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UNIV. OF CAMBRIDGE
Dept. of Engineering
SigProC Lab

Codes for efficient data storage on DNA molecules

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Your mission: save the world!

- Mankind is self-destructing
- We will lose all technology and knowledge
- Archive our information so it remains accessible when all current technology is lost

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My partners

David MacKay

Nick Goldman

Emily Hesketh

Roland Schwarz

Ewan Birney

DNA Storage

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Store information on DNA!

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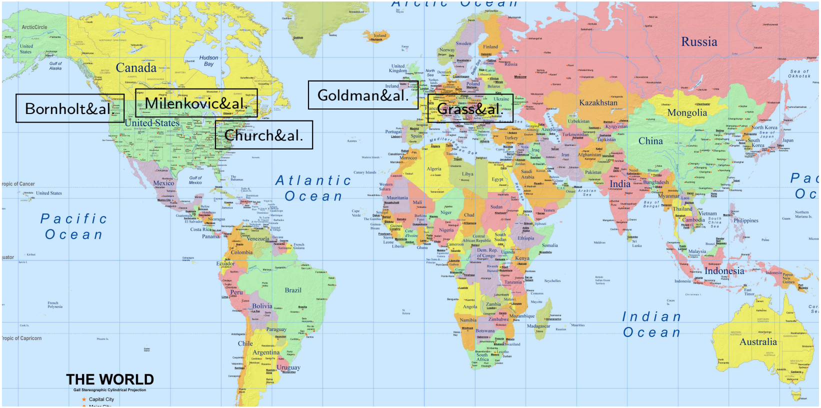


Bornholt&al.

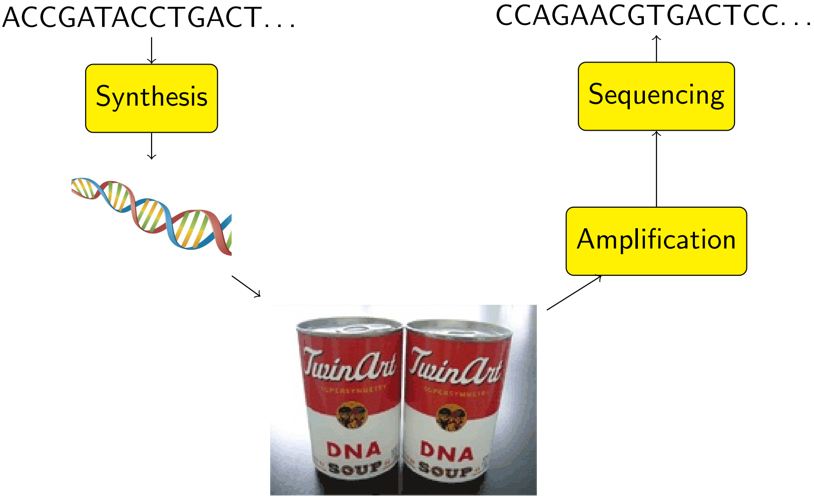
Milenkovic&al.

Goldman&al.

Grass&al.

Church&al.

DNA Storage



ACCGATACCTGACT. . .

Synthesis

Sequencing

Amplification

CCAGAACGTGACTCC. . .

DNA Storage

- Synthesis: order from a handful of companies, slow, expensive
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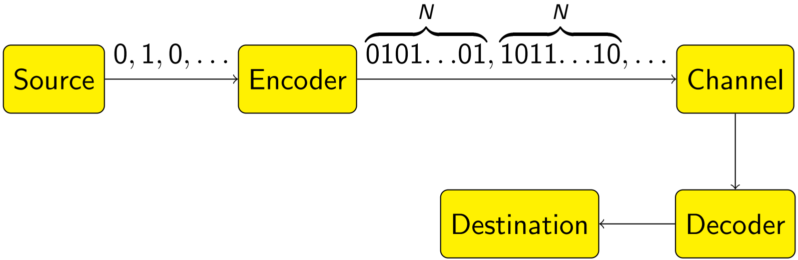
Current and future work:

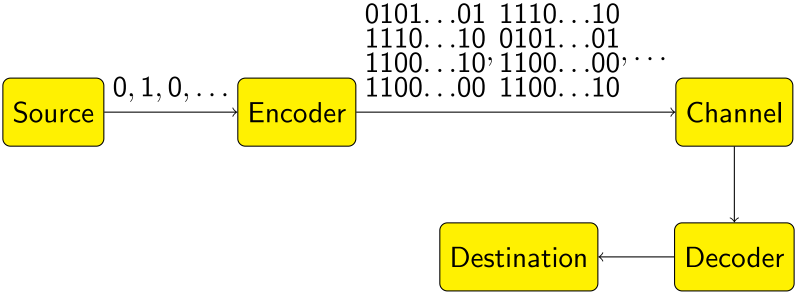
- Probabilistic characterisation of the storage channel
- Dedicated coding techniques
- Optimised data rates (kbit per \$) and reliability (10^{-n} error probabilities for $n = 6, 7, 8, \ldots$)

