# **IEEE VAST 2010 Challenge**

## DETAILED TASK DESCRIPTION FOR ALL CHALLENGES

## Read this first

Questions? See the discussion blog or send email to challengecommittee AT cs.umd.edu

The 2010 VAST Challenge consists of three Mini Challenges and a Grand Challenge. Contestants can choose to work on one, some, or all of the challenges. To successfully respond to the Grand Challenge, contestants must tie together all data sets with an overall scenario description using data elements from each of the four mini challenges, but are not required to submit to the mini-challenges.

The datasets used for these challenges are synthetic: that is, they are a blend of computer- and human-generated data. All datasets, whether real or synthetic, have anomalies. Some anomalies may be significant, some may not. Any anomalies reported should be supported by the proposed hypotheses. For example, "all first names start with a "M" may be interesting, but unless it is tied to the discussion of the situation, that anomaly has no place in your submission.

We have included all information necessary to form working hypotheses for the purpose of these challenges. No external data is needed to successfully perform the analysis. Be aware that using additional non-provided data may skew an otherwise successful solution.

The descriptions below provides the details for all the mini-challenges and the Grand Challenge, questions posed in each, and a description of what participants need to provide for answering each question. Each entry (Mini Challenge or Grand Challenge) is required to submit a video demonstrating how you conducted the analysis.

# **Definitions**

There are different formats/size for providing answers to the questions:

## **Short Answer:**

Short answers are only requested in the mini challenges.

A short answer is a text description of the answer and of how you arrived at the answer. It is limited to 150 words (including captions) and a maximum of 2 screen shots.

#### **Detailed Answer:**

Detailed Answers may be requested by the mini challenges and the Grand Challenge.

A Detailed Answer is a longer text description focusing on how you arrived at the answer with much more details than the Short Answer.

- For mini challenges, detailed answers are limited to 1000 words (including captions), with a maximum of 5 screen shots.
- For the Grand Challenge there is no size limit (but less than 5000 words is recommended with a maximum of 15 screen).

Detailed answers should provide the answer and describe in detail the PROCESS USED TO ARRIVE AT THE ANSWER.

Please check the **Guidelines** page before you prepare your answers.

#### Video

All entries are required to include a video with voice narration.

Maximum length (shorter is better):

- 4 minutes for Mini Challenge entries
- 15 minutes for Grand Challenge entries.

NOTE: If you submitted an entry to all three mini challenges you already have three videos for them. You may reuse all or parts of the 3 videos but should also leave enough time to show how you integrated the multiple datasets and come up with the grand challenge answers.

Please check the <u>Guidelines</u> page before you prepare your video.

# Debrief:

Debrief are requested only in the Grand Challenge. The debrief is basically the analytic product that a professional analyst would deliver after doing the analysis.

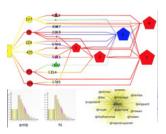
A debrief is a maximum of 2000 words narrative describing your hypothesis about the situation at hand. Include in your narrative the relationships of the various players. If there are uncertainties, you can suggest possible next steps to clarify those uncertainties.

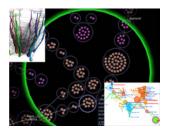
Please check the **Guidelines** page before you write your debrief.

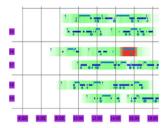
# Two-Page Summaries:

Two page Summaries are OPTIONAL, and they do not need to be submitted until after the results have been announced. They

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appear in the printed materials of the Symposium and also archived online.

These summaries allow you to give a general overview of your tools, significantly highlight novel features, provide references to papers and other relevant work and describe any new discoveries you made about your tools while working through the Challenge problem. Only the two-page summaries of the best entries (which are awarded an award) will be published in the Proceedings. Nevertheless, ALL submitted two-page summaries will be published online - along with your answer - in the VAST Benchmark Repository, whether or not they received an award.

