

Virtual Worlds and NWS Operations



<http://slidesha.re/vw-nws>

Eric Hackathorn
RITT Forum Presentation
February 16, 2011

what are virtual worlds?



3-D Visualizations

- Immersive storytelling
- Bringing NOAA's data and research to life

Social Interaction

- Communication
- Collaboration
- Community

Global Audience

- Scalable experiences
- Untapped market

NOAA's Meteora Island in Second Life®



Tsunami



Science On a Sphere®

Weather Map

Meeting Hall

Weather Balloon

Hurricane Ride



<http://www.esrl.noaa.gov/gsd/tob/virtualworlds.html>

<http://bit.ly/vgov>

vGov

mitigating societal impacts

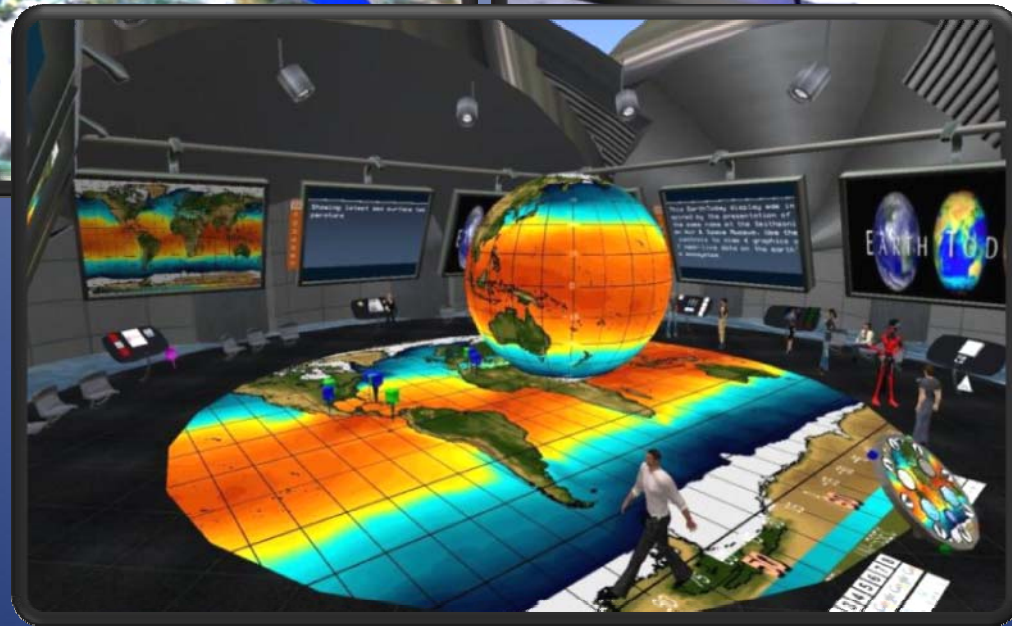
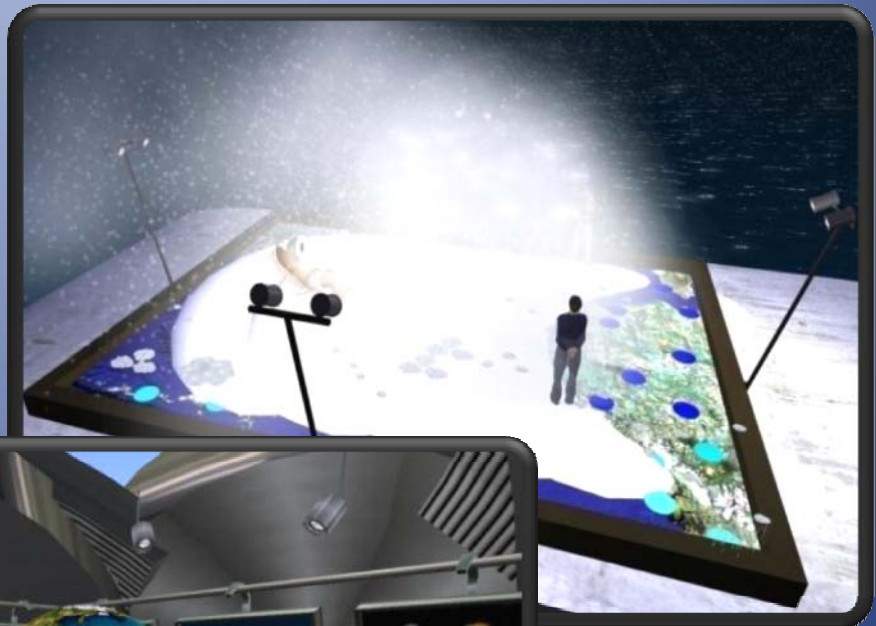
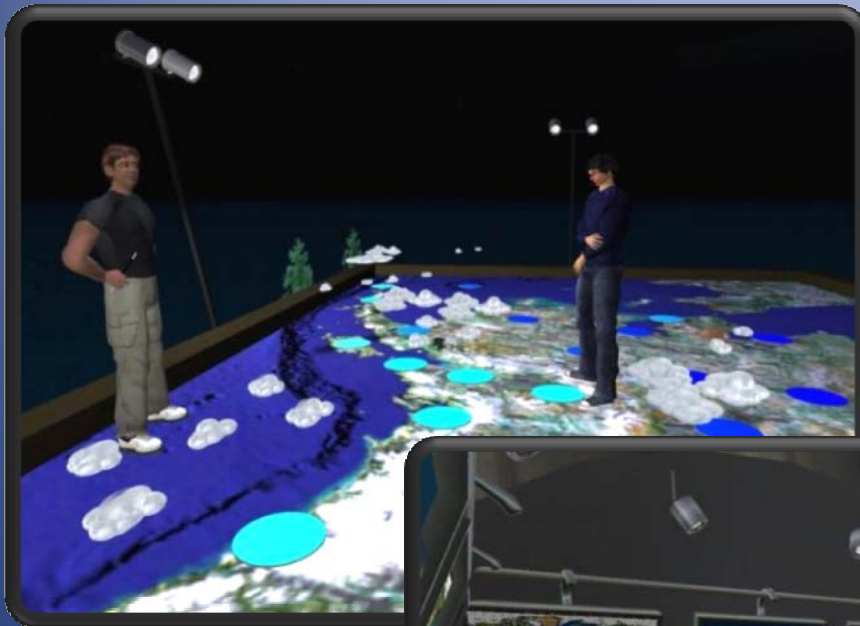
situational awareness