“Normal” symbol coding


Source
$0, 1, 0, \ldots$
Encoder
$\overbrace{0101\ldots01}^{N}, \overbrace{1011\ldots10}^{N}, \ldots$
Channel
Decoder
Destination

$$\boxed{N \gtrsim 10,000}$$

Packet coding

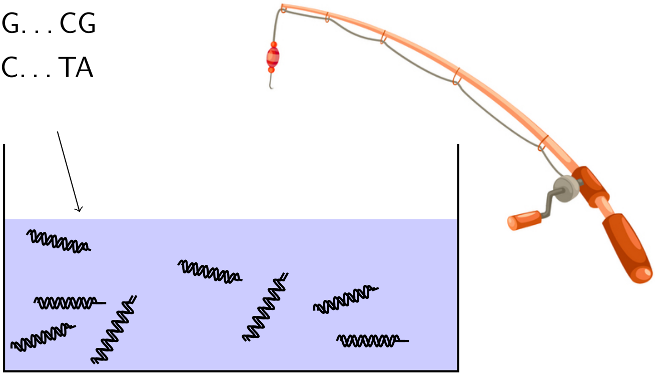

Source
$0, 1, 0, \ldots$
Encoder
$\begin{matrix}0101\ldots01\\1110\ldots10\\1100\ldots10\\1100\ldots00\end{matrix}, \begin{matrix}1110\ldots10\\0101\ldots01\\1100\ldots00\\1100\ldots10\end{matrix}, \ldots$
Channel
Decoder
Destination

$$\boxed{\text{Packet size} \simeq 8 - 10,000, \ \text{Codeword length} \simeq 100 - 10,000}$$

The DNA Soup Channel

$$\overset{N \simeq 200}{\longleftrightarrow}$$

1. ACGCA. . . AT
2. GGACT. . . TG
3. ATCTG. . . GA
4. TTACG. . . CG
5. GCTAC. . . TA
6. . . .



The DNA Soup Channel

- DNA is quaternary
- Synthesis/sequencing constraints dictate DNA strand lengths in the 100s
- Too short for proper coding
- Difficult but feasible size for “packet” coding
- But:

- Packet order is lost in the soup
- Identical packets (out of order) are indistinguishable

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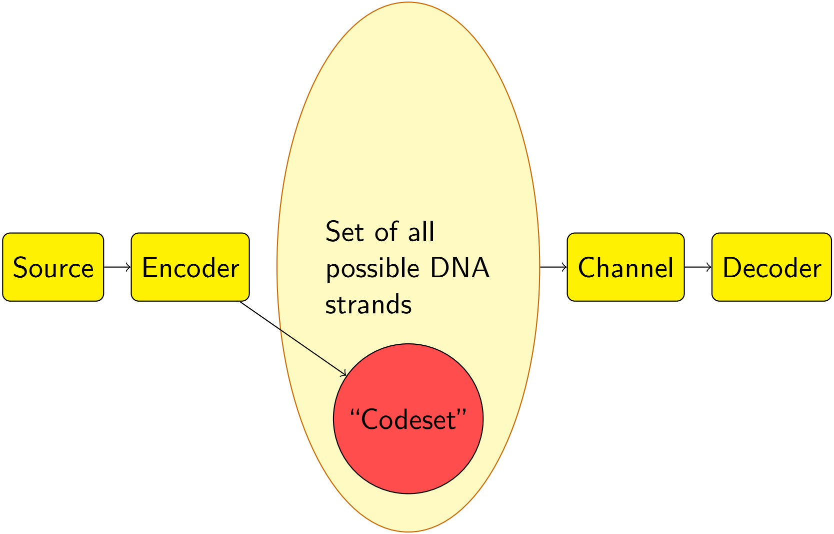
What are the theoretical limits for storage in the DNA soup channel?

Subset coding à la MacKay



Subset coding à la MacKay

- The decoder obtains (possibly repeated) noisy observations of the elements in the codeset.
- Its role is to determine which codeset the encoder selected.
- The “codesets” take up the role of “codewords” in traditional coding.

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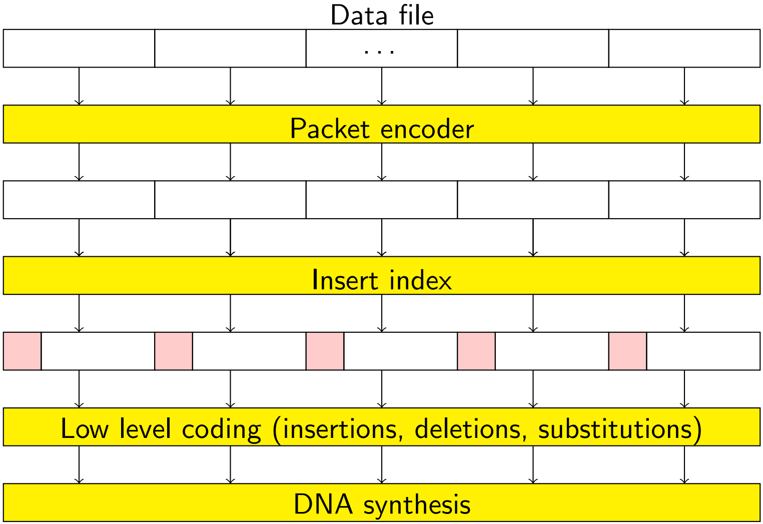
For the noiseless channel, optimal construction:

- Prefix of DNA packet runs through an index sequence 0,1,2,3,. . .
- Remaining portion of DNA packet determined by traditional encoder where the index maps the position of the symbol in the codeword
- This is equivalent to fountain coding, indexed Reed Solomon coding and indexed random linear coding.

Current system



Current system

- “Noisy fountain coding” through low-level high rate intra-packet coding (similar to [Venkiah, Poulliat Declercq] papers
- The “index” portion needs perfect protection or the system fails

This is not optimal and the “graal” of noisy DNA soup channel coding would be to invent a true codeset coding system.

Current work

- Channel measurement and estimation
- Evaluate low-level codes (Marker codes [Ratzer&MacKay], watermark codes [Davey&MacKay], convolutional codes)
- Evaluate packet encoders (Fountain, RS codes)
- Unequal error protection for the index
- Direct codeset coding for the noisy DNA soup channel

Ethical questions

- If "Mankind version 1.0" is so terrible, should we store our knowledge at all?
- Will future intelligent life know about Reed Solomon codes?
- Who says we are version 1.0?