The two-page summary should be formatted according to the general IEEE VGTC Guidelines <a href="http://www.cs.sfu.ca/~vis/Tasks/camera.html">http://www.cs.sfu.ca/~vis/Tasks/camera.html</a>

## MINI CHALLENGE 1: Text Records - Investigations into Arms Dealing

You have been charged with providing a forensic analysis of illegal arms dealing that may have taken place last year. The following contains intelligence reports and material drawn from other sources that will be of concern to you in your analysis. The information begins in 2008, and runs through early 2009. Please organize your analysis by country. In particular, we are interested in the following:

MC1.1 Summarize the activities that happened in each country with respect to illegal arms deals based on a synthesis of the information from the different report types and sources. State the situation in each country at the end of the period (i.e. the end of the information you have been given) with respect to illegal arms deals being pursued. Present a hypothesis about the next activities you expect to take place, with respect to the people, groups, and countries.

Provide a Detailed Answer.

MC1.2 Illustrate the associations among the players in the arms dealing through a social network. If there are linkages among countries, please highlight these as well in the social network. Our analysts are interested in seeing different views of the social network that might help them in counterintelligence activities (people, places, activities, communication patterns that are key to the network).

Provide a Detailed Answer.

#### Also for each mini challenge entry provide:

- a Video showing how you conducted the analysis
- the optional Two-Page Summary

#### MINI CHALLENGE 2: Hospitalization Records - Characterization of Pandemic Spread

There was a major epidemic outbreak that spanned several cities across the world in 2009. The disease tended to move fast and be fairly difficult to combat. Health officials are seeking help to analyze the illness across these countries to help characterize the spread of the disease.

You have been provided with hospital admittance and death records for cities involved in the epidemic. Please examine the following:

MC2.1: Analyze the records you have been given to characterize the spread of the disease. You should take into consideration symptoms of the disease, mortality rates, temporal patterns of the onset, peak and recovery of the disease. Health officials hope that whatever tools are developed to analyze this data might be available for the next epidemic outbreak. They are looking for visualization tools that will save them analysis time so they can react quickly.

Provide a Detailed Answer.

MC2.2: Compare the outbreak across cities. Factors to consider include timing of outbreaks, numbers of people infected and recovery ability of the individual cities. Identify any anomalies you found.

Provide a Detailed Answer.

# Also for each mini challenge entry provide:

- a Video showing how you conducted the analysis
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# MINI CHALLENGE 3: Genetic Sequences - Tracing the Mutations of a Disease

this case concerns a patient, identified by Interpol as Nicolai Kuryakin, admitted to a hospital in Paris after being removed from a flight to Moscow due to illness. The patient, now deceased, was admitted with an unidentified illness and later developed symptoms consistent with Drafa Fever. An autopsy confirmed the presence of the Drafa virus in the patient's bloodstream.

Investigators need your help to understand the evolution of the current Drafa virus outbreak, as it may shed some light on Nicolai's contacts. In question 1 and 2, you need to characterize the distance between genetic sequences and reconstruct the likely evolutionary paths. Public health organizations also need your help to understand how characteristics of the disease relate to the new virus strains. In particular, they would like to know what changes in genetic sequence make the symptoms more severe (question 3) and what changes make the virus most dangerous overall (question 4).

Technical Background on Viruses and Mutation

When the Drafa virus infects a host, it uses the host's cell machinery to replicate and evolve. When the virus replicates, it creates viral particles consisting of protein molecules. In this way, the virus makes copies of itself, growing the population of virus particles within the same host and eventually spreading to others. The proteins that make up these particles affect the ability of the virus to create disease, evade host defense mechanisms, and protect its genetic information. This genetic information includes the genes which can be thought of as the instructions on how to create the various viral protein molecules. Viruses can have very few to hundreds of such genes.

Since the Drafa virus has a high mutation rate, the genetic information contained within the virus is constantly changing. These mutations occur as a result of mistakes made during the viral replication process. The genetic code (also known as sequence) gets rewritten over time, resulting in a stronger or weaker virus. Each of these variations, if viable, creates a new viral strain or mutant.

A gene consists of a sequence of single molecules (each called a base or a nucleotide) and coded as A, T, C, or G. Triplets of these bases combine to form amino acids (for example GGC is Glycine and CAA is Glutamine) and amino acids combine to form proteins.

For this scenario, we are focusing on the genetic sequence information for a single Drafa gene, the one that codes for a surface protein on the virus. The location of this protein on the surface enables portions of it to interact with other protein molecules in the host. As such, evolution of this protein greatly affects the virulence of Drafa (the Drafa virus), its relative ability to cause disease.

