

Multi-View Channels and Applications

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Joint work with



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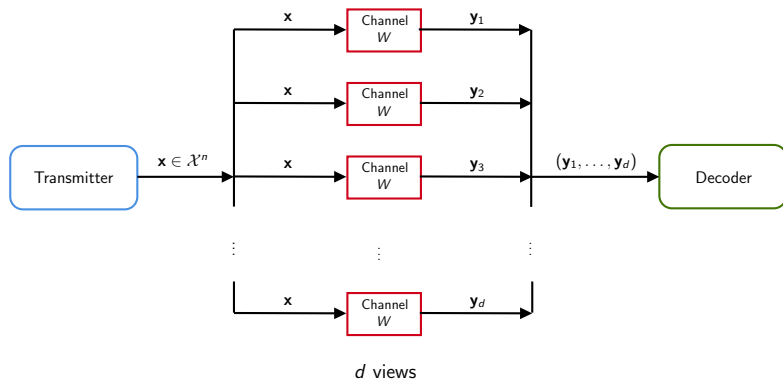


Itay Geva

M.Sc. Candidate
Technion, Israel

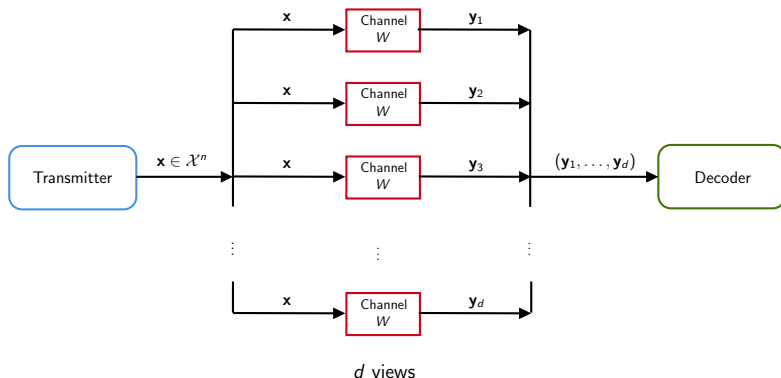
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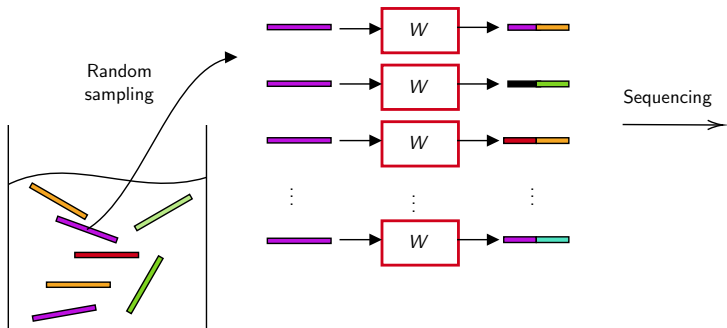


Q1: What rates are achievable with **vanishing reconstruction error probability**?

Q2: Can we use **A1** to obtain **achievable rates** over practical channel models for **modern storage media**?

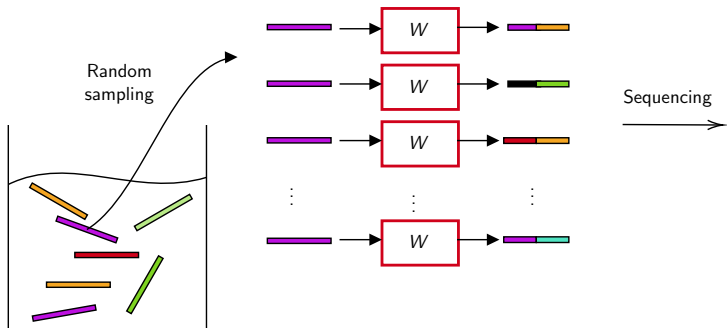
Where does this problem arise? - I

- ▶ Short molecules in a DNA pool are “amplified” by **Polymerase Chain Reaction** (PCR) and sampled multiple times [Shomorony and Heckel (2022)].



