Mark Heim of Loveland Wins for the Third Straight Time!


The judges once again awarded first prize to Mark Heim, now a senior at Thompson Valley High School. He received a gold medal of the Olympiad, a $1500 scholarship to be used at any certified American university or 4-year college, a $1000 UCCS Chancellor’s Scholarship for CMO Medalists, CASIO Cassiopeia Pocket Viewer, CASIO “Super-Calculator” Classpad 300, and Wolfram Research’s software Mathematica. This is the third straight victory for Mark, who won first prize last year, and tied for first prize 2 years ago with another three-time winner Bryce Herdt. In the 30 years of the Olympiad, we had only three 3-time winners: David Hunter, Bryce Herdt and Mark Heim.
From the left: Mark Heim, Alexander Soifer, and Bryce Herdt, April 29, 2005

Mark Heim and Hannah Alpert were the only Olympians who solved problem 22.4.(B). Moreover, they found solutions not known to me. Mark, in fact, proved a much stronger result than the problem asked for. I am looking at the article “Knowledge plus creativity equal math contest victory” by Bobbi Sankey published in The Slice on May 4, 2005. It captures my contemporaneous impression of Mark Heim’s paper, and his solution of problem 22.4.(B). Let me quote some of this article here:

Written by Soifer and local mathematician Ming Song, the problems required knowledge of far more than a few algebraic formulas. Even the judges gathered to listen to Soifer explain solutions to the five problems before beginning to critique students’ essays.

The Olympiad is not a speed competition. Many students sat in their chairs the full four hours. Problems increase in difficulty,
and students who can think outside the box have the best chance at solving them.

There are numerous ways to reach conclusions and in judging process, creativity is valued just as much as the correct answer.

This year, one student’s creativity set him apart from the hundreds of other competitors. He discovered a solution even judges hadn’t considered for one of the test’s most difficult problems.

According to Soifer, the high school senior wrote the best essay in Olympiad history, stunning judges and reaching far beyond what the problem required him to prove.

“I’ve seen thousands of papers in 22 years and it was just amazing,” he said. “He demonstrated use of group theory, terminology of computer science – where did he get all that? It was absolutely remarkable work. It was written by a mathematician.”

The mathematician is Mark Heim, a student at Thompson Valley High School in Loveland and the Olympiad’s first place winner. Heim is a familiar Olympian – he won first prize last year and tied for first place 2 years ago with three-time Olympiad winner Bryce Herdt of Mitchell High School.

“He is an independent thinker,” Soifer said. “He is ready to do research.”

Second prize was awarded to Sam Elder, a Freshman from Poudre High School. He received a silver medal of the Olympiad, a $1000 scholarship to be used at any certified American university or 4-year college, a $1000 UCCS Chancellor’s Scholarship for CMO Medalists, CASIO Cassiopeia Pocket Viewer, CASIO “Super-Calculator”, and Wolfram Research’s software Mathematica.

Third prize was presented to Hannah Alpert, a sophomore from Fairview High School. She received a bronze medal of the Olympiad, a $500 scholarship to be used at any certified American university or 4-year college, a $1000 UCCS Chancellor’s Scholarship for CMO Medalists, Wolfram Research’s software Mathematica, CASIO Cassiopeia Pocket Viewer, and CASIO “Super-Calculator”. Remember Hannah: you will meet her several more times in this book!

The judges also awarded 5 fourth prizes, 24 first honorable mentions, and 101 second honorable mentions.
Literary Awards were presented to Melisa Lizzaraga, a junior from St. Mary’s High School; Tim Henrie, a freshman from Sand Creek High School; and Crystal Kossow, a sophomore from Falcon High School. Here is one of the winners’ poem:

**A Writer in a Crowd**  
*by Crystal Kossow*

This is me,  
A writer in a crowd,  
Geniuses by my side  
Solving problems by the second  
As I search my mind for words,  
Words that will grab at you,  
To make you see.

I get straight A’s of course  
But for me it’s a struggle,  
Hours of notes, days of reading  
To have an answer  
But not understanding  
They see me as smart  
So they invite me here.

I go blank  
As I read the problem  
So I write  
To convey my thoughts  
So you may understand  
I am a writer in a crowd  
Geniuses by my side.