As the Drafa virus spreads from host to host, it mutates and evolves. Each mutation substitutes an existing base with a different one (for example, A changing to C, G changing to C, ...). Over time, this results in evolved viral strains (mutants) with a number of modified bases.

For the given scenario, diagnostic tests confirm that the current outbreak is a new evolved form of the Drafa virus. Viral mutants have been isolated from human blood samples in hospitals where patients are being treated, and laboratory sequencing techniques are being used to collect genetic information.

Mc3.1 What is the region or country of origin for the current outbreak? Please provide your answer as the name of the native viral strain along with a brief explanation.

Provide a Short Answer.

MC3.2 Over time, the virus spreads and the diversity of the virus increases as it mutates. Two patients infected with the Drafa virus are in the same hospital as Nicolai. Nicolai has a strain identified by sequence 583. One patient has a strain identified by sequence 123 and the other has a strain identified by sequence 51. Assume only a single viral strain is in each patient.

Which patient likely contracted the illness from Nicolai and why? Please provide your answer as the sequence number along with a brief explanation.

Provide a Short Answer.

**MC3.3** Signs and symptoms of the Drafa virus are varied and humans react differently to infection. Some mutant strains from the current outbreak have been reported as being worse than others for the patients that come in contact with them.

Identify the top 3 mutations that lead to an increase in symptom severity (a disease characteristic). The mutations involve one or more base substitutions. For this question, the biological properties of the underlying amino acid sequence patterns are not significant in determining disease characteristics.

For each mutation provide the base substitutions and their position in the sequence (left to right) where the base substitutions occurred. For example,

C → G, 456 (C changed to G at position 456)

 $G \rightarrow A$ , 513 and  $T \rightarrow A$ , 907 (G changed to A at position 513 and T changed to A at position 907)

A → G, 39 (A changed to G at position 39)

Provide a Short Answer.

**MC3.4** Due to the rapid spread of the virus and limited resources, medical personnel would like to focus on treatments and quarantine procedures for the worst of the mutant strains from the current outbreak, not just symptoms as in the previous question. To find the most dangerous viral mutants, experts are monitoring multiple disease characteristics.

Consider each virulence and drug resistance characteristic as equally important. Identify the top 3 mutations that lead to the most dangerous viral strains. The mutations involve one or more base substitutions. In a worst case scenario, a very dangerous strain could cause severe symptoms, have high mortality, cause major complications, exhibit resistance to anti viral drugs, and target high risk groups. For this question, the biological properties of the underlying amino acid sequence patterns are not significant in determining disease characteristics.

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For each mutation provide the base substitutions and their position in the sequence (left to right) where the base substitutions occurred. For example,

- C → G, 456 (C changed to G at position 456)
- G → A, 513 and T → A, 907 (G changed to A at position 513 and T changed to A at position 907)
- A → G, 39 (A changed to G at position 39)

Provide a Detailed Answer.

## Also for each mini entry provide:

- a Video showing how you conducted the analysis
- the optional Two-Page Summary

## Grand Challenge: Arms Dealing and Pandemic

In Mini-Challenge 1, you investigated illegal arms deals that involved several countries. In Mini-Challenge 2, you investigated a pandemic outbreak of a virus across several cities in the world. In Mini-Challenge 3, you investigated the source of a virus strain taken from a victim of the pandemic.

For the Grand Challenge, you are charged with investigating any possible linkage between the illegal arms dealing and the pandemic outbreak.

In particular, you need to address the following:

- 1. Briefly describe your hypothesized linkage between the arms dealing activity and the pandemic outbreak.
- 2. Where did the disease originate (as far as you can tell with the data)? Provide a time-based tracing of its spread among countries. If you have established linkages between arms dealers in certain countries and the pandemic, please indicate this.
- 3. We had countries with arms dealers identified in MC 1 that did not suffer pandemic outbreaks in MC 2. Provide a hypothesis as to why some countries that may have been involved with arms dealers did not suffer an outbreak?

Recall that we are particularly interested in how visualizations helped you with your analysis. Remember to explain in your process what visualizations you used and what insights were gained from these visualizations.

No additional data set is needed for the Grand Challenge (only the data provided in mini 1, 2 and 3).

#### For the grand challenge you need to provide:

- a debrief
- a Video showing how you conducted the analysis
- the optional Two-Page Summary

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