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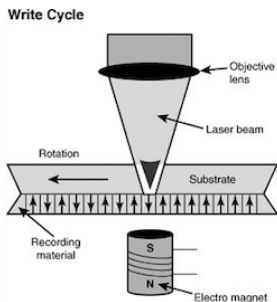
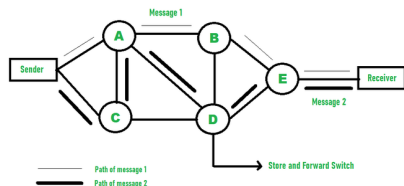
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- ▶ The capacity is determined by mutual information terms corresponding to **different # of views** of the input sequence; see [Lenz et al. (2019, 2020), Shomorony and Heckel (2022), Weinberger and Merhav (2022)].

Where does this problem arise? - II

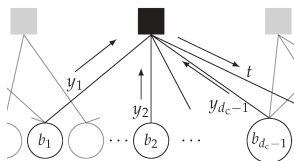
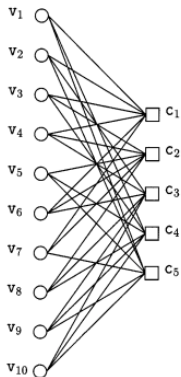
- ▶ Errors due to synchronization in packet-switched communications and in reading magneto-optical media



- ▶ Each output “run” at the end of (noisy) duplications corresponds to a multi-view channel [Mitzenmacher (2008), Cheraghchi and Ribeiro (2019)]

Where does this problem arise? - III

- ▶ More fundamentally, in the iterative decoding of LDPC codes [Gallager (1962), Richardson and Urbanke (2001)]



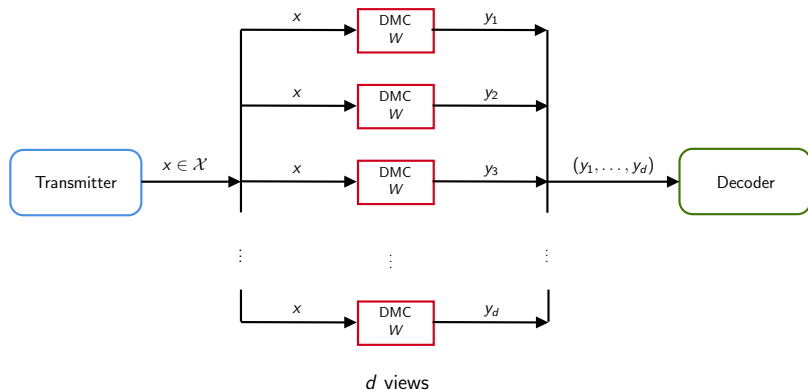
- ▶ A single variable node receives multiple “views” / estimates of its value, from different check nodes.

Answering **Q1** in the large view limit

A simpler setting: Multi-view DMCs

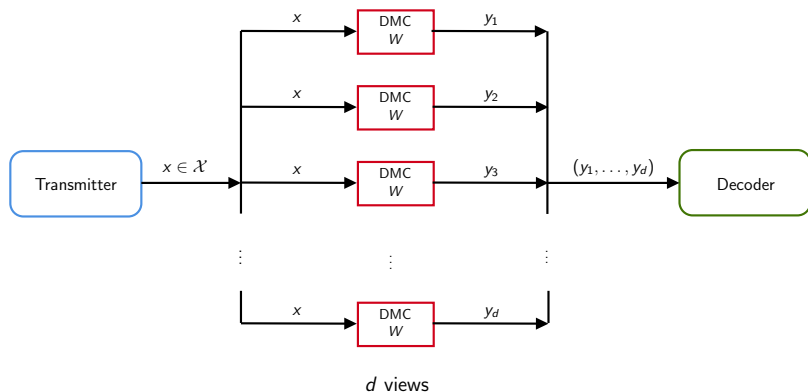
The setting, revisited

The decoder obtains d independent, noisy views of an input symbol.