This year’s Prize Fund of the Olympiad was generously donated by CASIO, Inc.; Wolfram Research, Inc.; Intermap Technologies, Inc.; Texas Instruments, Inc.; Air Academy School District 20; Harrison School District 2; Widefield School District 3; Colorado Springs School District 11; St Mary’s High School; Irving Middle School; Timberview Middle School; Sand Creek High School; Falcon High School; Ft. Collins High School; Mrs. Mary Sokol of Long Island, NY; Vice-Chancellor’s Office, Bookstore, and Chancellor’s Office—all from the University of Colorado Colorado Springs.
The Award Presentation Program included “Review of Solutions of the Olympiad Problems” by Alexander Soifer and his lecture “Geometric Cover-Up.”

The following guests of honor, hosts and sponsors addressed the winners and presented awards: Pamela Shockley-Zalabak, Chancellor; Rogers Redding, Vice Chancellor for Academic Affairs; Jim Henderson, Vice Chancellor for Student Success—all from the University of Colorado Colorado Springs; Honorable Congressman Michael Merrifield, State of Colorado; Matt Weiss, Director of Marketing and Education, CASIO, Inc.; Maggie Lopez, Assistant Superintendent, Colorado Springs School District 20; Gregory C. Hoffman, Director of Human Relations, Intermap Technologies, Inc.; and Alexander Soifer.

The Olympiad received congratulatory letters from Colorado Governor Bill Owens and Executive Director of the Department of Labor and Employment Jeffrey M. Wells. Let me reproduce for you the letter by Governor Owens. (There is a typo in this letter, the governor meant to greet the 22nd Olympiad, not the 23rd.)
On May 28, 2005, I attended Bryce Herdt’s high school graduation party. It was a delight to celebrate his achievements with his parents and two brothers.

Right after the Olympiad, on April 26, 2005, our senior judge Dr. Col. Bob Ewell sent me an astute if critical e-mail:

“I realize that technology is a wonderful thing, but watching you do the proofs using the pre-supplied drawings is like going to a concert and having the conductor put on a record. It feels like you are reading a proof instead of doing a proof as when you drew it out by hand. It’s not quite as satisfying.”
Indeed, the use of technology appears to be a zero-sum game. Fulfilling Bob’s desires, I reverted in part to “doing a proof” in front of our Olympians’ eyes.

Problems 22

22.1. Cover-up (A. Soifer). Can a square of area 2005 be covered by 401 squares of area 5 each?

22.2. Tea Time (M. Song). Is it possible to arrange the numbers 1–100 in a $10 \times 10$ grid so that the entries of any T-shaped figure consisting of four unit squares of the grid, called T-tetromino (depicted below) sum up to an even number?

![T-tetromino diagram]

22.3. One L of a Grid (A. Soifer). What is the minimum number of squares to be colored red in a $10 \times 10$ grid so that any L-shaped figure consisting of four unit squares of the grid, called L-tetromino, contains at least two red squares?

22.4. Red and White (A. Soifer).
(A) Each vertex of a regular 11-gon is colored red or white. Prove that there are two congruent monochromatic triangles of the same color.
(B) Each vertex of a regular 2005-gon is colored red or white. Prove that there are two congruent monochromatic 10-gons of the same color.

A polygon is called monochromatic if all of its vertices are colored in the same color. Distinct polygons may have some (but not all) vertices in common.
22.5. Love and Death (A. Soifer, inspired by Martin Klazar’s research).

(A) The DNA of bacterium *bacillus anthracis* (causing anthrax) is a sequence, each term of which is one of 2005 genes. How long can the DNA be if no two consecutive terms may be the same gene, and no two distinct genes can reappear in the same order? That is, if distinct genes $\alpha, \beta$ occur in that order (with or without any number of genes in between), the order $\alpha, \ldots, \beta$ cannot occur again.

(B) The DNA of bacterium *bacillus amoris* (causing love) is a sequence, each term of which is one of 2005 genes. No three consecutive terms may include the same gene more than once, and no three distinct genes can reappear in the same order. That is, if distinct genes $\alpha, \beta, \gamma$ occur in that order (with or without any number of genes in between), the order $\alpha, \ldots, \beta, \ldots, \gamma$ cannot occur again. Prove that this DNA is at most 12,032 long.

**Solutions 22**

22.1. Assume it can be done. Since $401 \times 5 = 2005$, we have no area to spare, and thus the covering squares must not intersect in inside points, and share sides exactly like in a square grid (Fig. 22.1.1).

![Fig. 22.1.1](image-url)

Look at a side of the large square: it must be partitioned into $n$ sides of small squares, and we get the equation $\sqrt{2005} = \sqrt{5}n$ for an integer $n$, i.e., $401 = n^2$, which is absurd. Thus, the covering cannot be done. ■
22.2. Solution by Ming Song.

