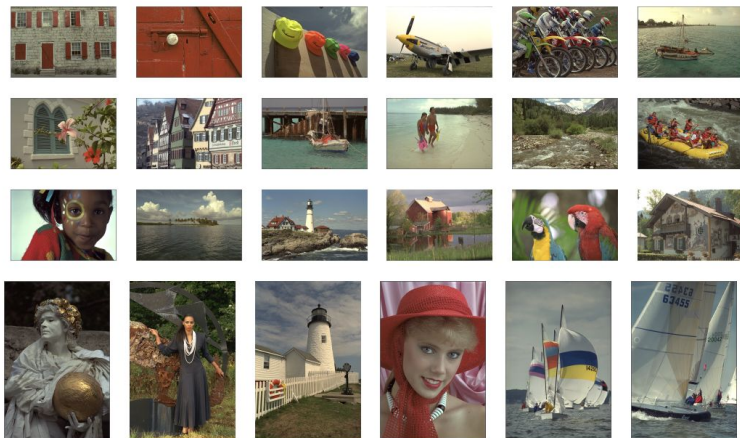
- **Goal** : Assess the quality of a learning based encoder based on JPEG DNA Standard Testing Conditions.
- These include :
 - An objective quality evaluation
 - Biochemical coding constraints
 - A subjective quality inspection

JPEG DNA call for proposal

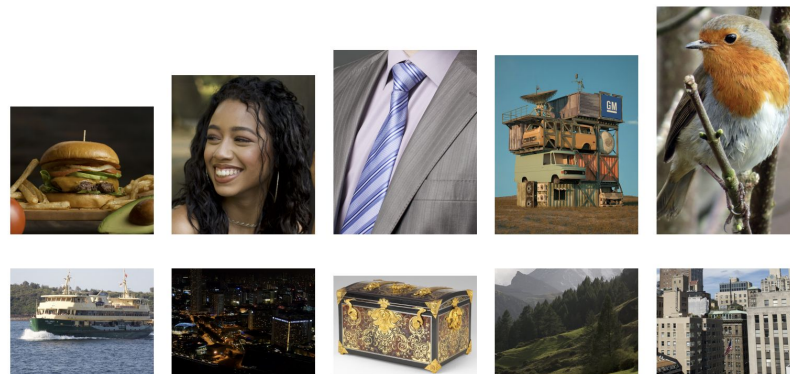
- Coders or transcoders respecting biochemical constraints:
 - Strand length limitations
 - Homopolymer runs
 - GC content balance
 - Repetition of patterns

- Baseline methods used for comparison:
 - Codec:
 - JPEG DNA benchmark codec
 - Transcoders:
 - JPEG DNA BC transcoder
 - Variable Length Direct Transcoder (Anchor 1)
 - Fixed Length Direct Transcoder (Anchor 3)

Data sets used for analysis

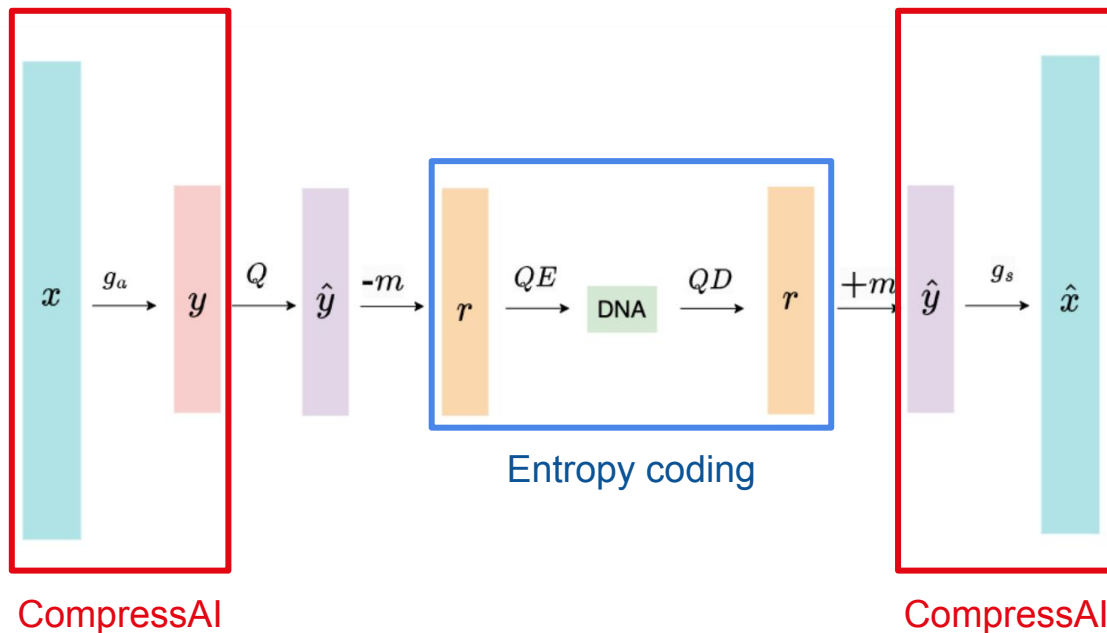


Kodak data set



JPEG DNA data set

Evaluated learning based autoencoder



Workflow of the autoencoder

- **CompressAI**: end-to-end learning-based compression autoencoder
- **Entropy coding**: quaternary encoding algorithm adapted from JPEG DNA Benchmark Codec

