



Entry Form
Please Type

Entries must be postmarked no later than September 15, 2009
Entries will not be returned

Entry Category

A category must be chosen for each entry or the submission will be disqualified. An entry cannot be submitted in multiple categories.

- ☐ Photography ☐ Illustrations ☒ Informational Graphics
☐ Interactive Media ☐ Non-interactive Media

Title of Work The Deadly Genomes

Please list the authors as they should appear in final print.

Name(s)

- | | | |
|----|----------------------|--|
| 1. | Martin Krzywinski | concept, visualization,
programming, design, layout |
| | _____
Please Type | _____
Role / Title |
| 2. | Jonathan Corum | layout, typography |
| | _____
Please Type | _____
Role / Title |
| 3. | Cydney Nielsen | concept, visualization |
| | _____
Please Type | _____
Role / Title |
| 4. | Ian Bosdet | research, layout |
| | _____
Please Type | _____
Role / Title |

(Use another sheet for additional team members.)

Contact Person

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How did you hear about the competition?

Through the website.



I (we) warrant that this entry is original and has been independently developed by me and/or members of my team and does not violate the copyright or other personal or proprietary right of another person or team of people. Further, I (we) attest that I (we) will be able to grant to *Science* and *Science Online* non-exclusive publication and web rights if our entry wins or places in the competition. Also, I (we) understand that if my entry wins or places in the competition, it will be shared with reporters covering the winners or the competition.

All members of the team must sign this form to be eligible.

(Digital/typed signatures may be submitted for hand-written signatures.)

Martin Krzywinski

Martin Krzywinski

Jonathan Corum

Cydney Nielsen

Ian Bosdet

Cydney Nielsen

Ian Bosdet

Contact person is responsible for distributing information received from the competition and/or sponsors to all other members of the team.



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I, Martin Krzywinski of Canada's Michael Smith Genome Sciences Center
Full Name *Name of Organization*

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Signature Martin Krzywinski Date 14 September 2009

(Your digital/typed signature on this line may be substituted for a hand-written signature.)

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Information about the Multimedia Material

NSF asks you to provide as much information as possible about each of your multimedia files, including descriptions, suggested credit and date. If there are any restrictions on the use of the material, please specify these clearly.

File Name(s)

Please list all file names.

High resolution poster (40" x 30", 300 dpi, 12,000x9,000 pixels)

hires/deadlygenomes.png

hires/deadlygenomes.tiff

hires/deadlygenomes.jpeg

Low resolution poster (10.67" x 8" , 300 dpi, 3200x2400 pixels)

lowres/deadlygenomes.png

lowres/deadlygenomes.tiff

lowres/deadlygenomes.jpeg

Web resolution (1000x750 pixels)

webres/deadlygenomes.png

webres/deadlygenomes.jpg

Entry form

deadlygenomes.doc

deadlygenomes.pdf

Caption Description

For each multimedia item, please include a brief non-technical description, which will be used for writing captions. Include any relevant keywords; use a separate page for additional space.

Some of the tiniest organisms on our planet are also the deadliest. Bacteria and viruses are the agents of widespread diseases like pneumonia and cholera and outbreaks of severe afflictions like hemorrhagic fevers, such as Ebola and Marburg. The combined global burden of disease caused by the organisms shown in the graphic is enormous, responsible for nearly 500 million cases and 10 million deaths annually.

Despite the diminutive size of the agents of these diseases, their genomes are both complex and varied. Smaller than that of a human genome – genomes of bacteria are about 1000 times smaller and those of viruses about 300,000 times smaller – they possess all the necessary biochemical blueprint for infection. Bacteria are self-contained single cell organisms capable of independent reproduction, respiration and voluntary movement. A virus, on the other hand, is nothing more than a strand of DNA or RNA surrounded by a protective protein coat. Virus genomes can be much smaller because the virus subverts its host's genome and biochemical machinery to create more copies of itself.

The graphic contrasts a variety of diseases by their death toll and mortality ratio statistics. For each disease, a visualization of the genome of the agent organism is shown, depicted as a path. This unique approach to genome visualization uses the structure of the genome to generate a unique



representation for each genome. The length of the path is proportional to the size of the genome, the curvature of the path at a given point is proportional to the repeat content and the color encodes the GC ratio (fraction of total bases that are guanine or cytosine).

Suggested Credit

Write how you would prefer to identify the copyright holder.