Consider any five numbers in the cross shape, as shown in Fig. 22.2.1. We are given that 
\[ a + b + c + d = \text{even} \] and 
\[ a + b + c + e = \text{even} \]. Thus, 
\[ d \text{ and } e \] have the same parity. Similarly \[ a, b, d \] and \[ e \] all have the same parity. Because \[ a + b + c + d = \text{even} \] and \[ a, b, \text{ and } d \] have the same parity, \[ c \] must have the same parity as \[ a, b, \text{ and } d \]. Thus, \[ a, b, c, d \] and \[ e \] all have the same parity. Since all squares on the board except the corners are part of a cross shape, 96 entries must all have the same parity. Since this is not true for the given numbers 1 through 100, we get the desired contradiction. ■

22.3. Coloring the 10 \( \times \) 10 grid in a chessboard fashion red and white helps: no matter where an L-tetromino is located on the grid, it will cover exactly two red squares. So, 50 red squares suffice.

Assume now that 49 squares have been colored red and have done the required job. Partition the grid into 24 L-tetrominoes and one 2 \( \times \) 2 square \( S \) in the middle of the board (Fig. 22.3.1).
Each L-tetromino contains at least two red squares. Thus, the 24 L-tetrominos of the tiling contain at least 48 red squares. This leaves at most one red square for the square $S$. But then an L-tetromino that shares three white squares with $S$ contains at most one red square, which contradicts our assumption. Thus, 50 red squares is the minimum.

22.4. (A). First Solution. The shape of such a triangle is uniquely determined by the number of sides of the regular 11-gon $P$ between the vertices of the inscribed triangle (Fig. 22.4.1), i.e., by the number of the integral partitions of 11 into the sum $a + b + c = 11$; $0 < a \leq b \leq c$.

For $a = 1$, we can choose $b = 1, 2, 3, 4, 5$, and so we get five distinct partitions;

For $a = 2$, we can choose $b = 2, 3, 4$, and we get three distinct partitions;

For $a = 3$, we can choose $b = 3, 4$, and thus get two partitions.
Thus, there are total of 10 non-congruent shapes of inscribed triangles. Should the vertices of the 11-gon \( P \) be colored red and white, we would get at least six vertices of the same color, say red, which gives us \( \binom{6}{3} = 20 \) distinct monochromatic red triangles. Since \( 20 > 10 \), we get at least two congruent all-red triangles.

Observe, we have proven a bit more: for each shape of a triangle, there are two monochromatic triangles of this shape, or there are at least three congruent monochromatic triangles. ■

22.4. (A). Second Solution. As in the previous solution, we have 20 distinct all-red triangles. We add to these triangles their images under rotations about the center of the 11-gon \( P \) that map \( P \) onto \( P \), for the total of 220 triangles, which we will call rotated triangles. The total number of the inscribed triangles is \( \binom{11}{3} = 165 \). Since \( 220 > 165 \), two of the rotated triangles coincide, but this means that for these two red monochromatic triangles, one triangle can be rotated into another, thus they are congruent.

Observe, we have proven a bit more: one of the two monochromatic congruent triangles can be rotated to coincide with another. ■

22.4.(B). The two methods have worked to solve problem 22.4(A). However, the first method fails here if one uses it without special care,
for \( \binom{1003}{10} < \binom{2004}{9} \). However, Hannah Alpert, a sophomore from Poudre High School, managed to make it work by reducing the number of types of triangles down from \( \binom{2004}{9} \). The second method works easily, as the following argument demonstrates.

Two-color red and white the 2005 vertices of the given polygon \( P \). At least 1003 vertices must be of the same color, say red, thus we get \( \binom{1003}{10} \) red monochromatic 10-gons. We add to these 10-gons their images under rotations about the center of \( P \) that map \( P \) onto \( P \), for the total of \( 2005 \times \binom{1003}{10} \) 10-gons, which we will call *rotated 10-gons*. The total number of the inscribed 10-gons is \( \binom{2005}{10} \). Since \( 2005 \times \binom{1003}{10} > \binom{2005}{10} \), two of the rotated 10-gons must coincide, but this means that for this pair of the red monochromatic 10-gons, one 10-gon can be rotated into another, thus they are congruent.

Observe: we have proven a bit more: one of the two monochromatic congruent 10-gons can be rotated to coincide with another. ■

In *Further Exploration* E26 you will find a much stronger result than problem 22.4.(B) asked for. It was found during the Olympiad by the winner Mark Heim!