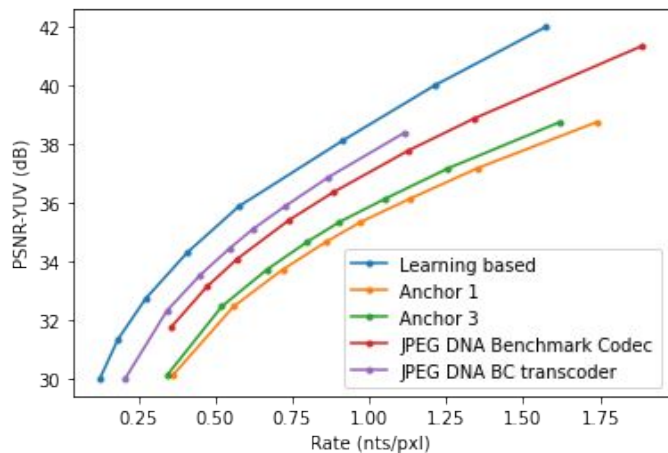
Image compression & encoding

- Anchors & JPEG DNA BC transcoder:
 - Images compressed at 8 different qualities with JPEG
 - Encoder applied to all images
- JPEG DNA benchmark codec & learning-based model:
 - Images encoded at 8 different qualities
 - Quality is a parameter of the encoding process (= alpha for the JPEG DNA BC)
- Quality levels and alpha values chosen so that the rates of all methods were in a similar range

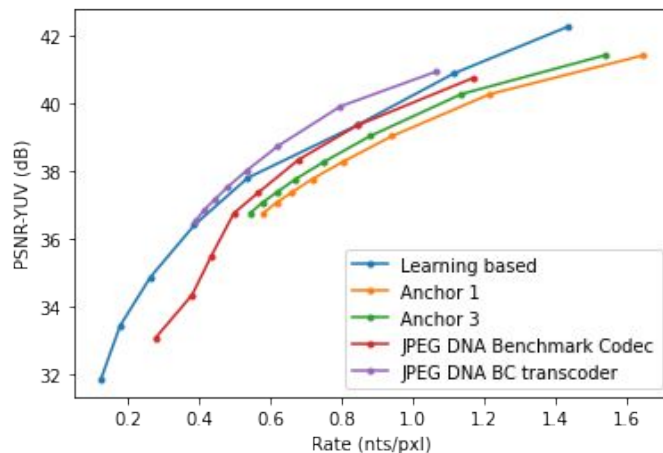
Objective quality evaluation

- Rate-distortion plot analysis:
 - PSNR-YUV
 - MS-SSIM
 - IW-SSIM
 - VIF
 - NLPD
 - FSIM
 - VMAF
- Run time analysis

- Peak Signal to Noise Ratio in the YUV color space
- Perceptual assessment of image quality



Kodak

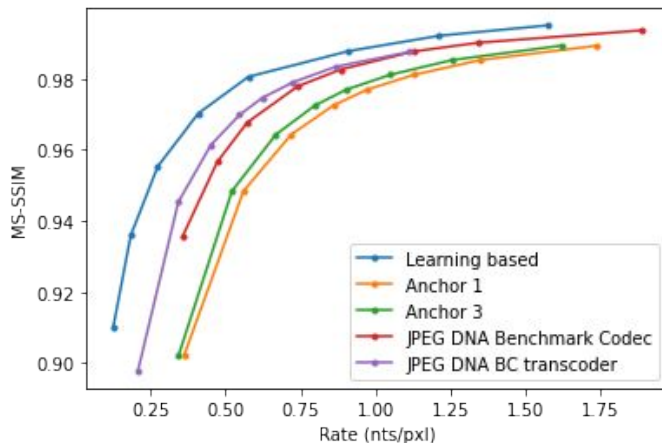


JPEG DNA

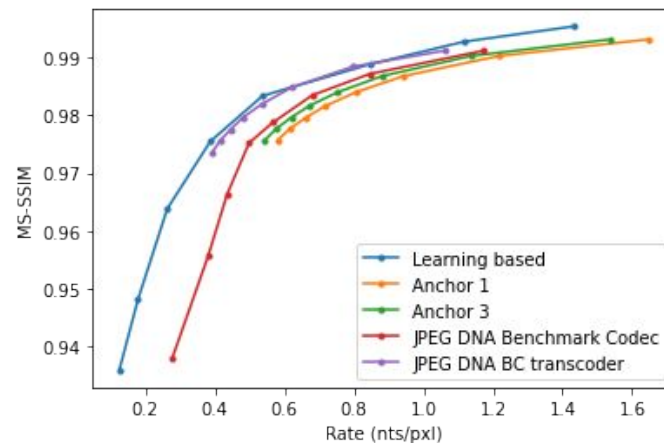
Average PSNR-YUV over the images of each data set, at different rates

MS-SSIM

- Multi-Scale Structural Similarity Index Measure
- Comparison of details between original and reconstructed image