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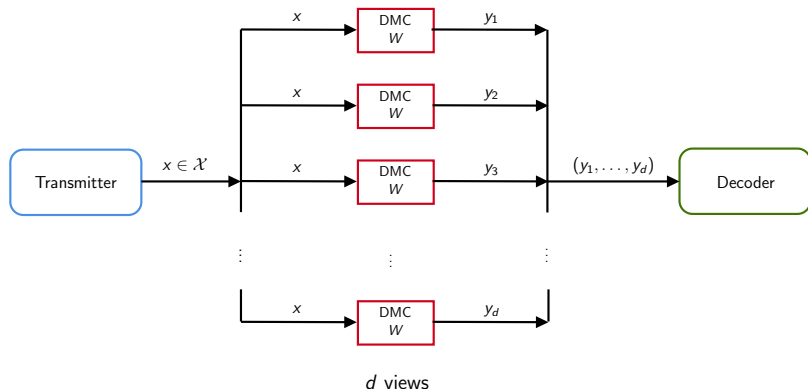
The decoder obtains d independent, noisy views of an input symbol.



Since a multi-view DMC is also a DMC, it suffices for us to focus on the transmission of a single symbol, for rate computations.

The setting, revisited

The decoder obtains d independent, noisy views of an input symbol.



Goal: Exact asymptotics of the mutual info. (+ capacity) and dispersion of such a multi-view channel, for arbitrary P_X .

What is known about this setting?

- ▶ Hellman and Raviv (1970), Kanaya and Han (1995): Exact asymptotics of information rates over DMCs with multiple views
- ▶ Levenshtein (2001): Characterization of $\#$ of views for exact reconstruction over comb. error channels and for reconstruction with **decaying** error prob. over multi-view DMCs

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- ▶ Mitzenmacher (2006): Calculation of the capacity of a multi-view binary symmetric channel (BSC)
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Our contributions:

1. Unified treatment of info. rate and channel dispersion



Finite-blocklength achievable rates with **fixed** error probability

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Our contributions:

2. Directly extensible proofs for **multi-letter** channels

Background

Some formalism

- ▶ Consider a DMC W with input alphabet \mathcal{X} and output alphabet \mathcal{Y} , both finite. Assume that $|\mathcal{X}|, |\mathcal{Y}|$ **do not** depend on d .
- ▶ The d -view **DMC** $W^{(d)}$ obeys the channel law

$$W^{(d)}((y_1, \dots, y_d) | x) = \prod_{i=1}^d W(y_i | x),$$

for $(y_1, \dots, y_d) \in \mathcal{Y}^d$ and $x \in \mathcal{X}$.

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- ▶ Fix a d -independent input distribution P_X . We are interested in:

$$I^{(d)} = I(X; Y^d) = H(X) - H(X | Y^d) \quad \text{[Mutual info.]}$$

and

$$V^{(d)} = \mathbb{E} \left[(\iota(X; Y^d) - I^{(d)})^2 \right], \quad \text{[Channel dispersion]}$$

where

$$\iota(X; Y^d) = \log \frac{P(Y^d | X)}{P(Y^d)}. \quad \text{[Info. spectrum]}$$

Building intuition: Multi-view BSC^(d)

Consider the d -view BSC(p), with binary input $X \in \{0, 1\}$:

$$Y = X + Z \pmod{2},$$

where $Z \sim \text{Ber}(p)$.