understanding the effects of droughts

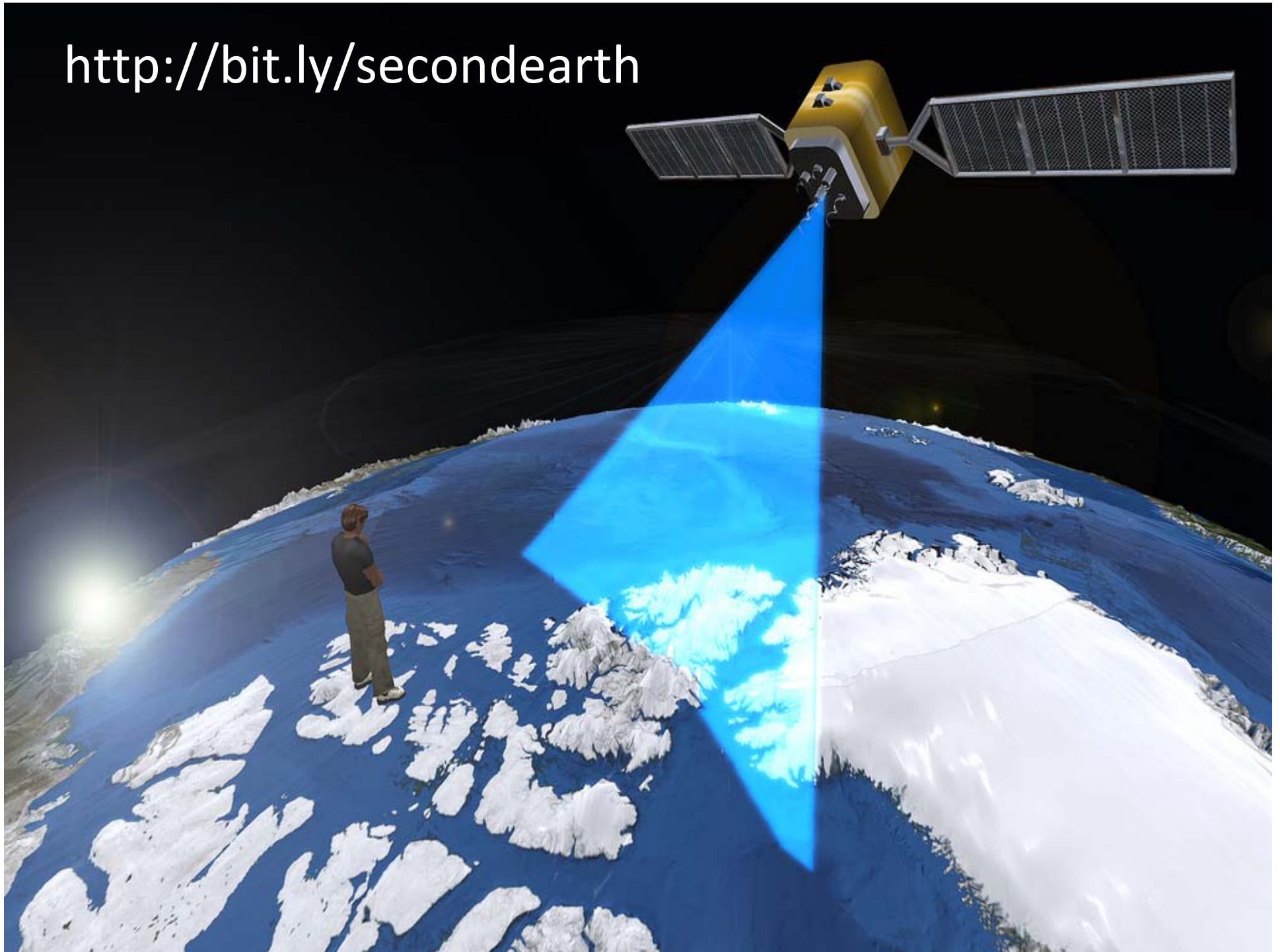
forecasting a virtual hurricane



virtual forecasting office