Kodak

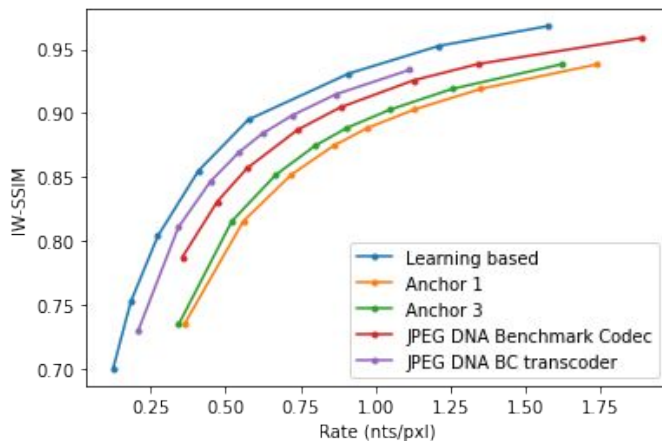


JPEG DNA

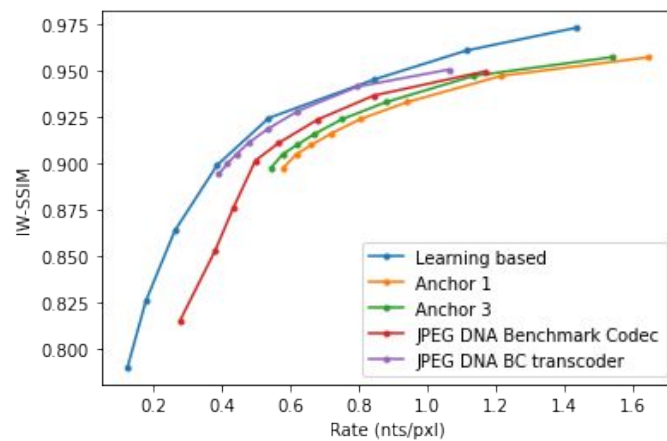
Average MS-SSIM over the images of each data set, at different rates

IW-SSIM

- Information content Weighted Structural Similarity Index Measure
- Grants more importance to the regions of the image with a higher information content



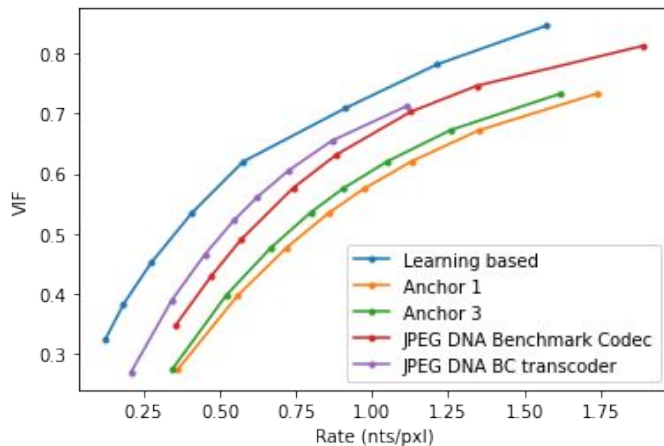
Kodak



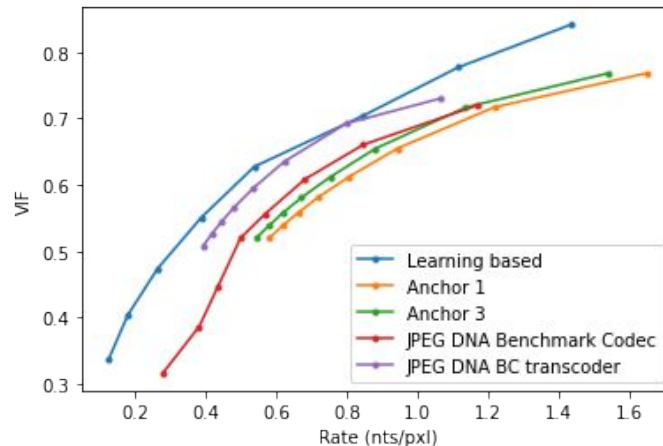
JPEG DNA

Average IW-SSIM over the images of each data set, at different rates

- Visual Information Fidelity
- Analysis of various statistical properties of the images: luminance, contrast, and texture
- Models the human perception of an image's quality



Kodak

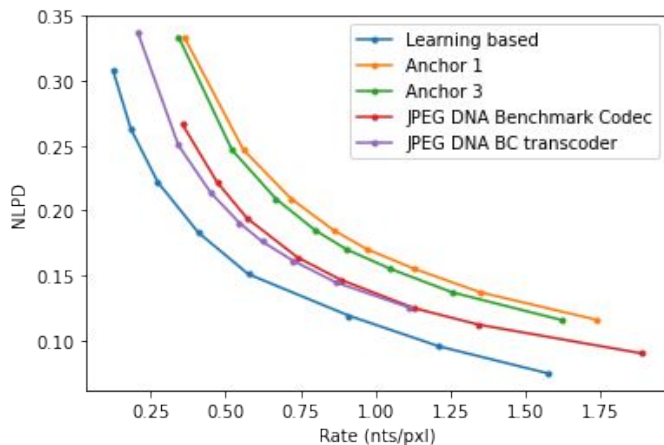


JPEG DNA

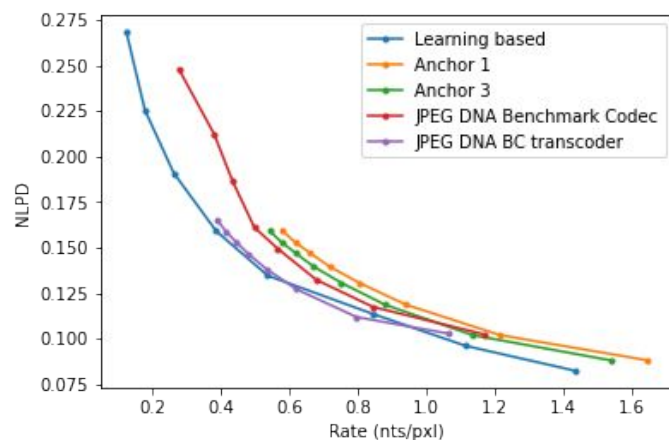
Average VIF over the images of each data set, at different rates

NLPD

- Normalized Laplacian Pyramid Distance
- 2 parameters taken into account : local luminance subtraction & local contrast gain control.
- Captures both local details and the global structure