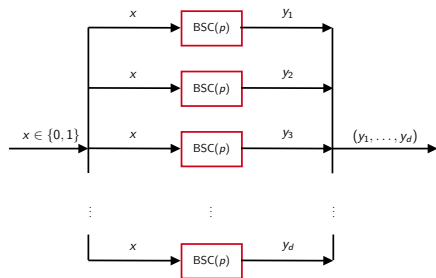
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Consider the d -view BSC(p), with binary input $X \in \{0, 1\}$:

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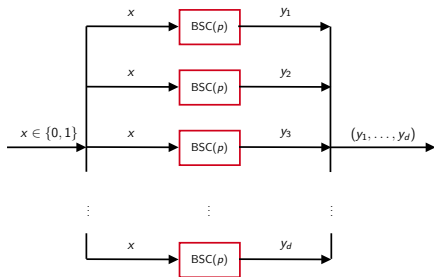
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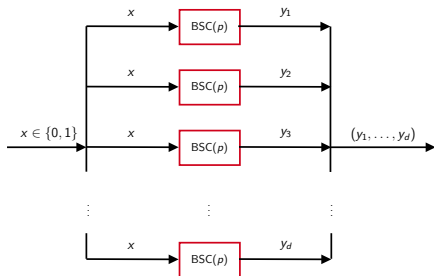
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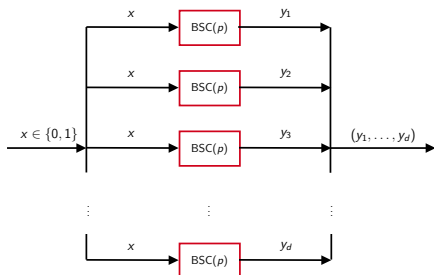
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$$\Pr[X \neq M] \leq \exp(-dZ(p)),$$

where $Z(p) = 2\sqrt{p(1-p)}$.

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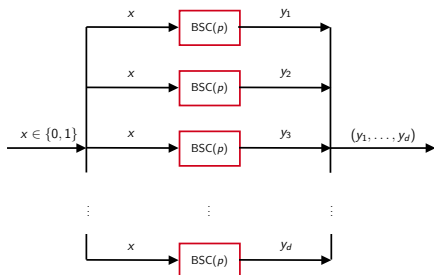
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Hence, for large d :

$$\begin{aligned} h_b(\Pr[X \neq M]) &\leq -2 \Pr[X \neq M] \cdot \log \Pr[X \neq M] \\ &= 2dZ(p) \cdot \exp(-dZ(p)). \end{aligned}$$

Building intuition: Multi-view BSC^(d)



This gives us

$$I(X; Y^d) \geq \log 2 - 2dZ(p) \cdot \exp(-dZ(p)).$$

Exponentially fast convergence to $H(X) = \log 2$

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Our Results

Our main result

- ▶ Intuitively, as d becomes large, we expect $I^{(d)} \approx H(X)$ and

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- ▶ For distributions P, Q on \mathcal{X} , define the **Chernoff information**

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Theorem

When $\mathcal{X}, \mathcal{Y}, P_X$ do not depend on d ,

$$I^{(d)} = H(X) - \exp(-d\rho + \Theta(\log d|\mathcal{X}|)), \text{ and}$$

$$\left| V^{(d)} - V(X) \right| = \exp(-d\rho + \Theta(\log d|\mathcal{X}|)),$$

where

$$\rho = \min_{x, x': x \neq x'} C(P_{Y|x}, P_{Y|x'}).$$

Interpreting the result

- ▶ The rate of convergence ρ of the mutual information and channel dispersion to their limits

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- ▶ For a binary-input memoryless symmetric (BIMS) channel W , the rate

$$\begin{aligned}\rho &= -\log \sum_{y \in \mathcal{Y}} \sqrt{P_{Y|0}(y|0)P_{Y|1}(y|1)} \\ &= -\log Z_b(W),\end{aligned}$$

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Hence, our earlier speed of convergence for the BSC^(d) is **tight**!

