

CSE 20

DISCRETE MATH

Fall 2020

<http://cseweb.ucsd.edu/classes/fa20/cse20-a/>

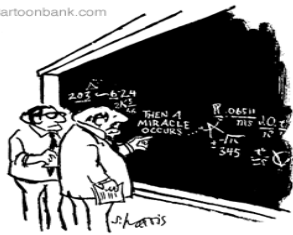
Today's goal

- Review content from first half of course
- Connect recurring examples to broader CS themes and learning outcomes of CSE 20

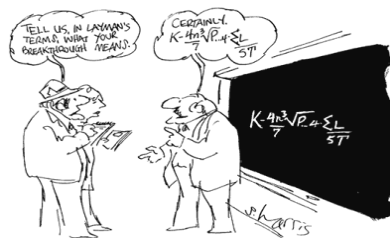
Recurring examples in CSE 20

- Netflix ratings and machine learning
- RNA and DNA: genomics and bioinformatics
- Codes: secret messages and error correction
- “Under the hood” of computers (e.g. circuits, color representation, data structures)

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"I think you should be more explicit here in step two."



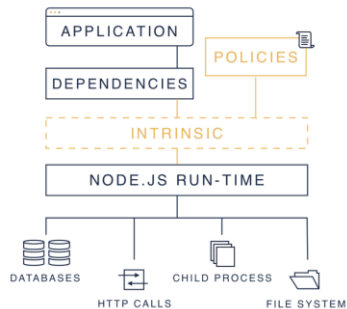
Building secure web applications

How it works

Unlike most runtime security solutions, which try to defend against application-level attacks by analyzing or monitoring behavior, Intrinsic protects against attacks by enforcing that your Node.js code only executes as expected.

Intrinsic is a new virtualization technology that lives in the Node.js language runtime. It blocks all privileged operations that are not whitelisted by your security policies.

Protecting your app is simple: include the Intrinsic library, write security policies, and Intrinsic makes sure your app runs safely.



Deian Stefan
UCSD CSE

“clean-slate approach to building secure, low-level systems and applications (e.g., remote shells and web servers), even if building secure systems applications is notoriously difficult”

Consider the following algorithm to introduce redundancy in a string of 0s and 1s.

Create redundancy by repeating each bit three times

```
1 procedure redun3( $a_{k-1}\cdots a_0$ : a binary string)
2 for  $i := 0$  to  $k-1$ 
3    $c_{3i} := a_i$ 
4    $c_{3i+1} := a_i$ 
5    $c_{3i+2} := a_i$ 
6 return  $c_{3k-1}\cdots c_0$ 
```

Decode sequence of bits using majority rule on consecutive three bit sequences

```
1 procedure decode3( $c_{3k-1}\cdots c_0$ : a binary string whose length is an integer multiple of 3)
2 for  $i := 0$  to  $k-1$ 
3   if exactly two or three of  $c_{3i}, c_{3i+1}, c_{3i+2}$  are set to 1
4      $a_i := 1$ 
5   else
6      $a_i := 0$ 
7 return  $a_{k-1}\cdots a_0$ 
```

Give a recursive definition of the set of outputs of the *redun3* procedure, *Out*,

Basis step: _____

Recursive step: _____

Roster method? Set builder notation?

Consider the message $m = 0001$ so that the sender calculates $redun3(m) = redun3(0001) = 000000000111$.

Introduce ____ errors into the message so that the signal received by the receiver is _____ but the receiver is still able to decode the original message.

What are correct ways to fill in the blanks?

- A. 2 errors, received signal is 000000000001
- B. 5 errors, received signal is 110111000111
- C. 4 errors, received signal is 100010010101
- D. More than one of the above
- E. None of the above

Building a circuit for line 3 in *decode* procedure: given three input bits, we need to determine whether the majority is a 0 or a 1.

How many inputs and outputs for this circuit?

- A. 1 input and 1 output
- B. 3 inputs and 1 output
- C. 1 input and 3 outputs
- D. 3 inputs and 3 outputs
- E. None of the above

Building a circuit for line 3 in *decode* procedure: given three input bits, we need to determine whether the majority is a 0 or a 1.

c_{3i}	c_{3i+1}	c_{3i+2}	a_i
1	1	1	
1	1	0	
1	0	1	
1	0	0	
0	1	1	
0	1	0	
0	0	1	
0	0	0	

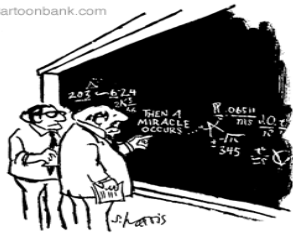
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c_{3i}	c_{3i+1}	c_{3i+2}	a_i
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1	1	0	
1	0	1	
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0	1	1	
0	1	0	
0	0	1	
0	0	0	