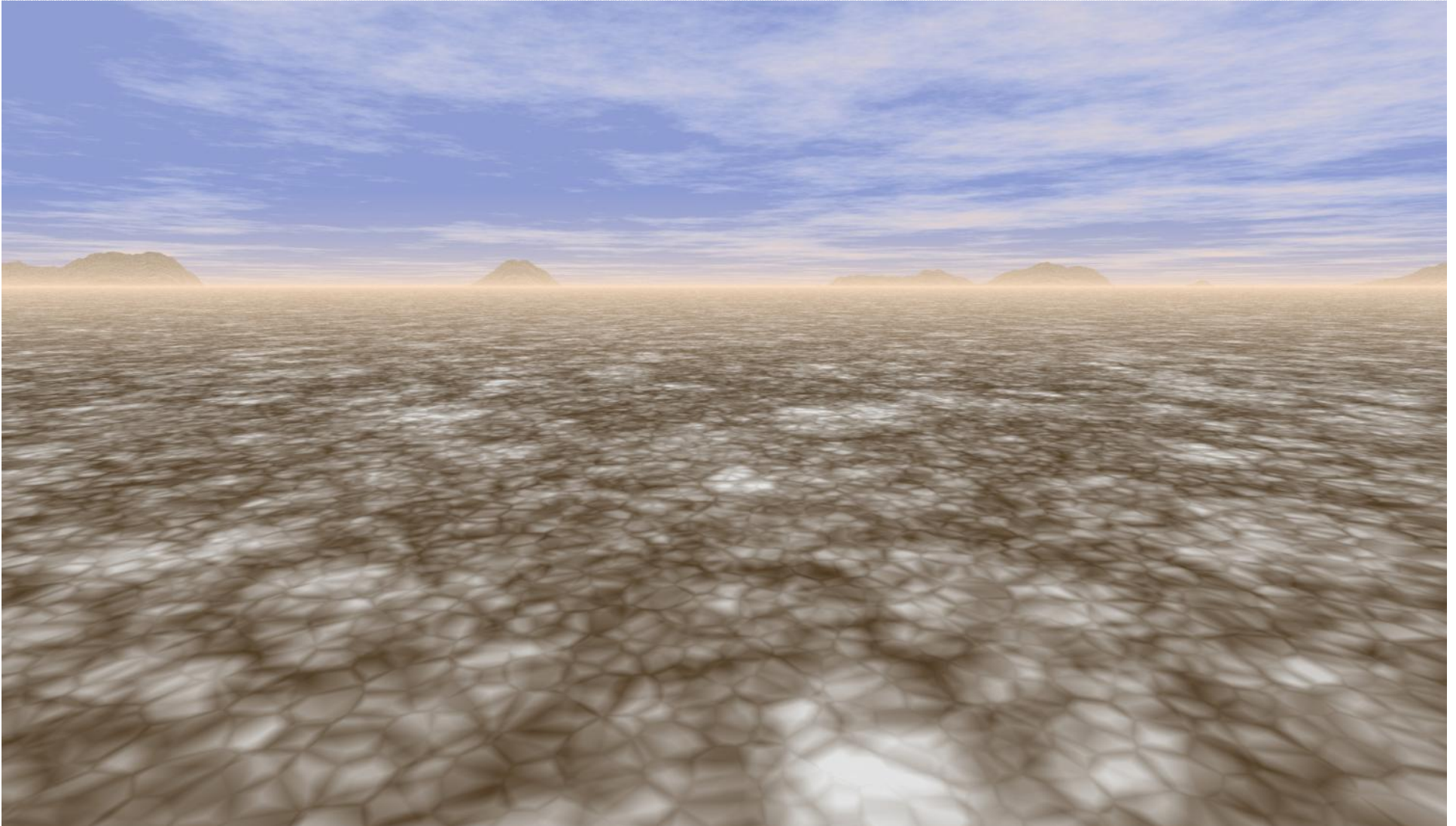


<http://bit.ly/secondearth>

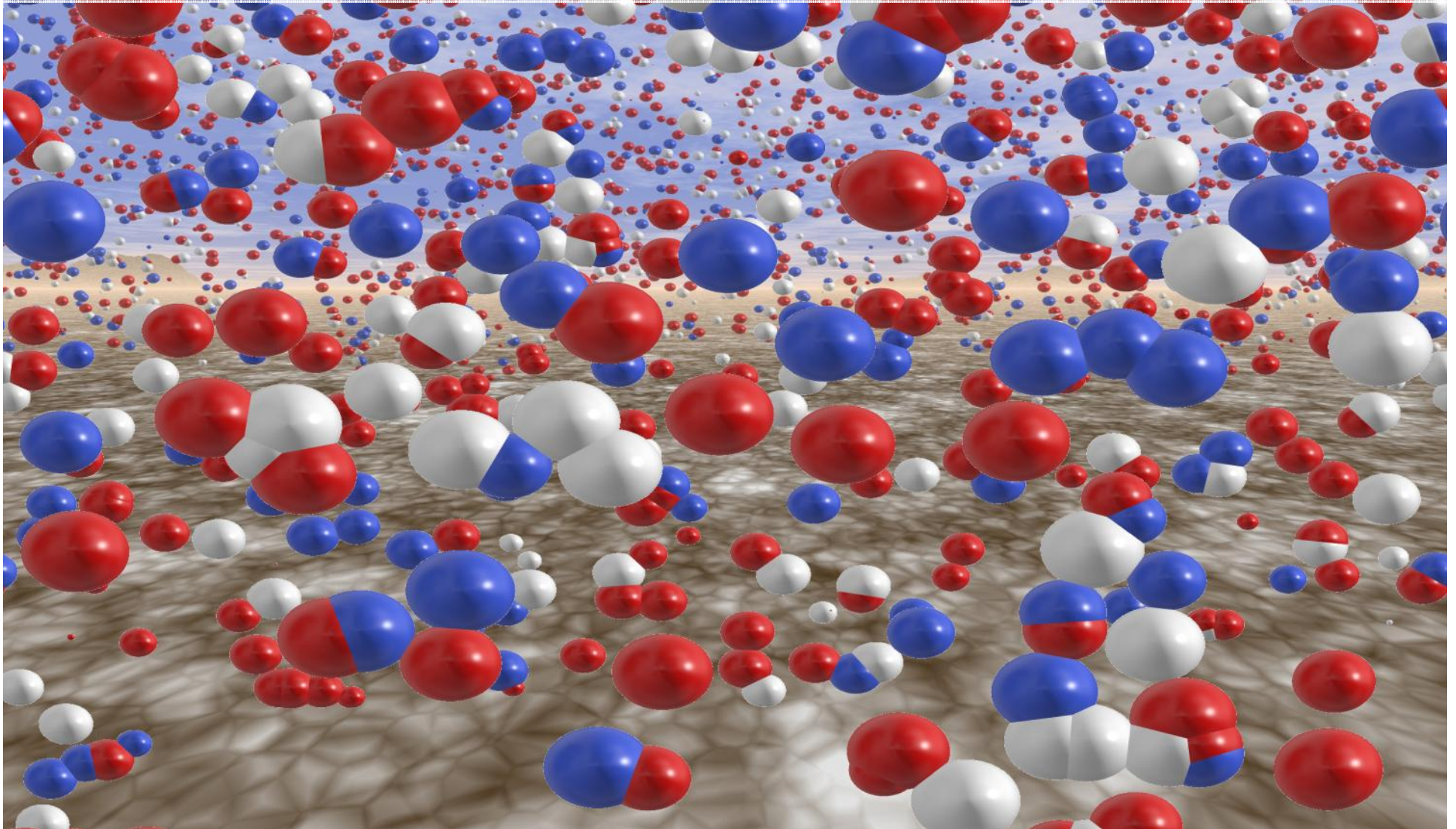