Kodak

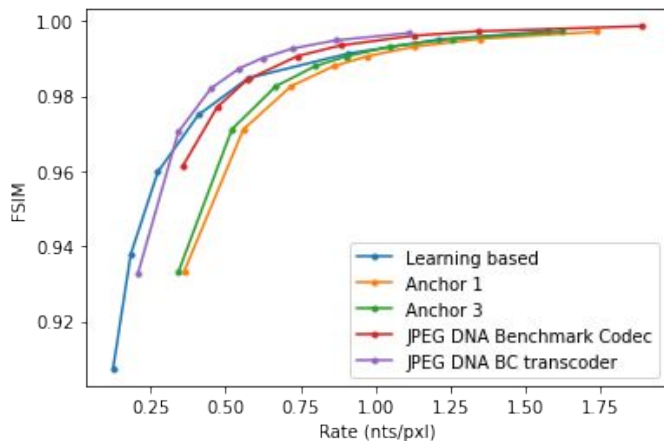


JPEG DNA

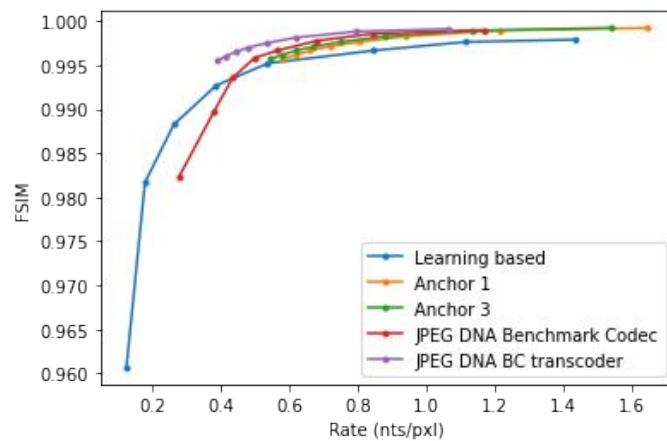
Average NLPD over the images of each data set, at different rates

FSIM

- Feature Similarity Index Metric
- 2 important low level features : phase congruency and image gradient magnitude
- Recreates the Human Visual System perception



Kodak

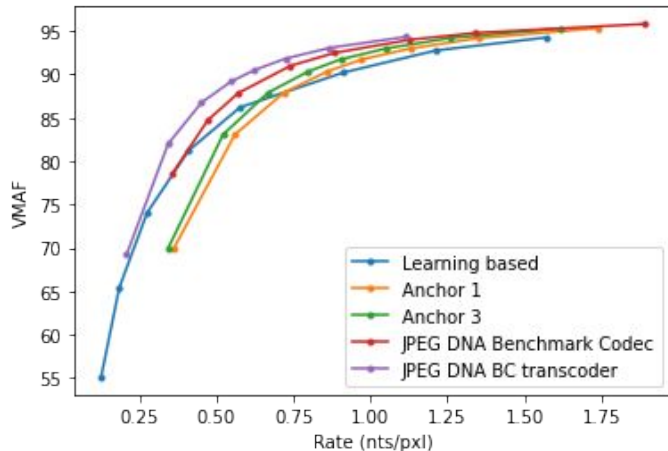


JPEG DNA

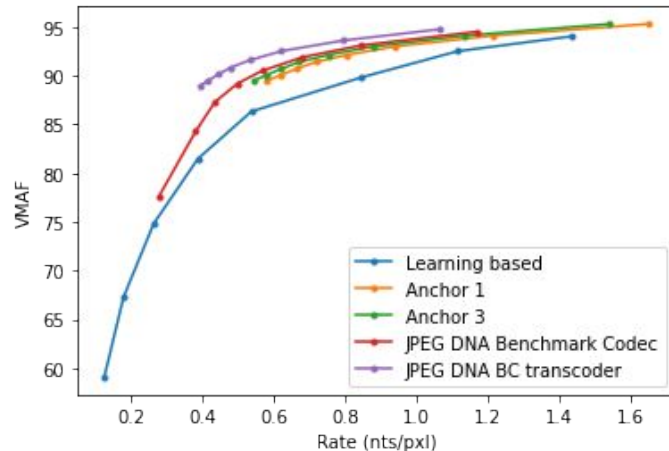
Average FSIM over the images of each data set, at different rates

VMAF

- Video Multimethod Assessment Fusion
- Machine learning model trained on subjective human ratings
- Multiple objective metrics fused



Kodak



JPEG DNA

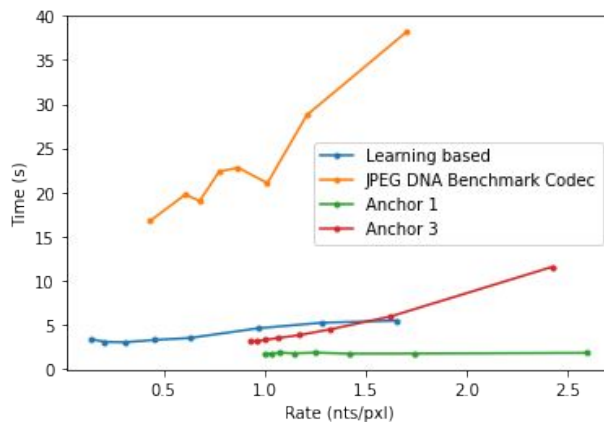
Average VMAF over the images of each data set, at different rates

- PSNR, SSIM, VIF and NLPD:
 - Learning-based is the highest performing model on the Kodak data set
 - JPEG DNA BC transcoder performs better on the JPEG DNA data set and catches up with the Learning-based model
- VMAF and FSIM, the most complex metrics :
 - Learning-based is the lowest performing model on the JPEG DNA dataset, and on the Kodak dataset at high rates
- Necessary subjective inspection to clear up contradictions