A finite blocklength corollary

- ▶ A characterization of finite-blocklength rates achievable over $W^{(d)}$, thus follows.
- ▶ For a **fixed** $\epsilon \in (0, 1)$ and blocklength $n \geq 1$, let
$$M^*(n, \epsilon) \leftarrow \text{largest } M \text{ s.t. } \exists \text{ length-}n \text{ code over } W^{(d)} \\ \text{with max. error } \epsilon.$$

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If W is “non-singular”, we have

$$\log |\mathcal{X}| - \frac{\log M^*(n, \epsilon)}{n} \leq e^{-d\rho + \Theta(\log d|\mathcal{X}|)} - \Phi^{-1}(\epsilon) \cdot \frac{e^{-d\rho/2 + \Theta(\log d|\mathcal{X}|)}}{\sqrt{n}} + \Theta\left(\frac{\log n}{n}\right).$$

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- ▶ In particular, choosing $d = \rho^{-1} \log n$, we can achieve rates

$$R_{n,\epsilon} \geq \log |\mathcal{X}| - O_\epsilon\left(\frac{\log n}{n}\right).$$

An Application: Achievable Rates Over Noisy
Nanopore Channels

What is the talk about?

- ▶ We are interested in nanopore-based DNA sequencing – a third generation technology in the sequencing of biopolymers.

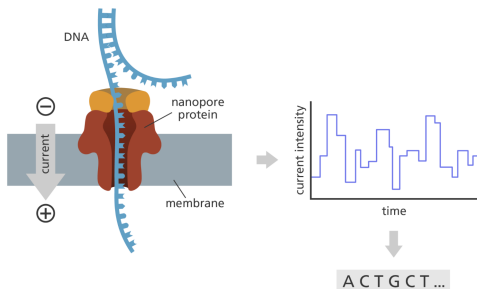


Image credit: Laura Olivares Boldú, Wellcome Connecting Science

- ▶ A nanopore sequencer can read strands of length 10–100 Kilo-bases, which is significantly larger than the read capability of other sequencers (≈ 100 bases).

How does a nanopore sequencer work?

- ▶ The bases of (single-stranded) DNA are “ratcheted” (translocated) through the nanopore, which is a microscopic pore.

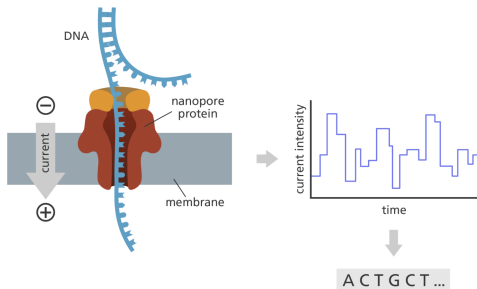


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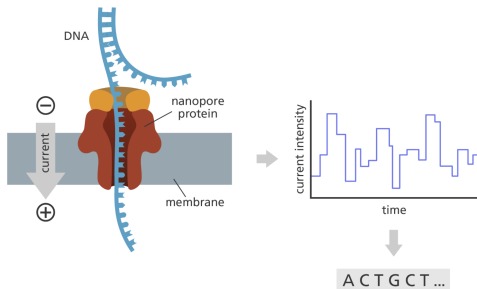


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- ▶ This traversal of bases creates electric current flow – a function of the bases in the nanopore – which can then be measured.
- ▶ Predictably, such measurements are **error prone**.

Error sources and modelling

The following types of errors corrupt nanopore reads:

[Mao, Diggavi, Kannan (2018); Hulett, Chandak, Wootters (2021); Hamoum et al. (2021); McBain, Viterbo, Saunderson (2024)]

1. Intersymbol interference (ISI): **non-trivial nanopore width**
2. “Backtracking” / “skipping”: **imperfect translocation speed**
3. Measurement noise: **random noise in current readings**

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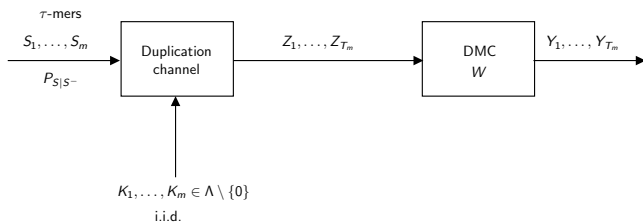
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These errors can be modelled by the following abstractions:

1. Intersymbol interference (ISI): **Block-Markov inputs**
2. “Backtracking” / “skipping”: **Insertion/deletion errors**
3. Measurement noise: **Memoryless noise**

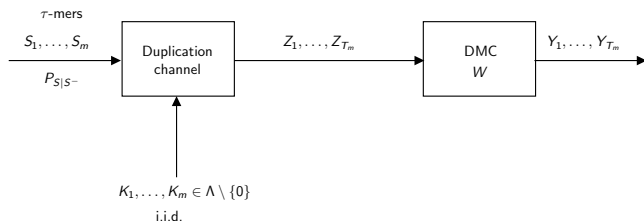
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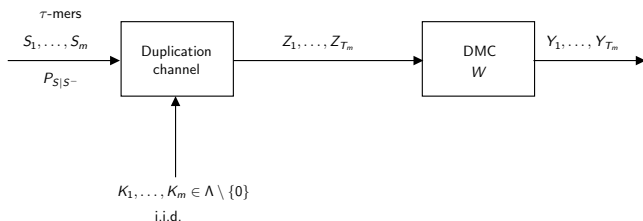


Quick description:

1. (S_1, \dots, S_m) : “de-Bruijn”-Markov input sequence of contiguous length- τ subsequences of input bases $B_1, \dots, B_{m+\tau-1} \in \mathcal{X}$
2. Each symbol S_i is **repeated** K_i times, leading to Z^{T_m} , where $T_m = \sum_{i \leq m} K_i$.
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Q: What information rates are achievable over such a channel W_{nn} ?

Contributions in our work

Theorem (McBain, Viterbo, Saunderson (2024))

The capacity of W_{nn} is

$$C(W_{nn}) = \sup_{P_{S|S^-}} \lim_{m \rightarrow \infty} \frac{1}{m} I(S^m; Y^{T_m}),$$

where the sup. is over all stationary and ergodic transition kernels $P_{S|S^-}$.

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Our contributions:

1. Explicit computation of the capacity without DMC noise
2. Computable bounds on capacity for general, noisy nanopore channels (NNCs)
3. Low-complexity, high-rate encoding/decoding algorithms when $W = EC$
4. Change-point detection-based decoder for high current measurement (“sampling”) rates

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4. Change-point detection-based decoder for high current measurement (“sampling”) rates

NNCs Under High Sampling Rates

Setup and intuition

- ▶ We focus on the setting of high “sampling rates,” or high rates of current measurements.
- ▶ The sampling rate is controlled by the system designer, e.g., a more recent Oxford Nanopore Technologies sequencer has a sequencing speed of 450 b/s.

[Wick, Judd, Holt (2019), Zeng et al. (2020)]

- ▶ High sampling rates give rise to several duplications of each base.
- ▶ Intuitively, this leads to several **noisy views** of each τ -mer, allowing for reliable recovery.

High sampling rate regime

- ▶ We recommend that the designer set sampling rates high enough so that

$$P_K(\ell_m \leq K \leq h_m) \geq 1 - \frac{1}{m^{1+\eta}},$$

for some $\eta > 0$, where $\ell_m = m^2(\ln m)^3$ and $h_m = \gamma m^2(\ln m)^3$, for some $\gamma > 1$.

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High sampling rate regime

- ▶ We recommend that the designer set sampling rates high enough so that

$$P_K(\ell_m \leq K \leq h_m) \geq 1 - \frac{1}{m^{1+\eta}},$$

for some $\eta > 0$, where $\ell_m = m^2(\ln m)^3$ and $h_m = \gamma m^2(\ln m)^3$, for some $\gamma > 1$.