**22.5. (A). First Solution.** Let us prove that in a DNA satisfying the two given conditions, there is a gene that occurs only once. Indeed, let us assume that each gene appears at least twice. For each gene select its first two appearances from the left and call them a *pair*. The first gene from the left \( \alpha \) is in the first pair. This pair \( \alpha \alpha \) must be separated, thus the pair of the second gene \( \beta \) from the left is nestled inside the first pair, for otherwise we would get a forbidden sequence \( \alpha \ldots \beta \ldots \alpha \ldots \beta \). The second pair must be separated, and thus the pair of the third gene from the left must be nestled inside the second pair, etc. As there are finitely many genes, we end up with a pair of genes (nested inside all other pairs) that is not separated, a contradiction.

We will now prove by mathematical induction on the number \( n \) of genes that the DNA that satisfies the two conditions and uses \( n \) genes is at most \( 2n - 1 \) gene long. For \( n = 1 \) the statement is true, as the longest DNA is \( 2 - 1 = 1 \) gene long.
Assume that a DNA that satisfies the required conditions and uses \( n \) genes is at most \( 2^n - 1 \) gene long. Now let \( S \) be a DNA sequence that satisfies the two conditions and uses \( n + 1 \) genes; we need to prove that it is at most \( 2(n + 1) - 1 = 2n + 1 \) gene long.

In the first paragraph of our solution, we proved that there a gene \( g \) that occurs only once in \( S \); we throw it away. The only violation that this throwing may create is making two copies of another gene adjacent—if so, we throw one of them away too. We get the sequence \( S' \) that uses only \( n \) genes. By the inductive assumption, \( S' \) is at most \( 2n - 1 \) gene long. But \( S \) is at most two genes longer than \( S' \), i.e., \( S \) is at most \( 2n + 1 \) gene long. The induction is complete.

We need to demonstrate that a DNA of length of \( 2n - 1 \) on \( n \) genes is attainable. But this is easy: just pick the following sequence \( 1, 2, \ldots, n-1, n, n-1, \ldots, 2, 1 \).

22.5. (A). Second Solution. We will prove by mathematical induction on \( n \) that the DNA that satisfies the problem conditions and uses \( n \) genes is at most \( 2n - 1 \) gene long. For \( n = 1 \) the statement is true, as longest DNA is \( 2 - 1 = 1 \) gene long.

Assume that for any positive integer \( k, k < n \), a DNA that satisfies the conditions and uses \( k \) genes, is at most \( 2k - 1 \) gene long. Now let \( S \) be the longest DNA sequence that satisfies the problem conditions and uses \( n \) genes. We need to prove that \( S \) is at most \( 2n - 1 \) gene long.

Let the first gene of \( S \) be 1, then the last term must be 1 as well, for otherwise we can make \( S \) longer by adding a 1 at the end. Indeed, assume that the added 1 has created a forbidden DNA. This means that we now have a subsequence \( a, \ldots, 1, \ldots, a, \ldots, 1 \) (with the added 1 at the end); but then the original DNA that started with 1, already had the forbidden subsequence \( 1 \ldots a \ldots 1 \ldots a \).

Let us consider two cases.

Case 1. If there are no more 1’s in the DNA, we throw away the first 1 and the last 1, and we get a sequence \( S' \) that uses \( n - 1 \) genes (no more 1’s). By the inductive assumption, \( S' \) is at most \( 2n - 1 \) genes long. But \( S \) is two genes longer than \( S' \), i.e., \( S \) is at most \( 2n + 1 \) genes long.

Case 2. Assume now that there is a 1 between the first 1 and the last 1. The DNA then looks as follows: \( 1, S', 1, S'', 1 \). Observe that if a gene \( m \) appears in the sequence \( S' \), it may not appear in the sequence \( S'' \), for this would create the prohibited subsequence \( 1 \ldots m \ldots 1 \ldots m \).
Let the sequence 1, $S'$, 1 use $n'$ genes and the sequence 1, $S''$, 1 use $n''$ genes. Obviously, $n' + n'' - 1 = n$ (we subtract 1 in the left side because we counted the middle gene 1 in each of the two sub-sequences). By the inductive assumption, the lengths of the sequences 1, $S'$, 1 and 1, $S''$, 1 are at most $2n' - 1$ and $2n'' - 1$ respectively. Therefore, the length of $S$ is $(2n' - 1) + (2n'' - 1) - 1$ (we subtract 1 because the gene 1 between $S'$ and $S''$ has been counted twice). But 

$$(2n' - 1) + (2n'' - 1) - 1 = 2(n' + n'') - 3 = 2(n + 1) - 3 = 2n - 1$$

as desired. The induction is complete.