Imagine a vast virtual work area....

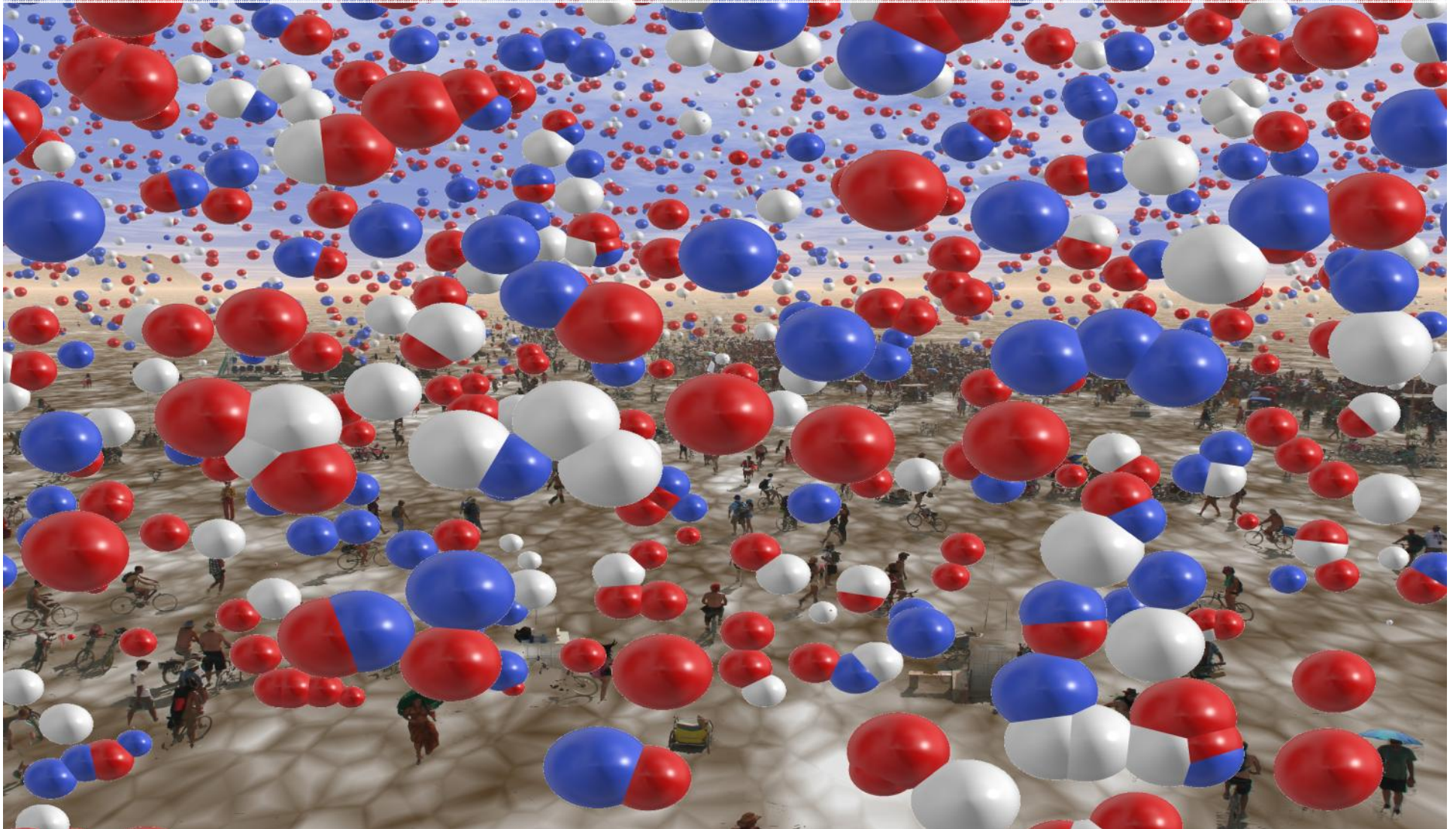
<http://im-tel.org/>



Populated with millions of data objects...