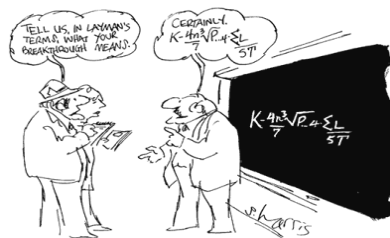
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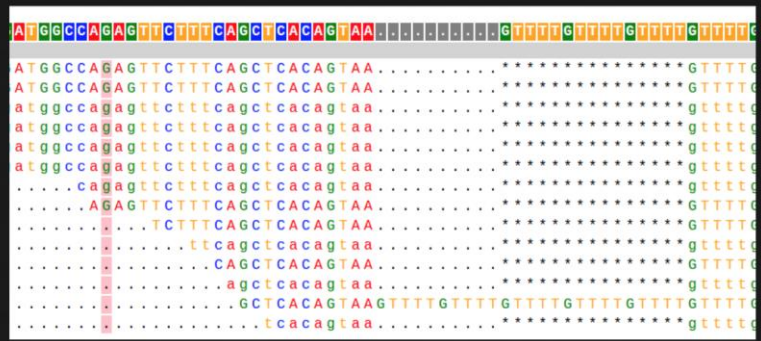


Genome Sequencing

pybamview

PyBamView is a python-based application that allows you to view BAM sequence alignments through your web browser. It was inspired by the [samtools tview](#) tool, and was motivated by the need to better visualize alignments with complex insertions/deletions across multiple samples, which is not handled well by current browsers such as IGV and the UCSC Genome Browser.

New! You can now generate alignment snapshots automatically on the command line using the `snappbam` utility, described [here](#).

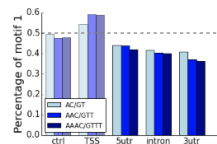


Melissa Gymrek
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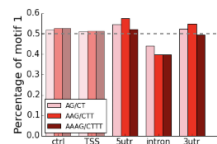
“complex genetic variants that underlie human disease. We are particularly interested in repetitive DNA variants known as short tandem repeats (STRs) as a model for complex variation.”

<https://mgymrek.github.io/pybamview/>

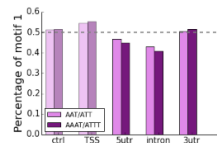
- AC/GT, AAC/GTT, AAAC/GTTT



- AG/CT, AAG/CTT, AAAG/CTTT



- AAT/ATT, AAAT/ATTT



Advances in cancer research using genomics

← → ↻ cytotrace.stanford.edu

CytoTRACE

- Run CytoTRACE
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Overview of CytoTRACE

CytoTRACE (Cellular (Cyto) Trajectory Reconstruction Analysis using gene Counts and Expression) is a computational method that predicts the differentiation state of cells from single-cell RNA-sequencing data. CytoTRACE leverages a simple, yet robust, determinant of developmental potential—the number of detectably expressed genes per cell, or gene counts. We have validated CytoTRACE on ~150K single-cell transcriptomes spanning 315 cell phenotypes, 52 lineages, 14 tissue types, 9 scRNA-seq platforms, and 5 species.

CytoTRACE framework

The diagram illustrates the CytoTRACE framework in three steps:

- 1**: A heatmap showing the number of expressed genes per single cell. The y-axis is labeled 'Predicted order' and the x-axis is 'Expected order'.
- 2**: A 3D plot showing 'Top genes (GCS)' and a heatmap of 'Top genes most associated with gene counts'. The y-axis is 'Predicted order' and the x-axis is 'Expected order'. A color scale at the bottom indicates 'Differentiation' from 'Less' (red) to 'More' (blue).
- 3**: A heatmap showing 'Smoothing of top genes by transcriptional covariance'. The y-axis is 'Predicted order' and the x-axis is 'Expected order'.

CytoTRACE prediction of bone marrow differentiation

The plot shows the differentiation of hematopoietic phenotypes. The axes are labeled 'FD1' and 'FD2'. The phenotypes are color-coded as follows:

- Stem and progenitors (red)
- Megakaryocyte-erythroid progenitors (orange)
- Erythroid progenitors/Erythroblasts (yellow)
- Erythrocytes (light orange)
- Granulocyte progenitors (blue)
- Granulocytes (light blue)
- Monocyte progenitors (green)
- Monocytes (light green)
- Macrophages (dark green)
- Immature B cells (purple)
- Mature B cells (light purple)

The plot is titled 'CytoTRACE Differentiation' and shows a clear trajectory of cell differentiation from stem and progenitors to various mature cell types.

Recurring example: RNA strands

Recall that S is defined as the set of all RNA strands, strings made of the bases in $B = \{\text{A, U, G, C}\}$. Consider the following predicates:

$Rep_{AC}(s, n) =$ “The RNA strand has at least n repeats of AC”

$Rep_{AAC}(s, n) =$ “The RNA strand has at least n repeats of AAC”

Translate to a formal statement, write its negation, and determine which is true.

If A has at least one repeat of AC then it has at least one repeat of AAC.

Negation is: _____

What is the logical structure of the statement?

- A. Statement is a conditional statement; its negation is also a conditional statement.
- B. Statement is a conditional statement; its negation is a conjunction.
- C. Statement is a universal quantification; its negation is also a universal statement.
- D. Statement is a universal quantification; its negation is an existential quantification.
- E. None of the above

Translate to a formal statement, write its negation, and determine which is true.

It is sufficient for a strand to have at least 3 repeats of AAC for it to have at least 2 repeats of AC.

Negation is: _____

Translate to a formal statement, write its negation, and determine which is true.

For at least one strand, it has at least 2 repeats of AC exactly when it has at least 2 repeats of AAC.

Negation is: _____

See you tomorrow

You can do this.