This proof allows us to find a richer set of examples of DNAs of length of $2n - 1$ (and even describe all such examples if necessary). For example:

1, 2, ..., $k$, $k + 1$, $k$, $k + 2$, ..., $k$, 2005, $k$, $k - 1$, $k - 2$, ..., 2, 1. ■

22.5.(B). Assume $S$ is the longest DNA string satisfying the problem conditions. Partition $S$ into blocks of three terms starting from the left (the last block may be incomplete and have fewer than three terms, of course). We will call a block extreme if a gene from the given set of genes \{1, 2, ..., 2005\} appears in this block for the first or the last time. There are at most $2 \times 2005$ extreme blocks.

We claim that there are no complete \(i.e., 3\text{-gene}\) non-extreme blocks.

Indeed, assume the block $B$, which consists of genes $\alpha, \beta, \gamma$ in some order, is not extreme (in the original DNA string $S$ these three genes do not have to be consecutive). This means that the genes $\alpha, \beta, \gamma$ each appears at least once before and at least once after appearing in $B$. We will prove that then the DNA would contain the forbidden subsequence of the type $\sigma, \tau, \omega, \sigma, \tau, \omega$. Let $A$ denote the ordered triple of the first appearances of $\alpha, \beta, \gamma$ (these three genes may very well come from distinct 3-blocks). Without loss of generality we can assume that in $A$ the genes $\alpha, \beta, \gamma$ appear in this order. Let $C$ denote the ordered triple of the last appearances of $\alpha, \beta, \gamma$ in some order. Let us look at the 9-term subsequence $ABC$ and consider three cases, depending upon where $\alpha$ appears in the block $B$.

Case 1. If $\alpha$ is the first gene in $B$ (Fig. 22.5.1), then we can choose $\beta$ also in $B$ and $\gamma$ in $C$ to form $\alpha, \beta, \gamma$ which with $\alpha, \beta, \gamma$ from $A$ gives us the forbidden sequence $\alpha, \beta, \gamma \alpha, \beta, \gamma$. 

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Case 2. Let $\alpha$ be the second gene in $B$ (Fig. 22.5.2). If $\beta$ follows $\alpha$ in $B$, then with $\gamma$ from $C$ we get $\alpha$, $\beta$, $\gamma$, which with $\alpha$, $\beta$, $\gamma$ from $A$ produces the forbidden sequence $\alpha$, $\beta$, $\gamma$, $\alpha$, $\beta$, $\gamma$. Thus, $\beta$ must precede $\alpha$ in $B$. If the order of the genes $\beta$, $\gamma$ in $C$ is $\beta$, $\gamma$, then we can combine an $\alpha$ from $B$ with this $\beta$, $\gamma$ to form $\alpha$, $\beta$, $\gamma$, which with $\alpha$, $\beta$, $\gamma$ from $A$ gives us the forbidden $\alpha$, $\beta$, $\gamma$, $\alpha$, $\beta$, $\gamma$. Thus, the order in $C$ must be $\gamma$, $\beta$. Now we can choose $\alpha$, $\gamma$ from $A$ followed by $\beta$, $\alpha$ from $B$, followed by $\gamma$, $\beta$ from $C$ to get $\alpha$, $\gamma$, $\beta$, $\alpha$, $\gamma$, $\beta$, which is forbidden.

Case 3. Let $\alpha$ be the third gene in $B$ (Fig. 22.5.3), and is thus preceded by $\beta$ in $B$. If the order in $C$ is $\beta$, $\gamma$, then we get $\alpha$, $\beta$, $\gamma$ from $A$ followed by $\alpha$ from $B$ and $\beta$, $\gamma$ from $C$ to get the forbidden $\alpha$, $\beta$, $\gamma$, $\alpha$, $\beta$, $\gamma$. Thus, the order in $C$ must be $\gamma$, $\beta$, and we choose $\alpha$, $\gamma$ from $A$, followed by $\beta$, $\alpha$ from $B$, and followed by $\gamma$, $\beta$ from $C$ to form the forbidden $\alpha$, $\gamma$, $\beta$, $\alpha$, $\gamma$, $\beta$. 

Fig. 22.5.1

Fig. 22.5.2

Fig. 22.5.3
We are done, for the DNA sequence consists of at most $2 \times 2005$ extreme 3-blocks plus perhaps an incomplete block of at most two genes—or 12,032 genes at the most.

For a much stronger bound, obtained by Martin Klazar of Prague, read *Further Exploration* E23. ■
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