Analyzed by thousands of people...



Pull Mode

Rank: 317 Score: 2534

Soloist Beginner Puzzle 8 (<150): Fruit Fly

Group Competition

#	Group Name	Score
1	Rice Biochemistry	9174

a b c d e

12 4 3 6 7 9 10 11

<http://bit.ly/folditgame>

Shake Sidechains Wiggle All Wiggle Backbone Wiggle Sidechains Freeze Protein Remove Bands Disable Bands Align Guide Reset Structures Reset Puzzle Help Glossary

Chat - Group Chat - Puzzle Chat - Global

auto show auto show auto show

The image is a screenshot of the Foldit game interface. At the top, it displays the player's rank (317) and score (2534) for a 'Beginner Puzzle 8 (<150): Fruit Fly'. A group competition table shows 'Rice Biochemistry' as the top group with a score of 9174. Below this, five protein structure puzzles (a-e) are shown as ribbon models. The main part of the interface is a large 3D molecular model of a protein structure, with various components labeled with numbers 3 through 12. A URL 'http://bit.ly/folditgame' is overlaid on the model. At the bottom, there is a toolbar with icons for actions like 'Shake Sidechains', 'Wiggle All', 'Wiggle Backbone', 'Wiggle Sidechains', 'Freeze Protein', 'Remove Bands', 'Disable Bands', 'Align Guide', 'Reset Structures', 'Reset Puzzle', 'Help', and 'Glossary'. On the far right, there are chat windows for 'Chat - Group', 'Chat - Puzzle', and 'Chat - Global', each with an 'auto show' option.

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Predicting protein structures with a multiplayer online game

Seth Cooper, Firas Khatib, Adrien Treuille, Janos Barbero, Jeehyung Lee, Michael Beenen, Andrew Leaver-Fay, David Baker, Zoran Popović & Foldit players

Affiliations | Contributions | Corresponding authors

Nature 466, 756–760 (05 August 2010) | doi:10.1038/nature09304
Received 22 January 2010 | Accepted 30 June 2010

People exert large amounts of problem-solving effort playing computer games. Simple image- and text-recognition tasks have been successfully ‘crowd-sourced’ through games^{1,2,3}, but it is not clear if more complex scientific problems can be solved with human-directed computing. Protein structure prediction is one such problem: locating the biologically relevant native conformation of a protein is a formidable computational challenge given the very large size of the search space. Here we describe Foldit, a multiplayer online game that engages non-scientists in solving hard prediction problems. Foldit players interact with protein structures using direct manipulation tools and user-friendly versions of algorithms from the Rosetta structure prediction methodology⁴, while they compete and collaborate to optimize the computed energy. We show that top-ranked Foldit players excel at solving challenging structure refinement problems in which substantial backbone rearrangements are necessary to achieve the burial of hydrophobic residues. Players working collaboratively develop a rich assortment of new strategies and algorithms; unlike computational approaches, they explore not only the conformational space but also the space of possible search strategies. The integration of human visual problem-solving and strategy development capabilities with traditional computational algorithms through interactive multiplayer games is a powerful new approach to solving computationally-limited scientific problems.

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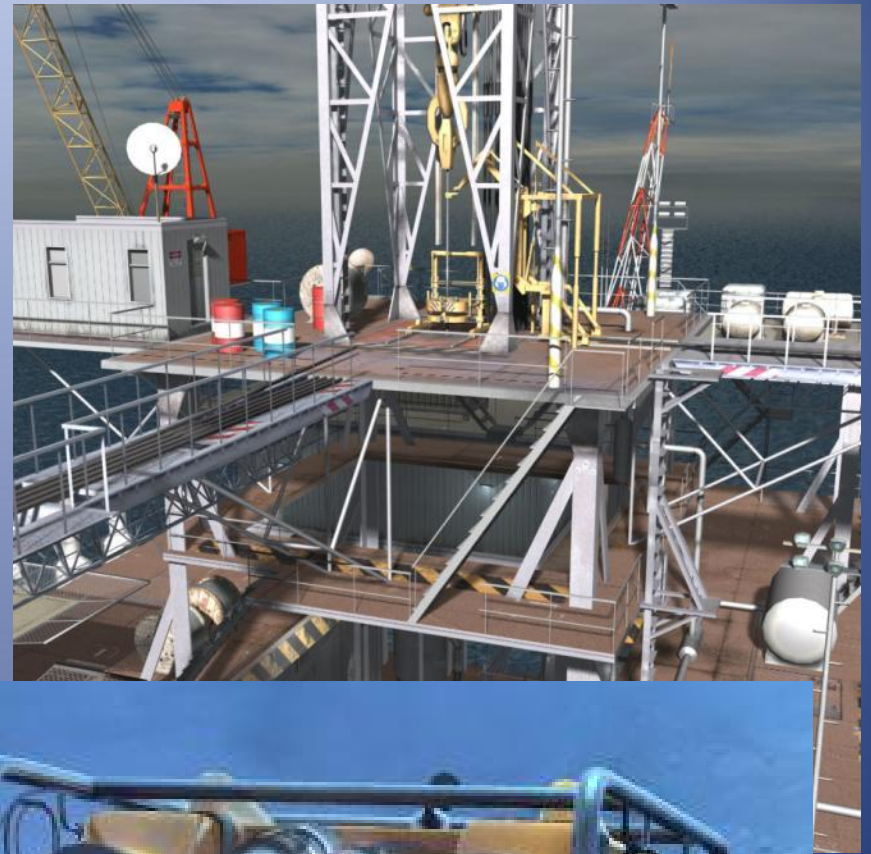
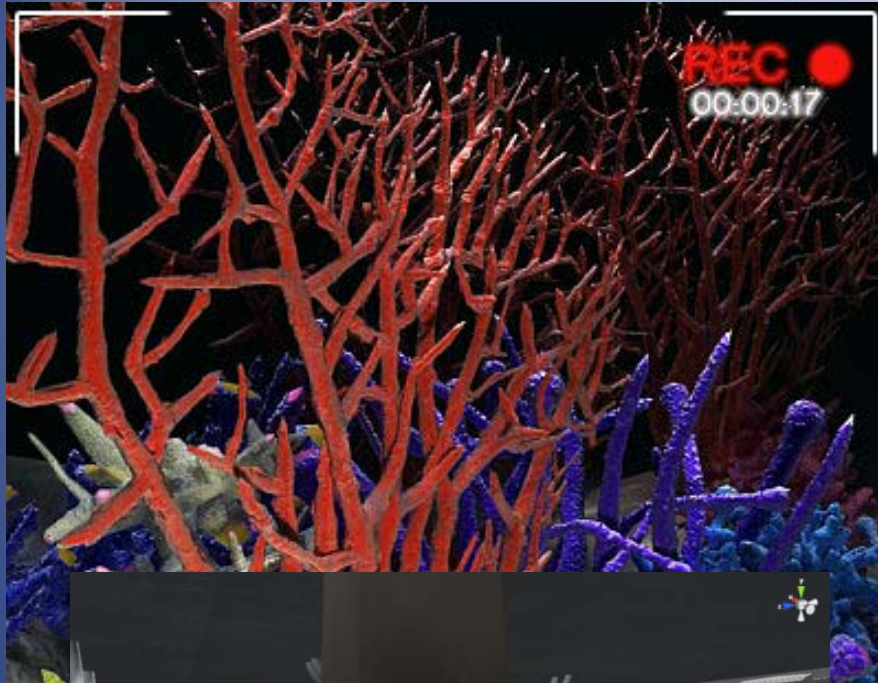
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“The integration of human visual problem-solving and strategy development capabilities with traditional computational algorithms through interactive multiplayer games is a powerful new approach to solving computationally-limited scientific problems.”

