



# Visualization of space-time patterns of West Nile virus

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CPSC 533c: Information Visualization

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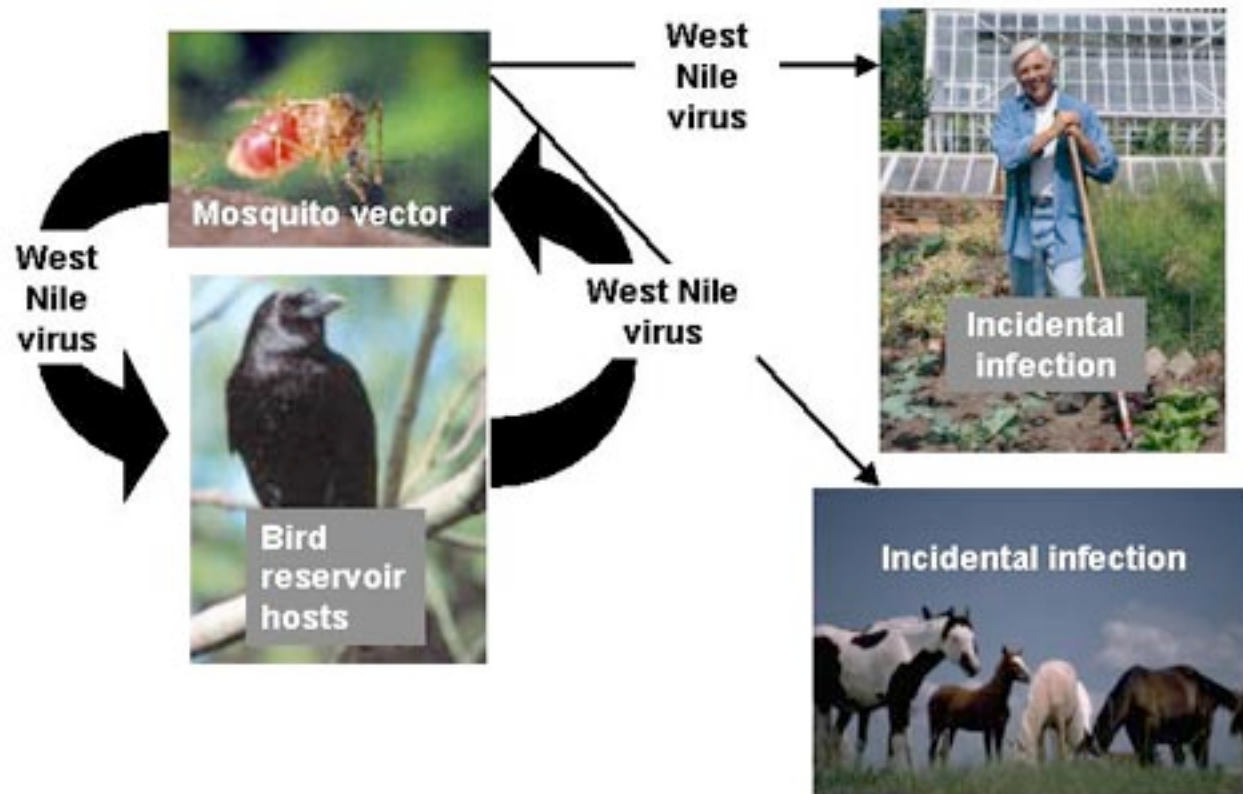


## West Nile Virus

- **Introduced in North America in 1999**
- **Transmitted by mosquitoes**
  - These mosquito species are highly ornithophilic
- **Corvids (crows, jays) are primary reservoir**
  - High mortality
- **Amplification cycle as mosquitoes feed on infected birds**
- **Humans infected by mosquitoes as a side-effect**
- **Theorized spillover effect as birds die off and mosquitoes switch to feeding on humans**
  - Would result in observable lag between bird deaths and human infections