(Examples: "John Smith, Best University" or "John Smith, Biology Department, Best University")

Martin Krzywinski, Cydney Nielson, Ian Bosdet (Canada's Michael Smith Genome Sciences Center) and Jonathan Corum (13pt)

Related URL(s)

<http://mkweb.bcgsc.ca/deadlygenomes>

Does This Material Show NSF-Supported Research? Yes ☐ No ☒

If yes, please explain and, if possible, provide the NSF grant number.

Grant #

Date of Material

Please narrow down the creation date as closely as possible, even if you can give only the decade.

September 2009

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no restrictions



Applicant Questionnaire
Please Type

This questionnaire will be used by the judges to help evaluate your entry.
Please submit with each entry. Include a succinct answer to each question asked.

1. Title of Entry

The Deadly Genomes

2. Give a clear, definitive description of the entry as it would appear in a magazine

Genome visualization of deadly bacteria and viruses and the epidemiological profile of the associated outbreak and widespread disease and infection.

3. Size Information

Actual Subject Size

Bacteria (organism ~1 micron, genome ~1-10 Mb)

Virus (organism ~0.01 microns, genome ~10kb)

Printed Size

Poster size is 40" x 30". The length of the genome path is proportional to the size of the genome.

Scale of Object

At 40"x30", 1" of the genome path corresponds to approximately 4.2 kb (1 cm = 1.7kb). Thus, a 10kb virus genome has a length of 2.4" (6 cm) while a 3Mb bacteria such as cholera has a length of 714" (60 feet or 18 meters).

4. What is the purpose of the entry?

The purpose of this graphic is to relate worldwide disease incidence and mortality statistics to the structure and variation of the genomes of the corresponding agent organisms. The graphic is designed to (a) draw the audience to think about the variety of disease incidence and mortality profiles, (b) contrast these profiles with their perception of the disease and (c) show them insight into the causative genomes.

The epidemiological data acts as the quantitative support for the figure. These statistics partition the diseases into distinct subsets (such as widespread/fatal, widespread/not-fatal, rare/ fatal, etc) and provide contrast between deadly but rare diseases, such as Ebola, with widespread but less fatal inflictions like malaria. The reader will notice that the number of times a disease appears in the news is much more a function of its mortality (y-axis) than the actual death count (x-axis).

The genome visualization provides a means to compare the size and structure of the genomes of the bacteria and viruses. Each genome is drawn as a path making direct visual inspection of local structure possible and allowing for comparisons between genomes. The relative difference in size between virus and bacterial genomes is evident, as is the variation in size among various bacteria. Variation in GC content, both global and local, can be distinctly seen in each path. For example, the GC-poor (19%) malaria genome of *Plasmodium falciparum* appears orange whereas the GC-rich (66%) *Mycobacterium tuberculosis*, the agent of tuberculosis, is vividly purple.



5. For what audience was the entry created?

The entry is targeted at the broad, public audience and does not require any technical background to understand. The diseases chosen are all in the public eye and most will be easily recognized. The poster will be of great interest to individuals with an interest in microbiology, virology, epidemiology and human health.

6. Explain how your entry fulfills each criterion:

Answers should be clear and concise not using more than a TOTAL of 300 words.

Remember, judges may not be familiar with the area of science represented in the entry.

Please use clear, non-technical language.

Visual Impact

The poster's foreboding title – The Deadly Genomes – is designed to draw in the audience and presents them with a visual depiction of the genomes of bacteria and viruses that cause disease. Each genome path is intricate, unique and beautiful and compels the eye into close examination in a hunt for patterns and shapes. The placement of the visualizations on the poster is based on the incidence and mortality of the disease, making a unique connection between genome structure, disease and worldwide disease burden.

Effective Communication

We have anchored the visual presentation on information that is familiar to a non-technical audience, who will easily recognize almost all of the diseases shown. By using these familiar elements as visual entry points, we then present the epidemiological characteristics of the disease as a plot showing the worldwide death count and mortality rate. The audience will be drawn into the relationship between the position on the plot with their own perception of their risk to the disease. The visualization of the disease agent's genome adds an organic element to the design. The genome paths are used to draw the audience into the poster, inviting them to explore each path and compare shapes. The legend provides sufficient information to understand how the shape of the path is derived and why it is important, without burdening the audience with technical details.

Freshness/Originality

The graphic achieves the difficult task of generating a meaningful visual representation of the whole genome of an organism. The genome is shown as a path (this is a unique approach to genome visualization), using fundamental and meaningful genome characteristics such as GC and repeat content (both have functional implications). The resulting paths can be used to visually compare genomes or to appreciate the intricacy in structural variation within a single genome.