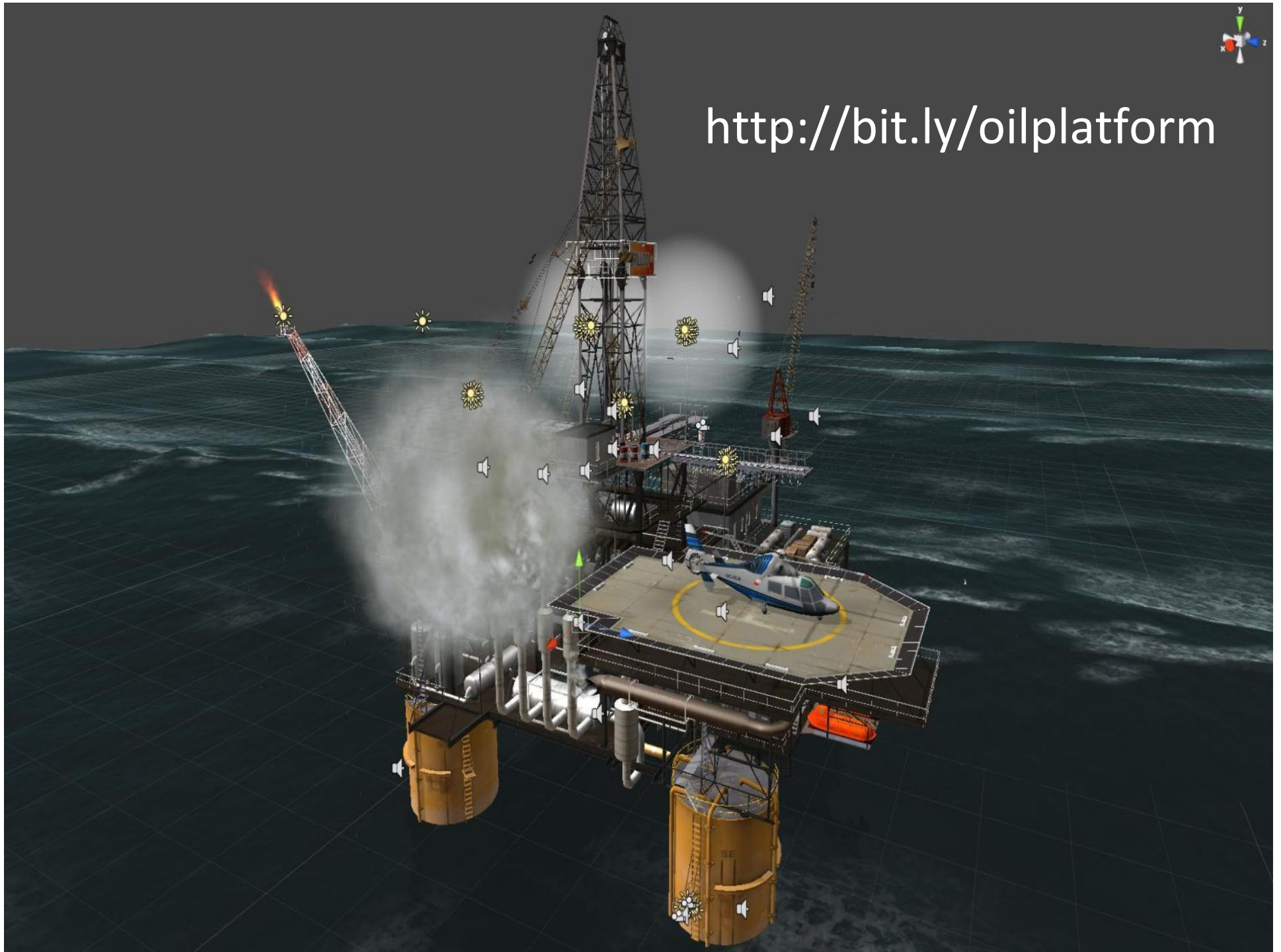
<http://www.nature.com/nature/journal/v466/n7307/full/nature09304.html>