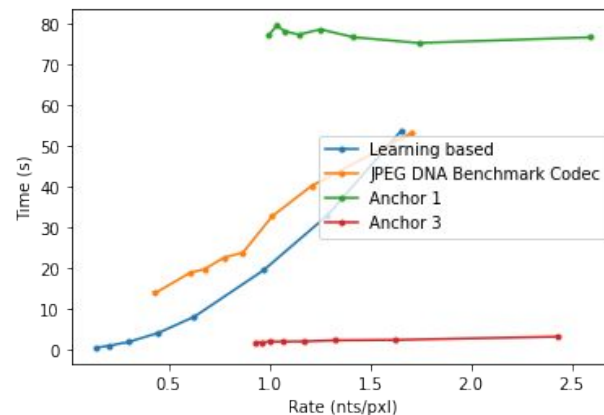
Run time analysis

Model	Encoding time (s)	Decoding time (s)
Anchor 1	1.756	77.356
Anchor 3	4.842	2.308
JPEG DNA Benchmark Codec	28.178	22.350
Learning-based	3.926	15.32

Average encoding and decoding times for the image 1 of the JPEG DNA data set at different rates



Encoding

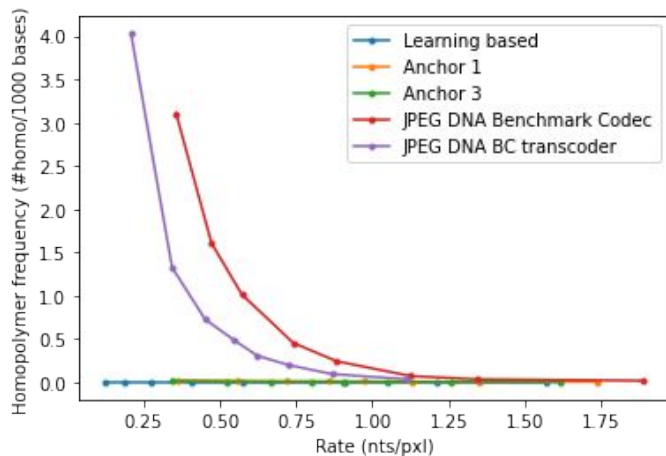


Decoding

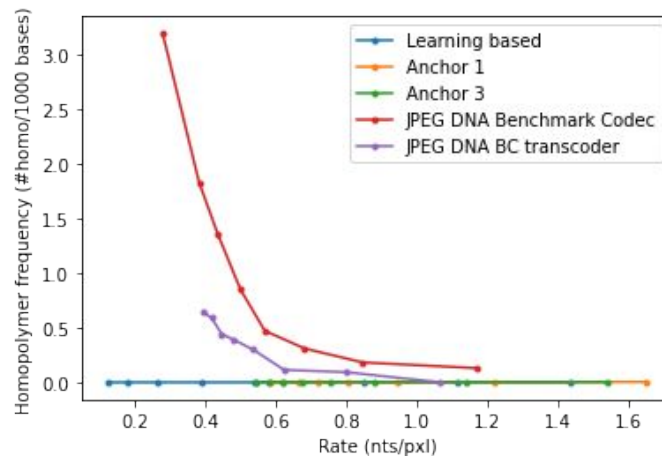
Encoding and decoding times in regards of rate, for image 1 of the JPEG DNA data set

Homopolymer frequency

- Number of individual homopolymers per 1000 nucleotides



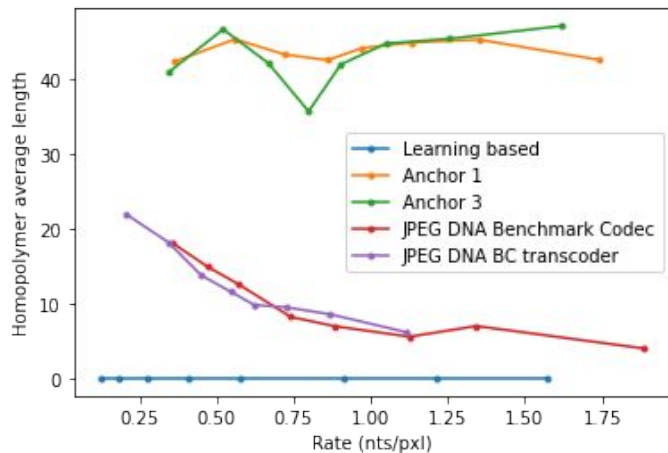
Kodak



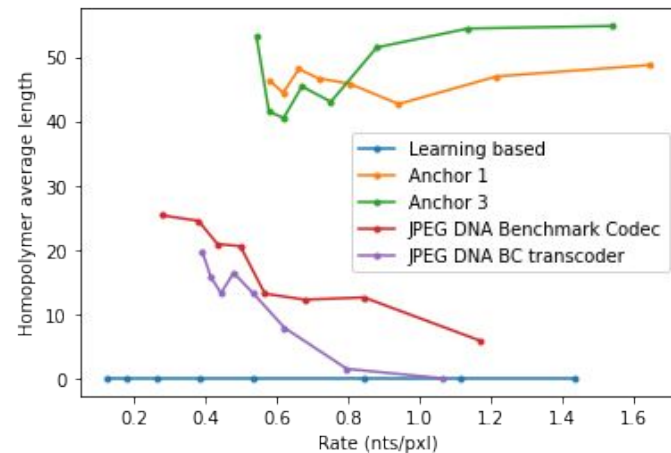
JPEG DNA

Average homopolymer frequency, for all generated DNA, at different rates

Homopolymer length



Kodak

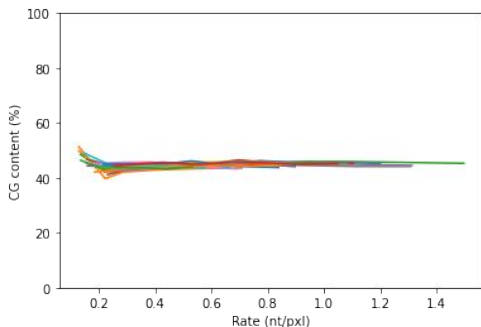


JPEG DNA

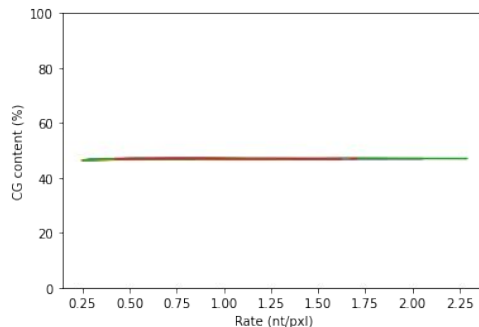
Average homopolymer length, for all generated DNA, at different rates

