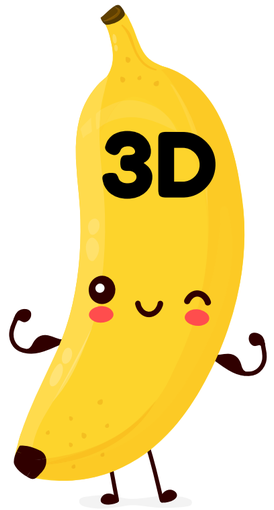
Unlocking the Power of ncRNA: Predicting Pathogenic SNPs for Next-Generation Treatments



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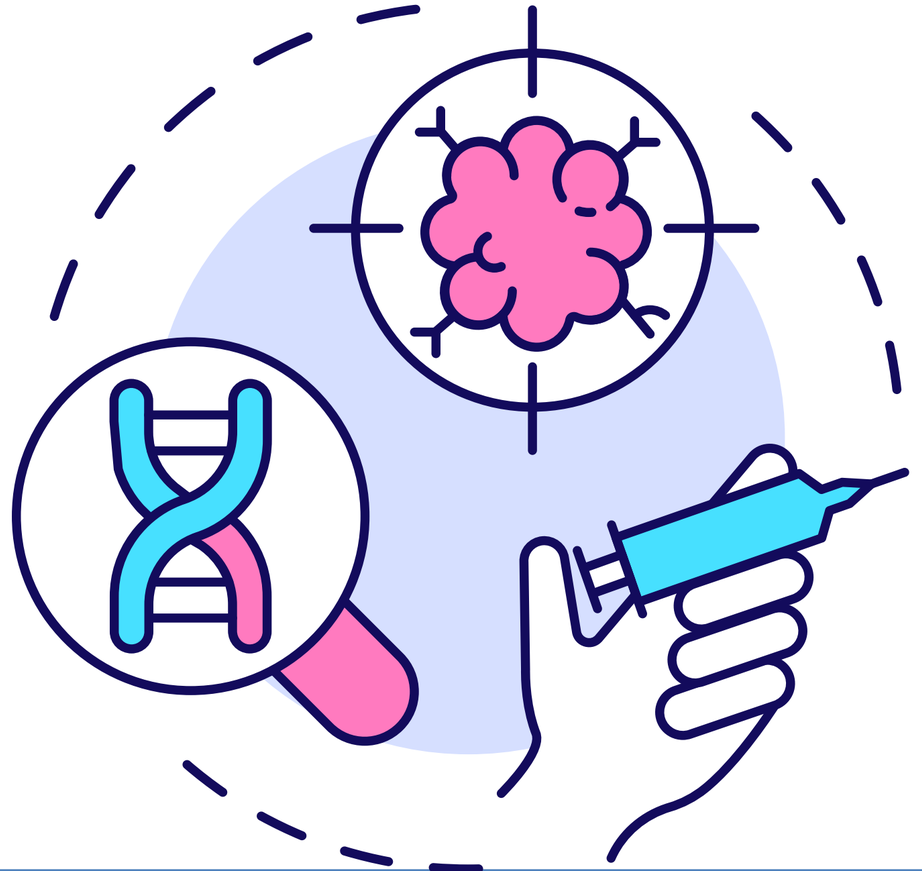
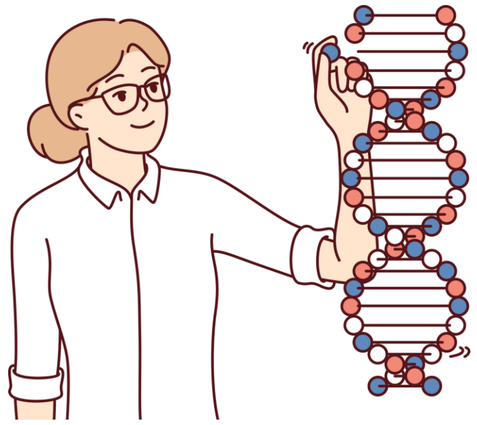


What is non-coding RNA (ncRNA)?

Does not code for proteins but regulates gene expression.

Why it matters: ncRNAs help control processes like gene regulation, splicing, and tumor suppression.