# West Nile Virus

## West Nile Virus Transmission Cycle



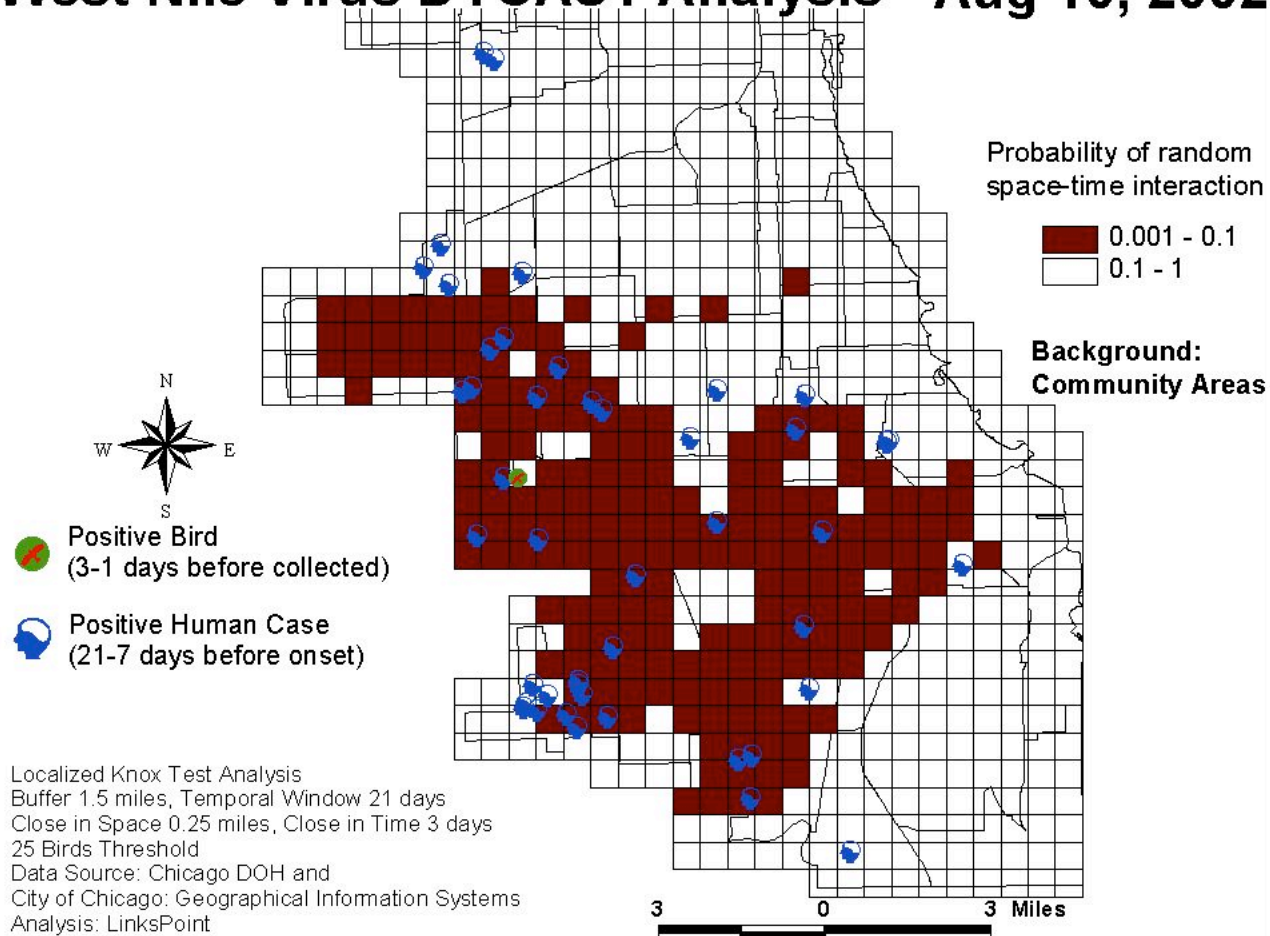
Source: The Centers for Disease Control and Prevention;  
<http://www.cdc.gov/ncidod/dvbid/westnile/cycle.htm>

## Dynamics of WNV in the field

- **Public reporting of dead birds can be used to track WNV activity**
- **DYCAST (Dynamic Continuous-Area Space-Time) system**