CG bases content -Kodak

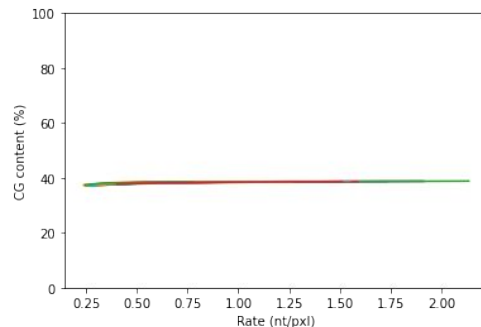
- Target CG content : between 40% and 50%.



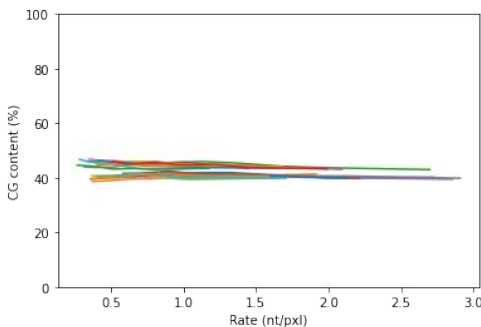
BC transcoder



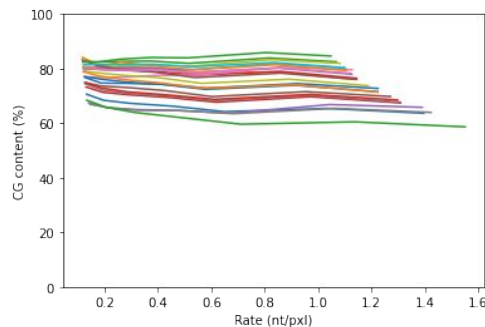
Anchor 1



Anchor 3



JPEG DNA benchmark codec

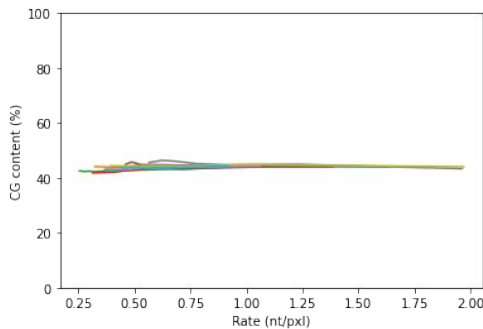


Learning-based

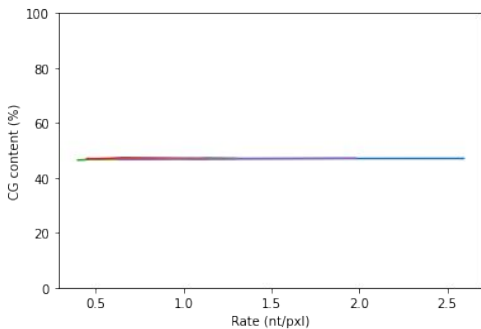
CG content of the DNA generated for all the images of the Kodak data set

CG bases content -JPEG DNA

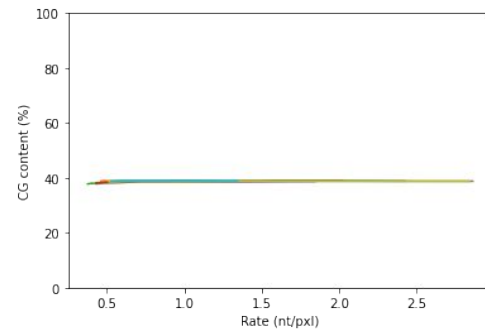
- Target CG content : between 40% and 50%.