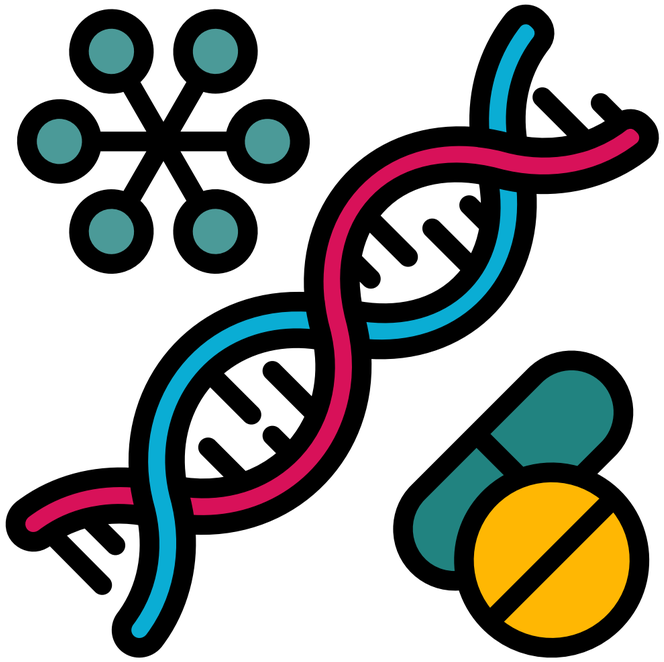
ncRNA is a hidden layer of genetic regulation that could unlock new treatments.



Why Focus on ncRNA in Cancer?

ncRNA, can uncover new biomarkers and therapeutic targets that are missed by traditional protein-coding gene-based approaches.

ncRNA variants can influence cancer progression in ways that protein-coding mutations cannot fully explain.



What are SNPs?

SNP (Single Nucleotide Polymorphism) is a change in a single base pair in the DNA sequence. Example:

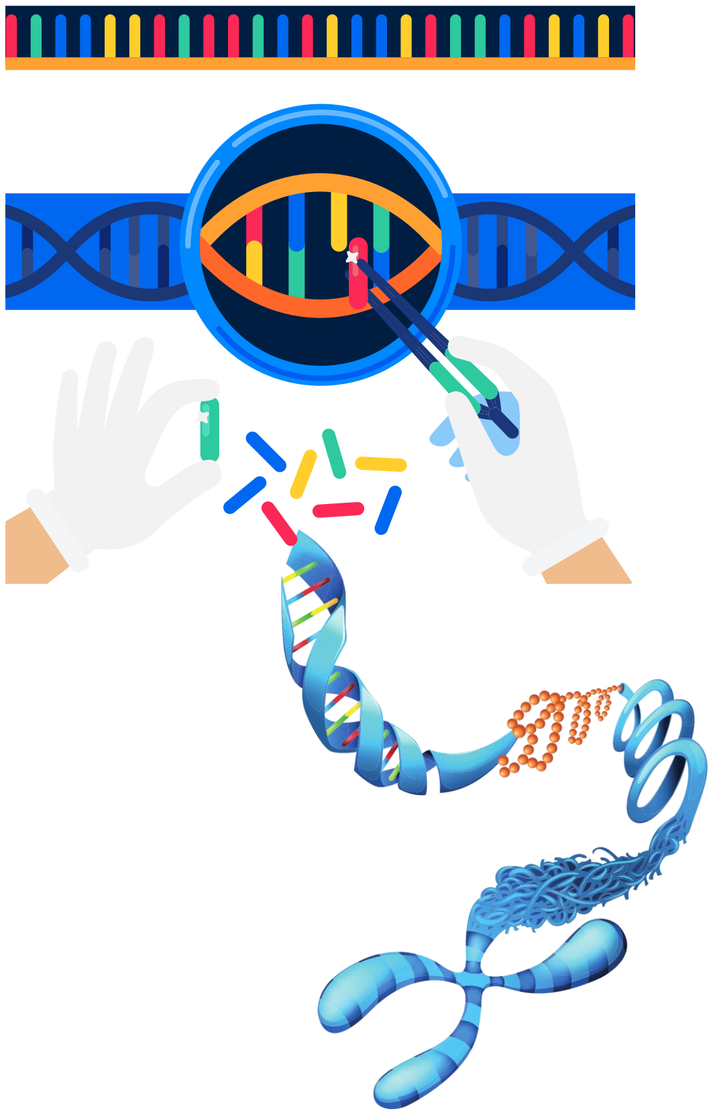
Original: AAGCCTA

SNP Variant: AAGCTTA

Some SNPs can be pathogenic (disease-causing), while others may have no effect.