  - Identifies clusters of dead birds within lattice cells
  - Result: daily raster map of WNV activity
  - WNV activity = high risk of human infection
  - Binary risk/no risk classification (“lit” / ”not lit”)

# DYCAST Results

## West Nile Virus DYCAST Analysis Aug 10, 2002

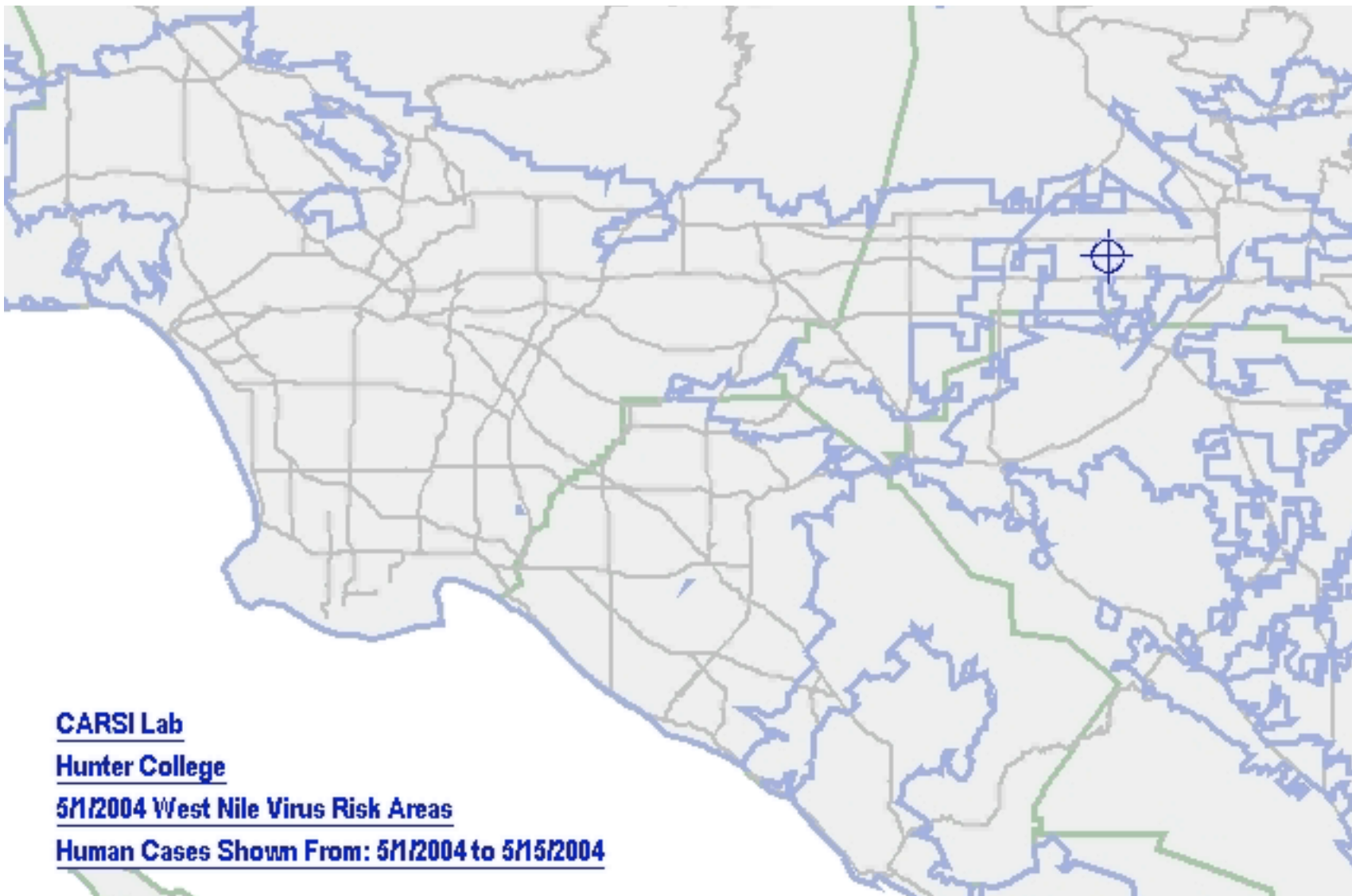
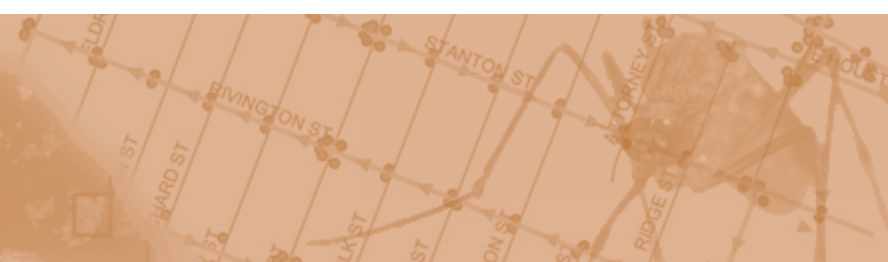