- Interactive learning potential
- Leveraging the crowds in games and simulations
- Competition awards successful “players”
- Creates repeat customers hungry for NOAA’s data

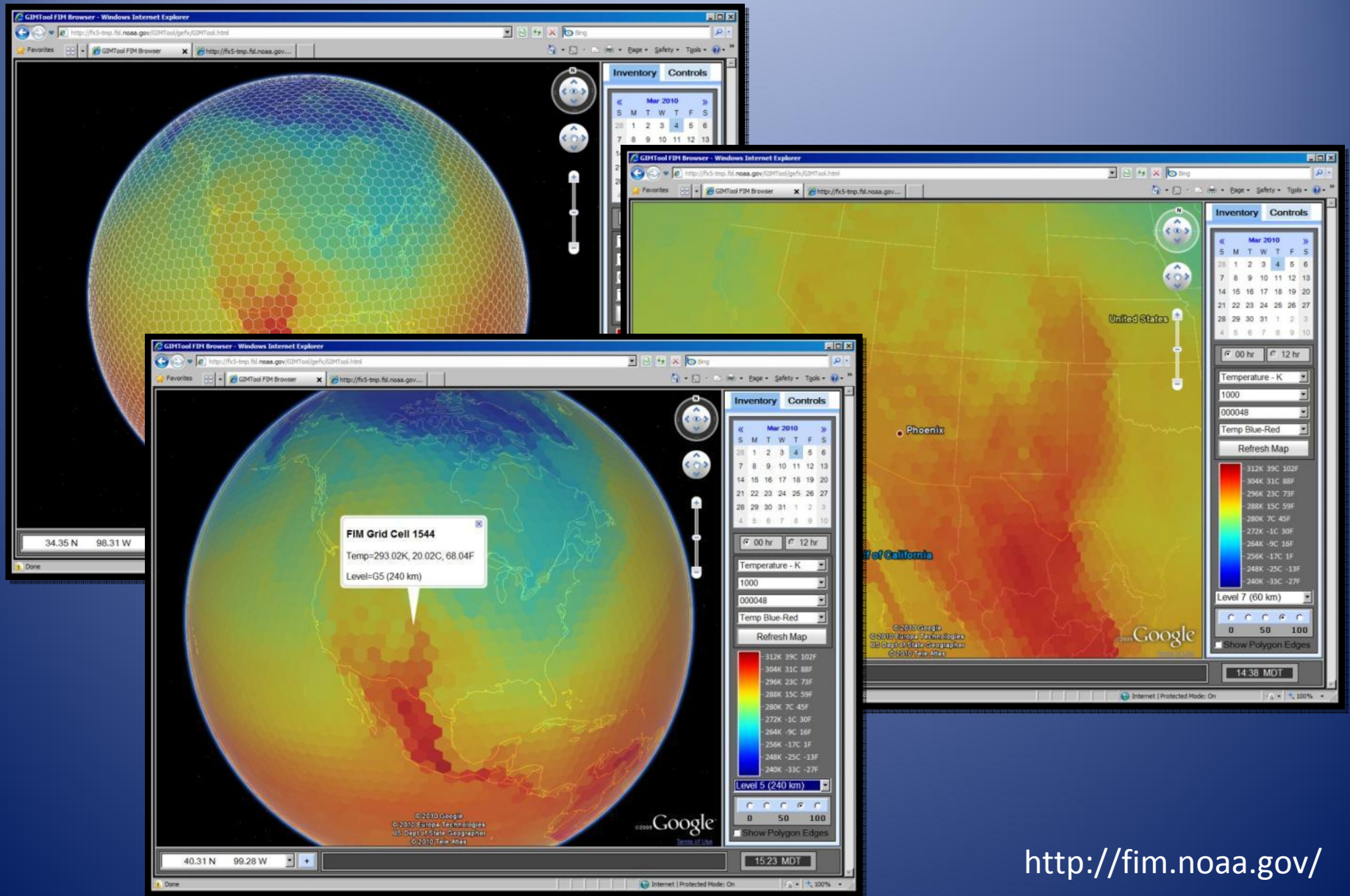




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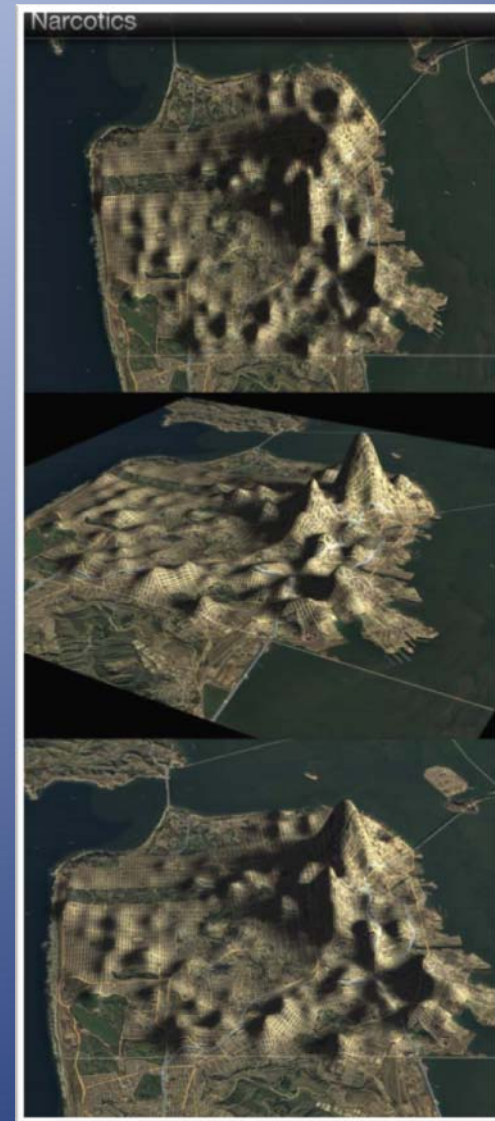


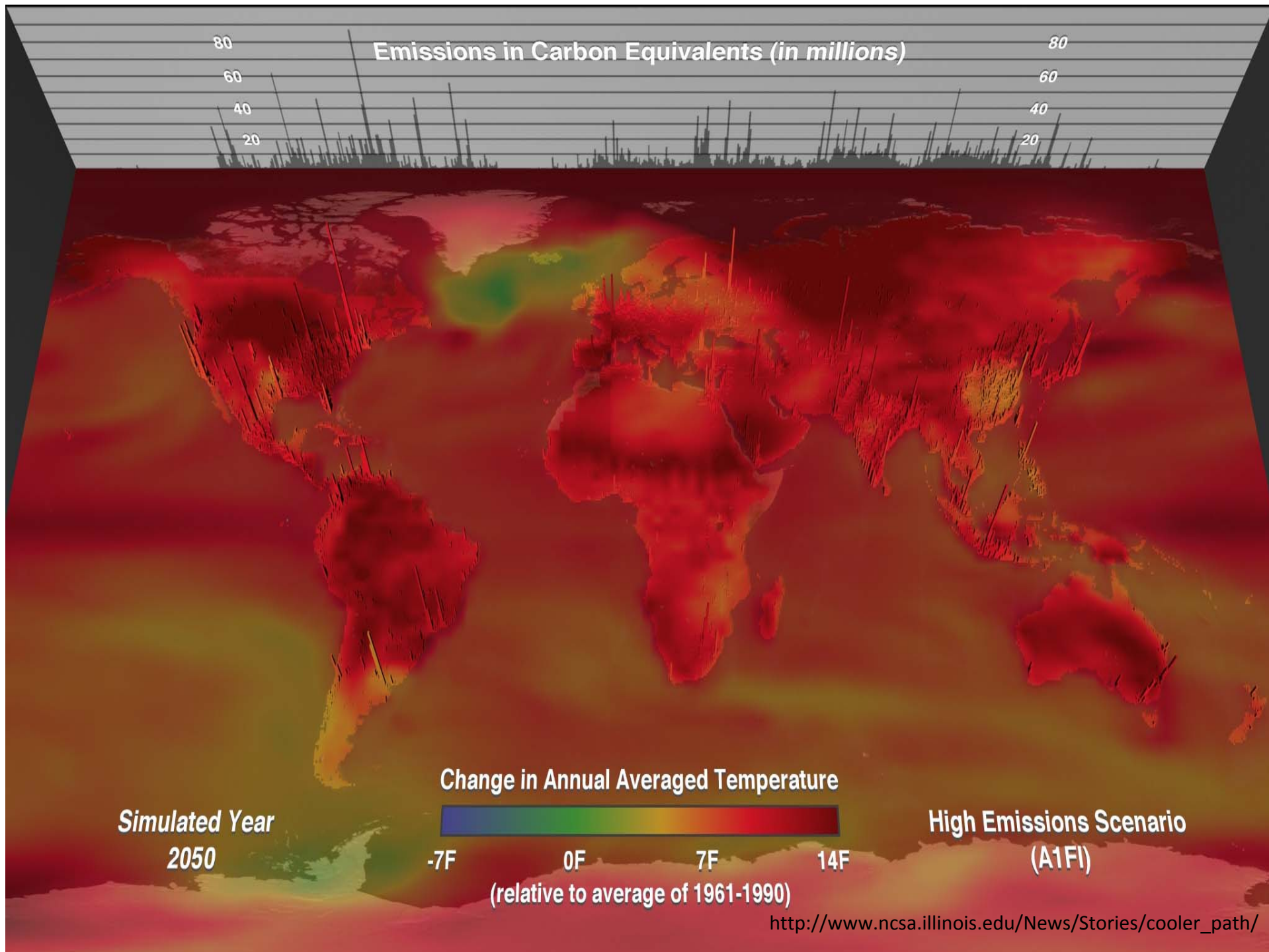
cloud-based visualizations of large data sets



<http://fim.noaa.gov/>

data viz examples







An Executive Guide for Keeping Up with Virtual Worlds

- Contact me!
- Join a virtual world and create an avatar
- Ask your kids about virtual worlds
- Attend the Federal Consortium for Virtual Worlds:
<http://www.ndu.edu/iCollege/fcvw/index.htm>
- Bookmark several virtual world news sites
- Check out:
<http://www.esrl.noaa.gov/gsd/tob/virtualworlds.html>



Questions?

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