- ▶ Our decoder computes change-point instants and employs a **MAP decoder** between change-points.

see [Laszlo et al. (2014)] for a change-point detection-based decoder in nanopore sequencing

- ▶ The existing analysis of multi-view information rates helps us obtain a handle on MAP error probability between change-points.

Our change-point detection-based decoder DECODE

Fix a **false-alarm probability** $\alpha_m = \frac{1}{m^3(\ln m)^4}$ and a **trimming length** $c_m = m(\ln m)^2$.

$$Y_1 \quad Y_2 \quad Y_3 \quad Y_4 \quad \dots \quad Y_{T_1-1} \quad Y_{T_1} \quad Y_{T_1+1} \quad \dots \quad Y_{T_2} \quad Y_{T_2+1} \dots Y_{T_m}$$

Our change-point detection-based decoder `DECODE`

Fix a **false-alarm probability** $\alpha_m = \frac{1}{m^3(\ln m)^4}$ and a **trimming length** $c_m = m(\ln m)^2$.

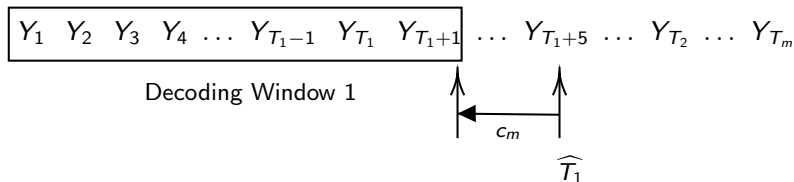
$$Y_1 \quad Y_2 \quad Y_3 \quad Y_4 \quad \dots \quad Y_{T_1-1} \quad Y_{T_1} \quad Y_{T_1+1} \quad \dots \quad Y_{T_1+5} \quad \dots \quad Y_{T_2} \quad \dots \quad Y_{T_m}$$

\uparrow
 \widehat{T}_1

- Use the Shiryaev algorithm to obtain a change-point estimate with false-alarm prob. α_m .

Our change-point detection-based decoder DECODE

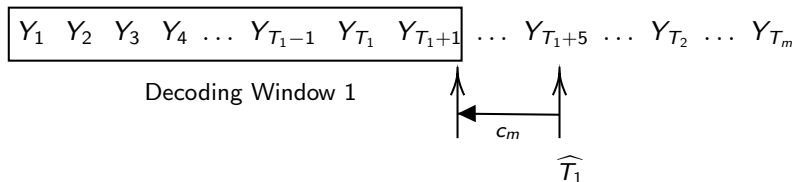
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- ▶ Use the Shiryaev algorithm to obtain a change-point estimate with false-alarm prob. α_m .
- ▶ Trim by c_m to obtain the **decoding window**.
- ▶ Use the **MAP decoder** in the decoding window to obtain an estimate of the first τ -mer.

Our change-point detection-based decoder **DECODE**

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- ▶ Use the Shiryaev algorithm to obtain a change-point estimate with false-alarm prob. α_m .
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Recurse from the end of the window.

Main result

With the aid of properties of the Shiryaev algorithm, we obtain the following results:

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Theorem

For any no-self-loop de Bruijn Markov $P_{S|S^-}$, in the high sampling-rate regime,

$$\lim_{m \rightarrow \infty} \Pr [\text{DECODE}(Y^{T_m}) \neq S^m] = 0.$$

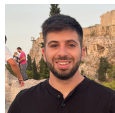
Theorem

In the high sampling-rate regime, rates of up to $C_{\tau}^{\text{no-noise, no-loop}}$ are achievable using DECODE.

Ongoing/Future work

- ▶ How many points can we pack into a (high-dimensional) probability simplex that are ϵ -separated in Chernoff distance?
 - ▶ Chernoff sep. \equiv Rate of $\rightarrow H(X)$
 - ▶ Points in prob. simplex \equiv Messages in composite DNA storage

- ▶ Concatenated multi-view channels? Feedback?



Thank You!