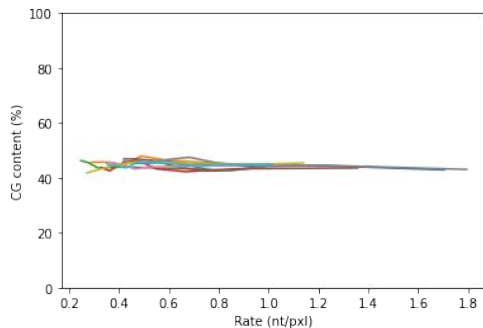
BC transcoder



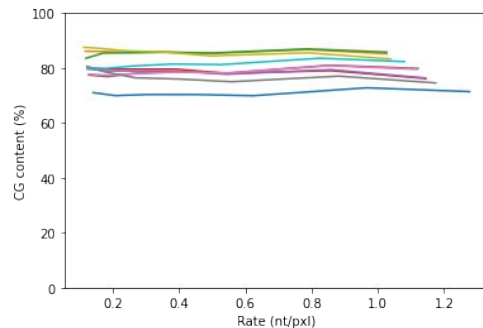
Anchor 1



Anchor 3



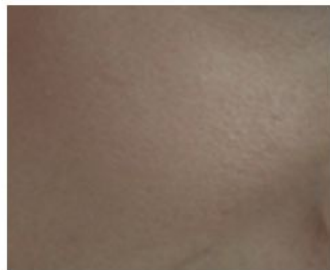
JPEG DNA benchmark codec



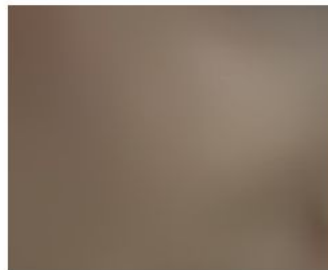
Learning-based

CG content of the DNA generated for all the images of the JPEG DNA data set

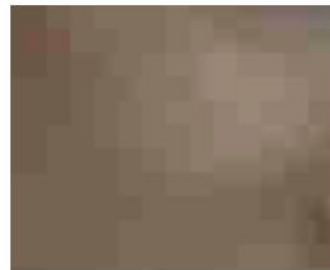
Subjective inspection



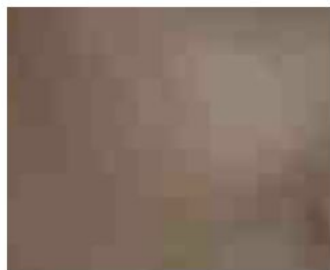
(a) Original



(b) Learning-based,
rate = 0.26 nts/pxl



(c) Benchmark codec,
rate = 0.32 nts/pxl



(d) BC transcoder,
rate = 0.27 nts/pxl



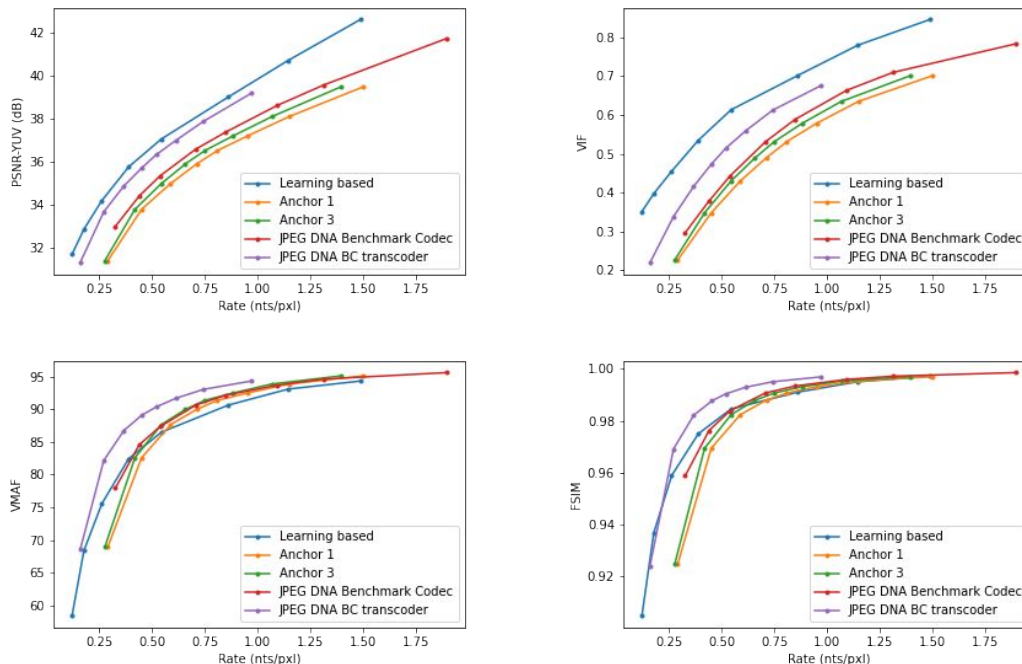
(e) Anchor 1, rate =
0.29 nts/pxl



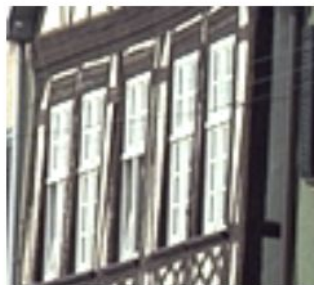
(f) Anchor 3, rate =
0.27 nts/pxl

■ Skin detail of the image 4 of the Kodak data set, decoded by the different models at a similar rate

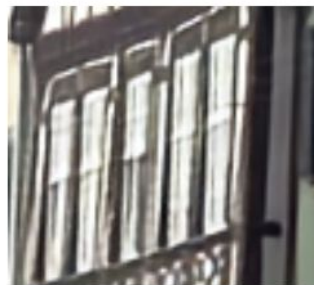
Rate-distortion plots for the image 4 of the Kodak dataset