## Analysis problems

- **What is the relationship between WNV activity in birds and human cases of WNV?**
- **What patterns of WNV activity are predictors of human cases?**
- **Do different areas have different relationship between WNV activity and human cases?**
  - Lag between dead birds and human onset may vary according to climate, population density, etc



# DYCAST Animation



CARSI Lab  
Hunter College  
5/1/2004 West Nile Virus Risk Areas  
Human Cases Shown From: 5/1/2004 to 5/15/2004

# Scientific Visualization vs Information Visualization

- **The visual representation is given (x, y and t)**
- **However, animation or 3D visualization is difficult to use**
- **Similarities may not be adjacent in space or time**
  - Other forms of juxtaposition are necessary
- **Use a derived variable, or in this case, a time-series**
  - Human case “risk histories”
  - Sequence of daily risk values for the cell in which a human occurs



# Risk Histories

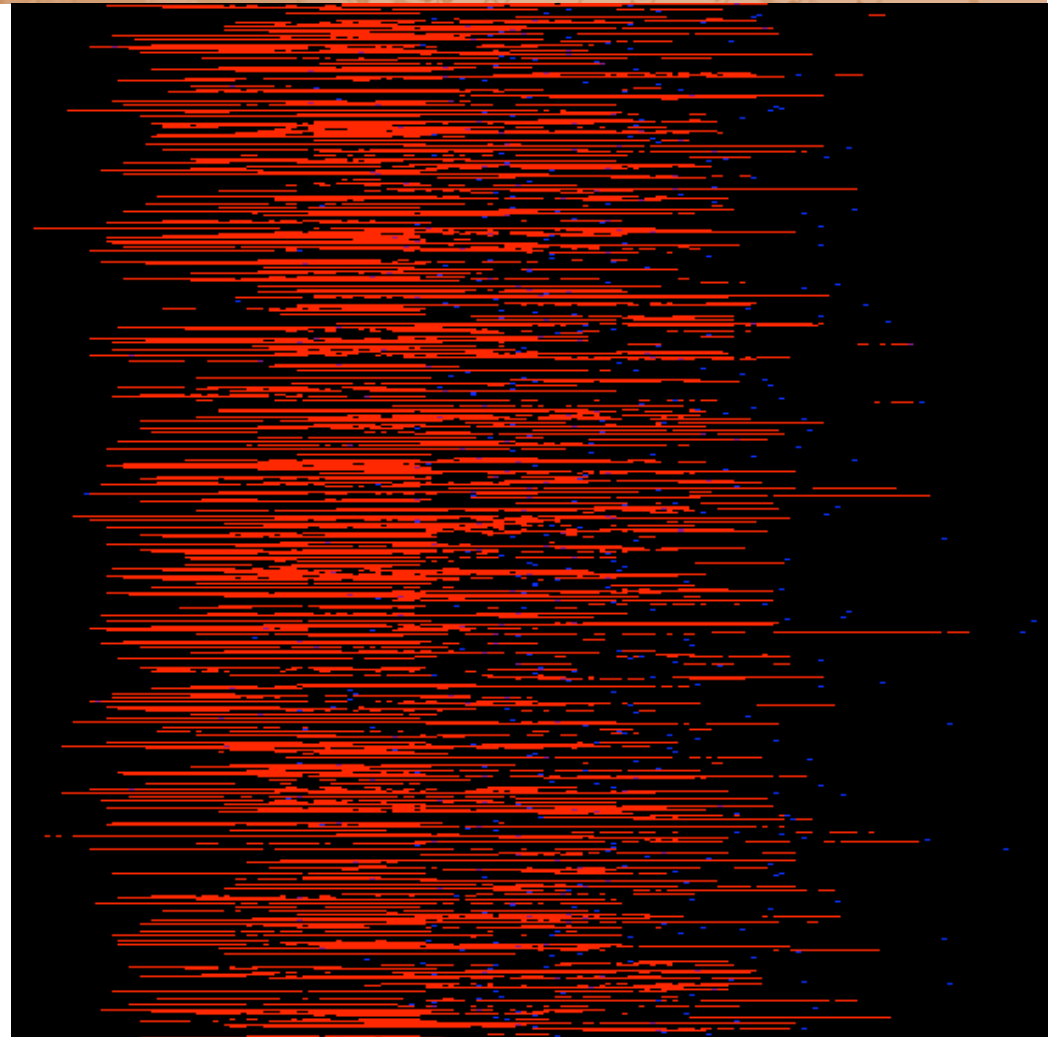
X dimension: time

Y dimension: individual  
human cases

Red: risk

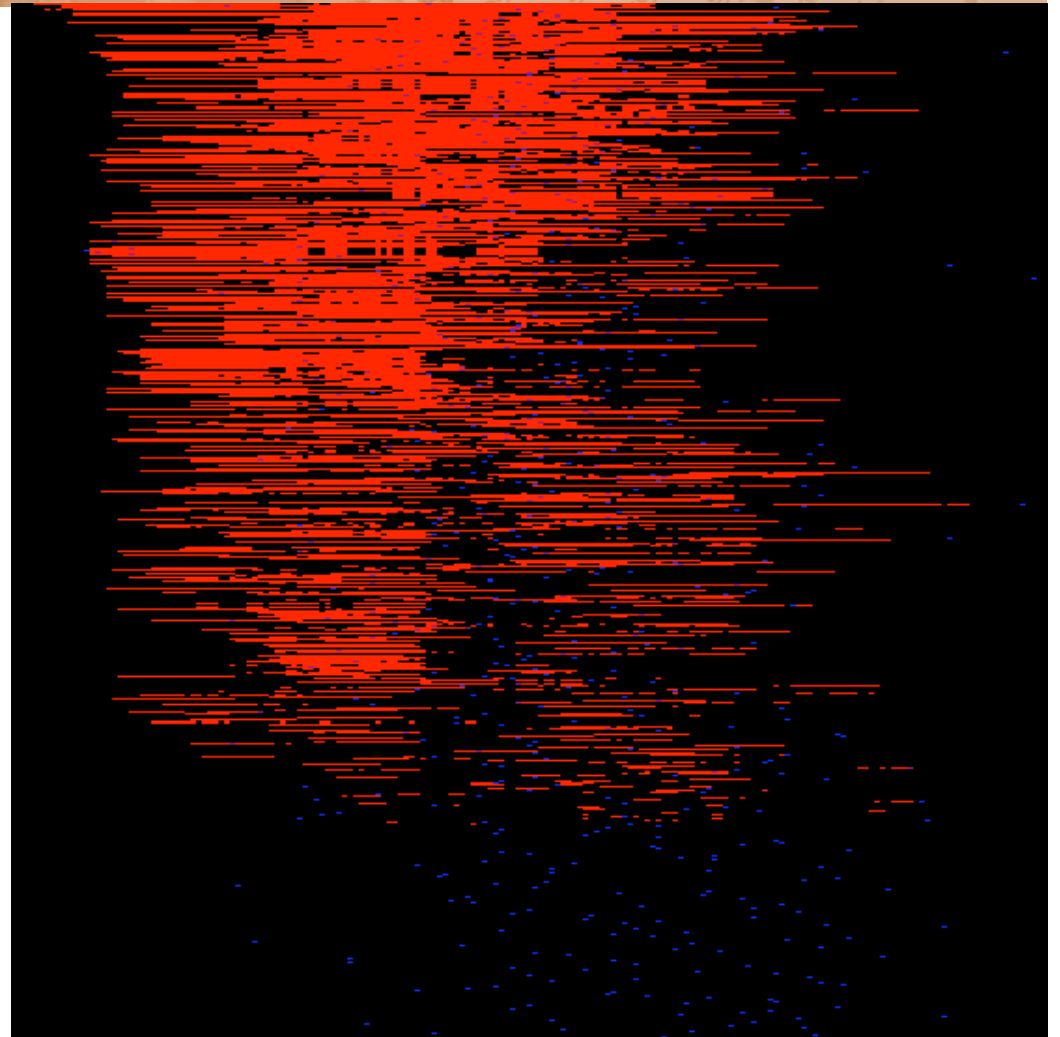
Black: no risk

Blue: date of  
human  
onset



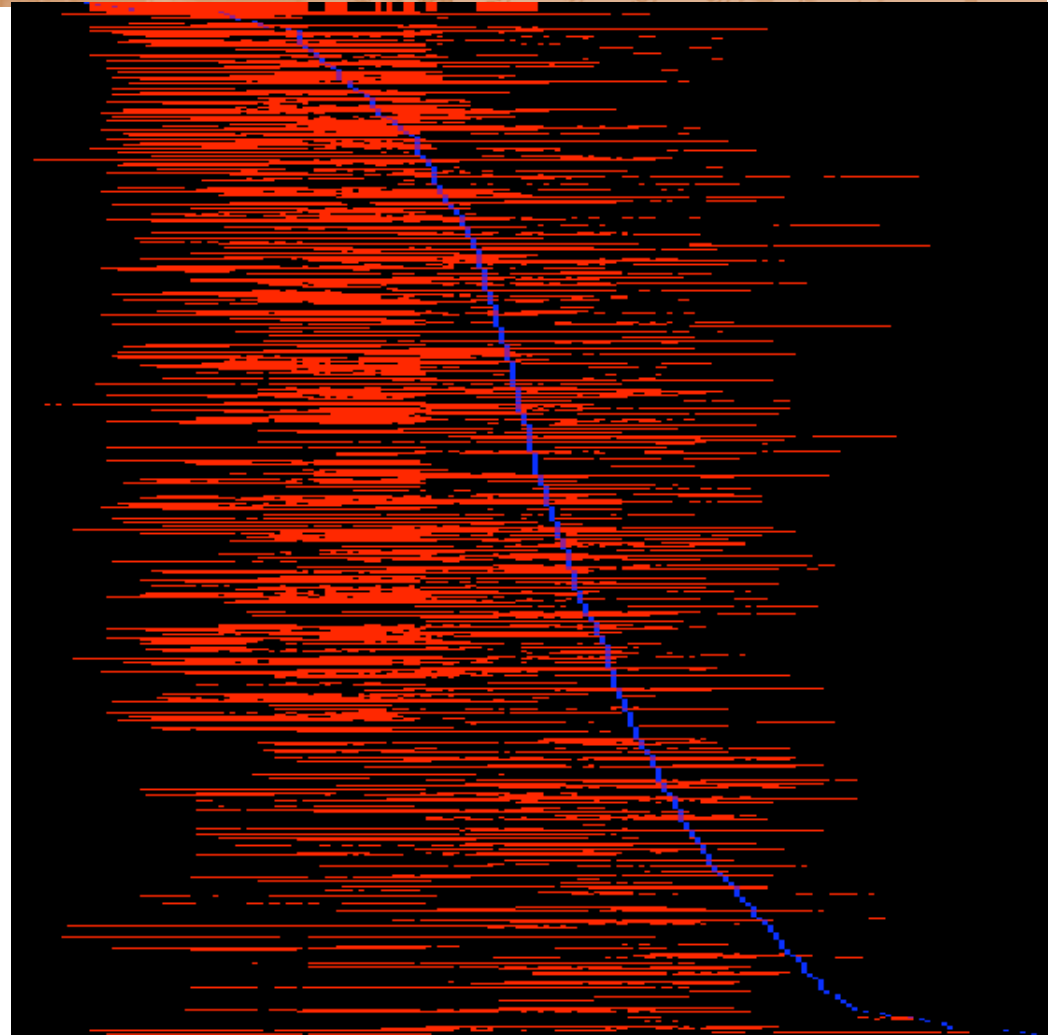
# Risk Histories

Sorted according to  