The Challenge: Predicting Pathogenic SNPs in ncRNA

- Cancer treatments are often not personalized, leading to poor outcomes for some people.
- ncRNA mutations are understudied compared to protein-coding mutations.
- Predict which SNPs are pathogenic and personalize cancer treatment.



Our Solution

1: Deep Learning for ncRNA Analysis

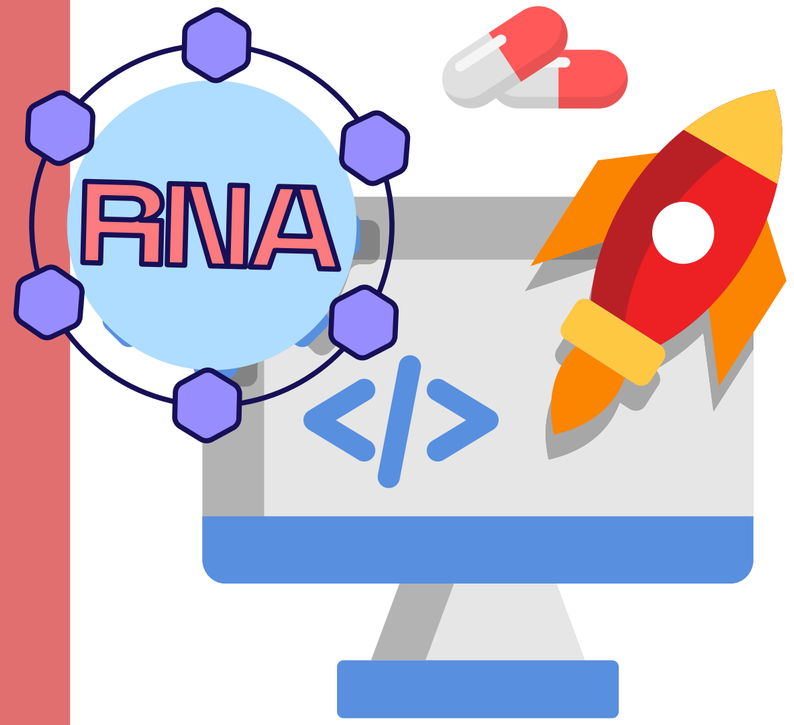
- Using AI to assess how SNPs affect ncRNA structure and function.
- RNA-FM model: Encodes ncRNA sequences into features that capture both sequence and evolution information.

2: Focus on Pathogenic SNPs

How It Works: Predicting Pathogenic SNPs

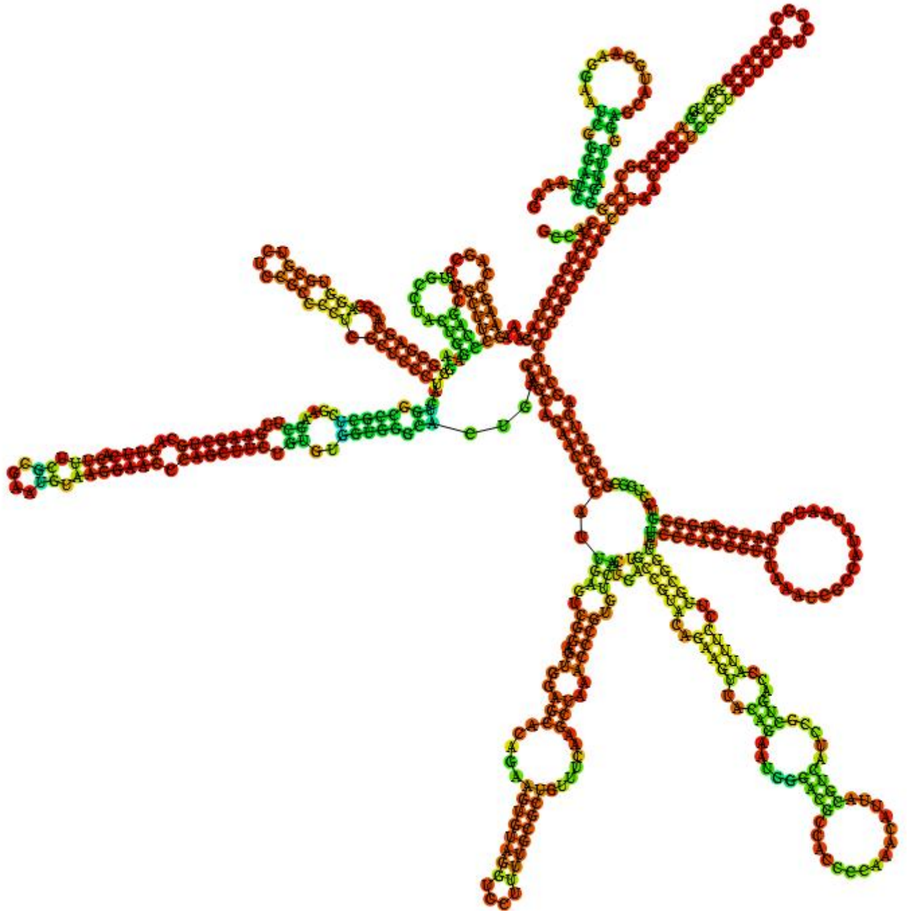
We used data from:

- ncRNA-eQTL: SNPs linked to gene expression and cancer survival.
- dbSNP: A large database of known SNPs.
- Rank genes based on how many pathogenic SNPs are present in a patient's ncRNA.
- Biomarker-based stratification helps personalize treatment decisions for cancer patients.



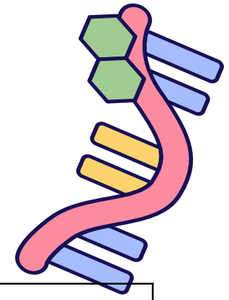
Identifying New Drug Targets in ncRNA

- SNPs in ncRNA disrupt its secondary structure, changing the loops and effecting the function.
- These structural changes are druggable regions, ideal for targeted therapies.
- RNA-FM helps identify these vulnerabilities by predicting the RNA structure.



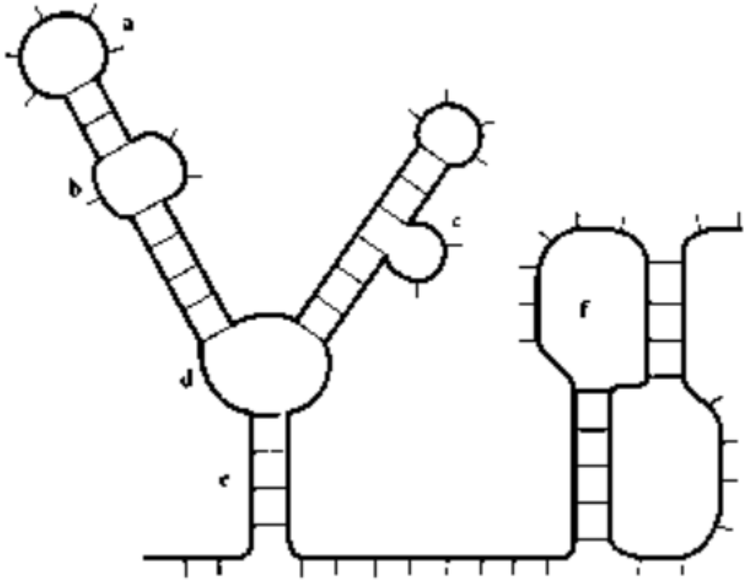
http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi

Mocked Results



	Cancerous SNP	Regular SNP
Hairpin Loop	10	18
Internal Loop	15	22
Multibranched Loop	11	20
Stem	40	21
Pseudoknot	30	19

Various RNA secondary structure patterns



a. hairpin loop
b. internal loop
c. bulge loop
d. multibranched loop
e. stem
f. pseudoknot
(http://ludwig-sun2.unil.ch/~bsondere/nussinov/)

This is what we hope the results will look like: the cancerous SNPs are in structurally significant parts of the RNA. We will examine regular SNPs as a negative control, and hopefully they will be evenly distributed over all RNA structures.

Conclusion: Transforming Personalized Cancer Treatment

- Our solution predicts pathogenic SNPs in ncRNA to guide personalized cancer treatments.
- Better understanding of ncRNA's role in cancer helps optimize therapy and improve patient outcomes.
- Using ncRNA variants to develop more precise, tailored next generation treatments.