PSNR-YUV, VIF, VMAF & FSIM of the image 4 of the Kodak at different rates



(a) Original



(b) Learning-based,
rate = 0.48 nts/pxl



(c) Benchmark codec,
rate = 0.64 nts/pxl



(d) BC transcoder,
rate = 0.56 nts/pxl



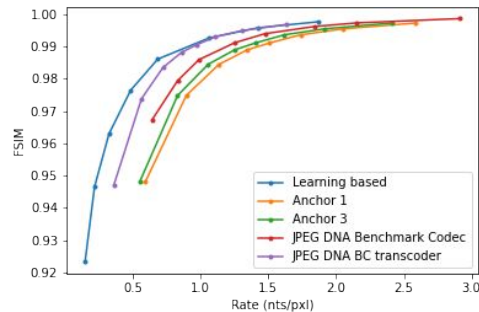
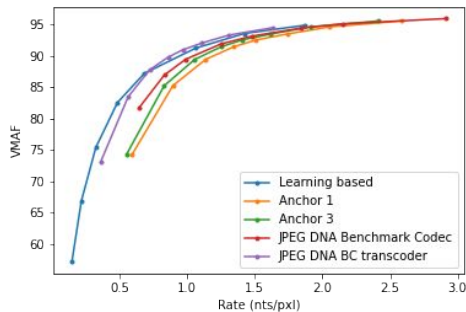
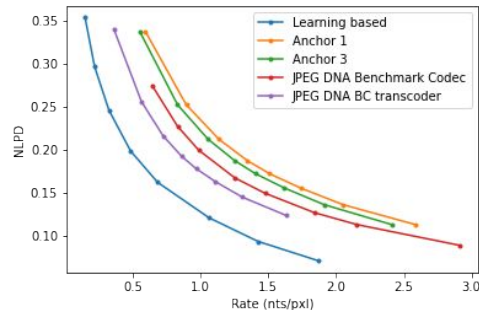
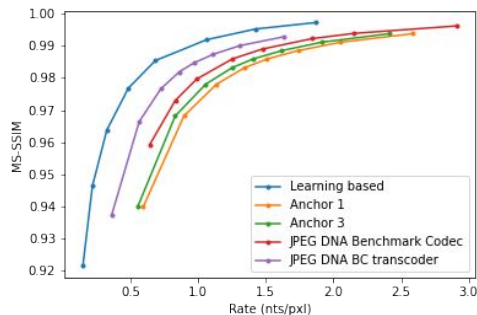
(e) Anchor 1, rate =
0.59 nts/pxl



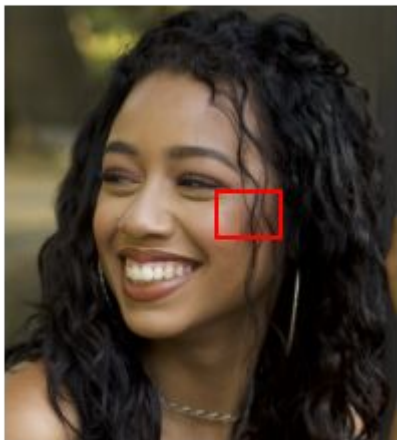
(f) Anchor 3, rate =
0.55 nts/pxl

Window detail of the image 8 of the Kodak data set, decoded by the different models at a similar rate

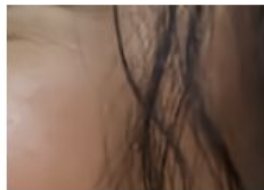
Rate-distortion plots for the image 8 of the Kodak dataset



MS-SSIM, NLPD, VMAF & FSIM of the image 8 of the Kodak dataset at different rates



(a) Original



(b) Learning-based,
rate = 0.50 nts/pxl



(c) Benchmark
Codec, rate = 0.49 nts/pxl



(d) BC
transcoder,
rate = 0.53
nts/pxl



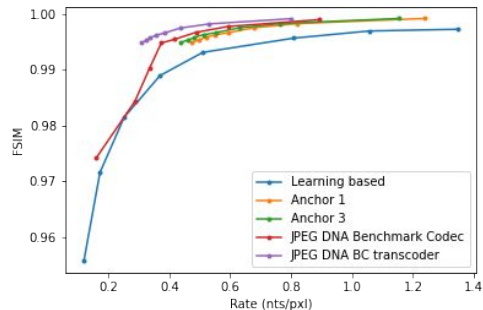
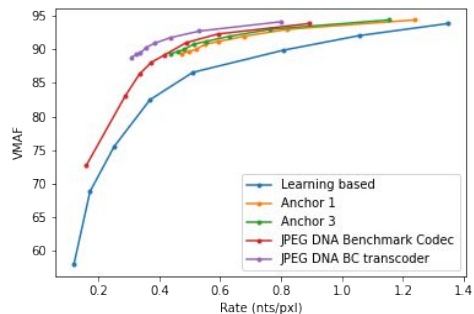
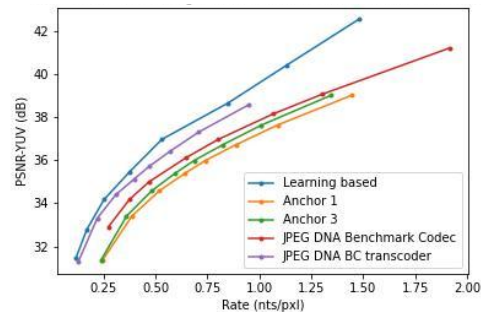
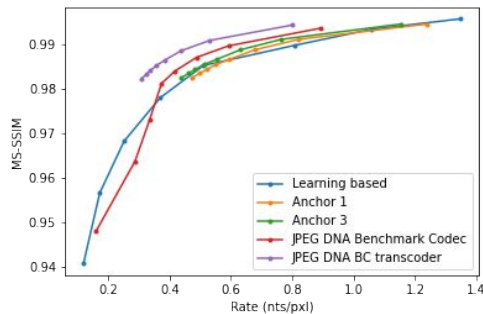
(e) Anchor 1,
rate = 0.55
nts/pxl



(f) Anchor 3,
rate = 0.51
nts/pxl

Skin & hair detail of the image 2 of the JPEG DNA data set, decoded by the different models at a similar rate

Rate-distortion plots for the image 2 of the JPEG DNA dataset



MS-SSIM, PSNR-YUV, VMAF & FSIM of the image 2 of the JPEG DNA at different rates

Learning-based autoencoder performance recap

- + Good performance on simple metrics
- Poor performance on advanced metrics
- + No homopolymers
- High CG content
- + Good visual evaluation

Project potential next steps

- Retrain the model using different networks
- Switch to more advanced autoencoders like JPEG AI
- Pattern repetition analysis in the generated DNA
- Lowering CG content in the generated DNA
- Integration of error detection & correction in the decoder



Multimedia Signal Processing Group

EPFL

<https://mmspg.epfl.ch/>

Thank you!

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