number of lit cells



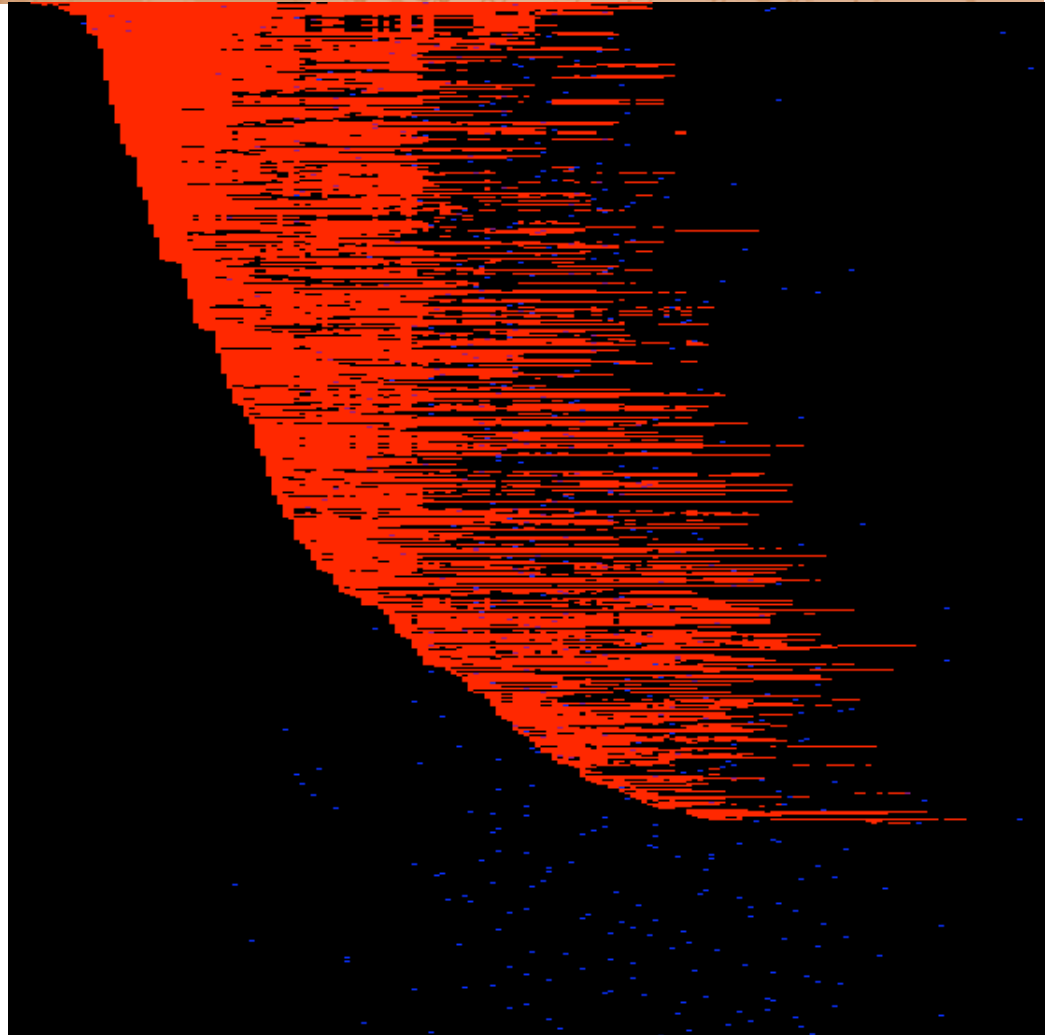
# Risk Histories

Sorted according to date of human onset



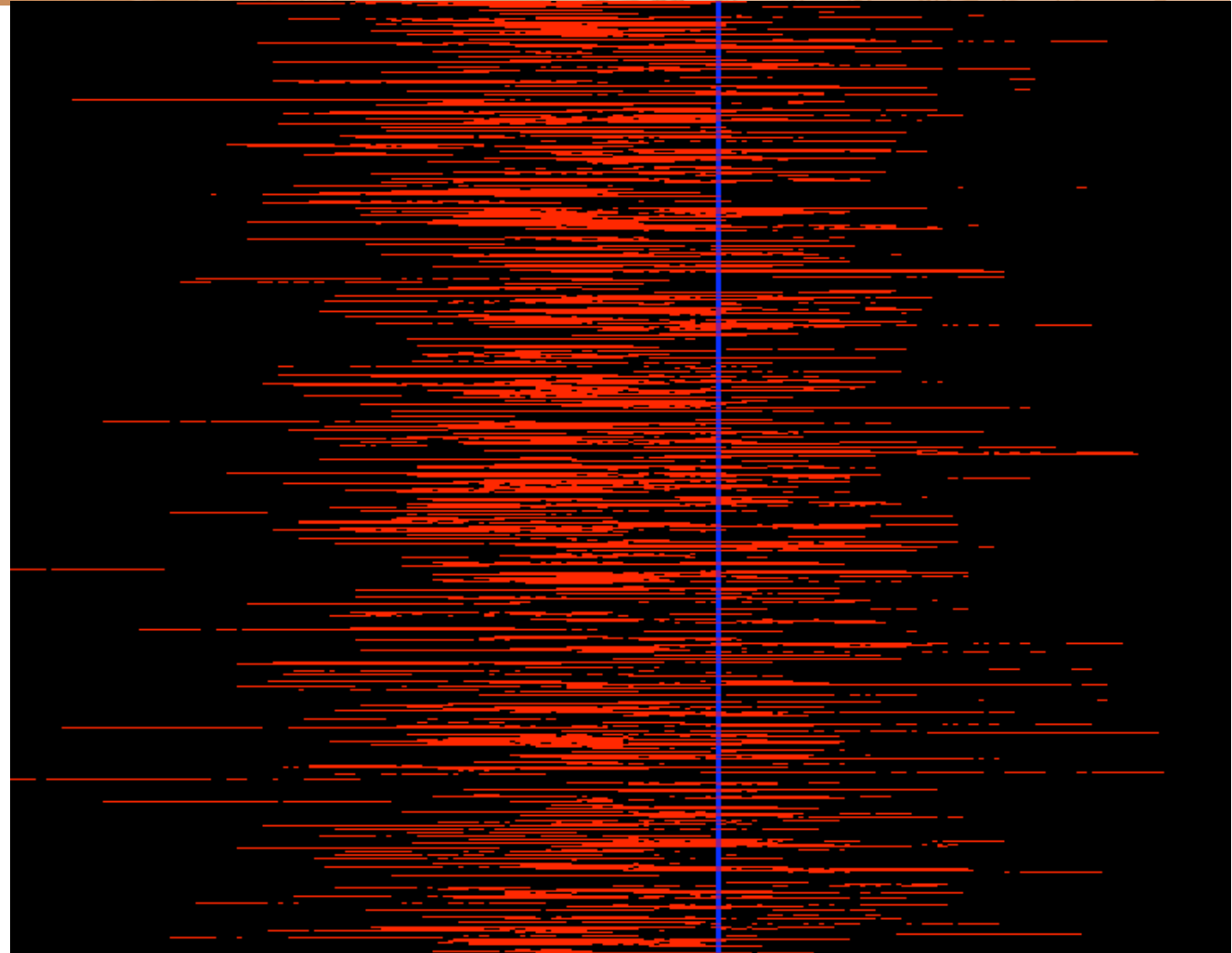
# Risk Histories

Sorted according to date of first risk



# Risk Histories

Shifted to align  
human onsets

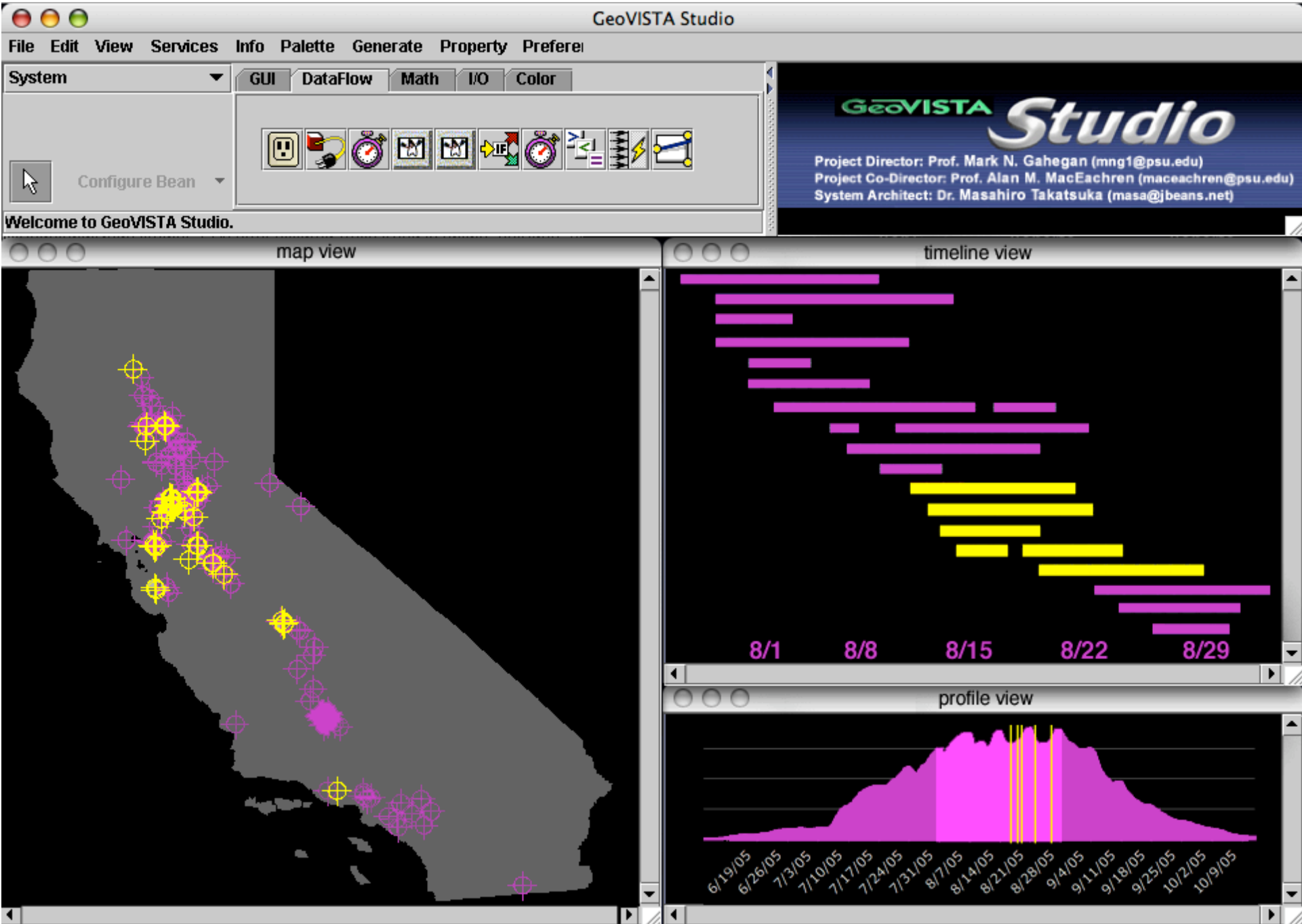






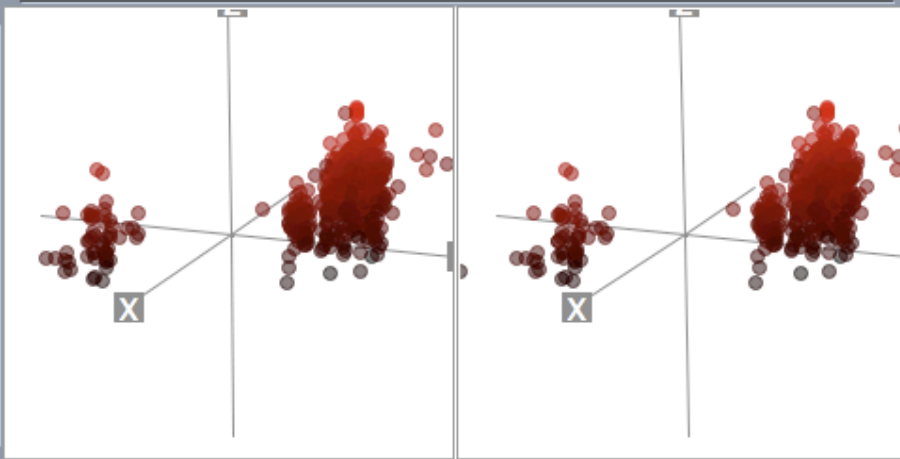
## Extracting Meaning: What Good Is It?

- **Are similar risk histories *spatially* correlated?**  
If so, what underlying circumstances do they have in common?
  - **Phase one: use linked views to explore spatial relationships**
  - **Phase two: use automated clustering to discover similarities in risk histories**
-

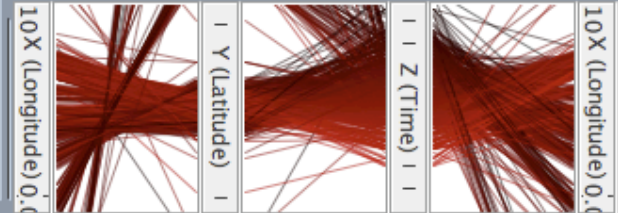


Data Sets

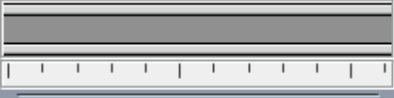
- human2004 (553)
- human2005 (686)



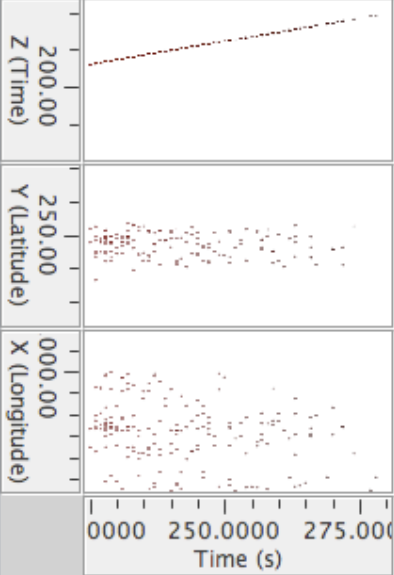
T	X	Y	Z
254.0	270.0	1266.0	254.0
266.0	279.0	1265.0	266.0
233.0	288.0	1244.0	233.0
259.0	290.0	1295.0	259.0
237.0	305.0	1171.0	237.0
225.0	306.0	1161.0	225.0
212.0	357.0	1142.0	212.0



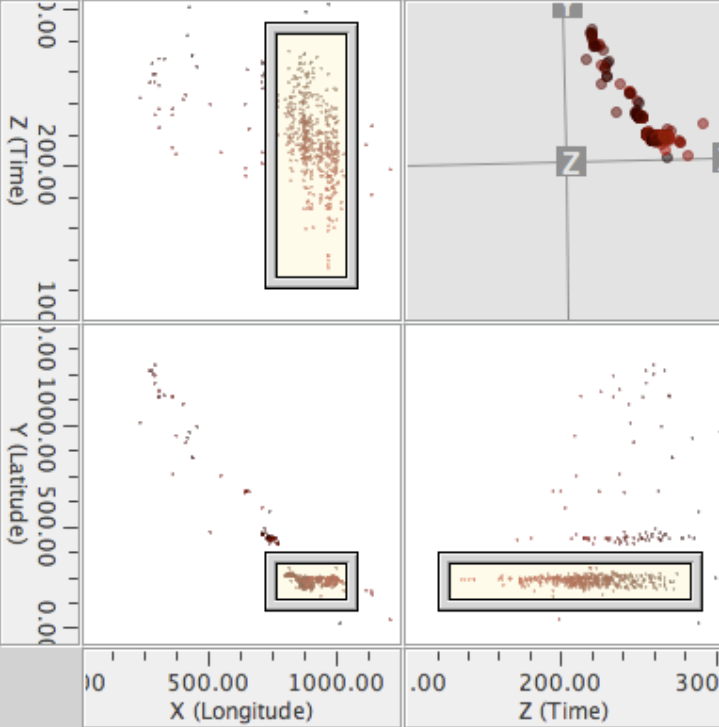
Time Slider



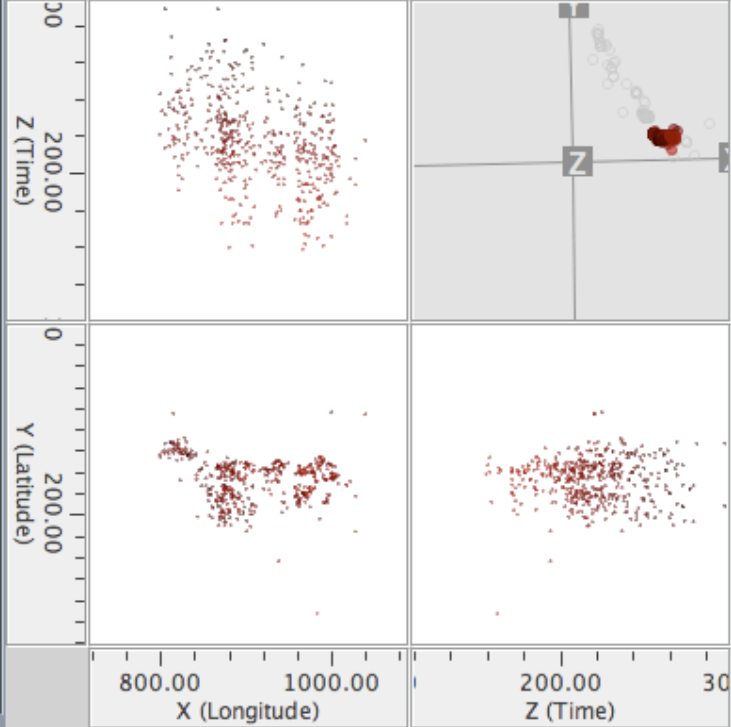
Time Series



Cube



Cube (Zoom)



# Project Progress Summary

- **Completed goals:**
  - Command-line utilities to extract risk histories
  - Implement sorting
- **In progress:**
  - Select visualization toolkit, assemble layout
- **To do:**
  - Develop interface between toolkit and command-line
  - Create linkages between views
  - Clustering of risk histories