Genomics: Insight and Recommendations

Health Information Technology Standards Advisory Committee (HITSAC)

Aaron Black
Director of Informatics
Inova Translational Medicine Institute
May 12th, 2016
Presentation Outline

• Introduction
  – Personal background
  – Inova Translational Medicine Institute (ITMI)

• Challenges

• Opportunities

• Process Recommendations

• Questions and Comments
– Personal Background
  • Consulting
  • Start-Up Company
    – Medical Billing
  • The Cancer Genome Atlas (TCGA)
  • Inova Translational Medicine Institute
TCGA Network – Data Generation and Sharing
ITMI: Mission and Vision

Improve health of the diverse communities we serve through application of genomics and associated molecular science to drive “computation assisted”, intelligent individualized care

- Applied genomics
- Predictive wellness
- Disease risk management
- Pharmacogenomics

STARTED IN 2011
Research on the integration of genomic information into the practice of medicine

- >90 FTEs
- ~1/3 Clinical
- 1/3 IT/Informatics
- 1/3 Lab technical
3,476 families are enrolled in our studies

Preterm Birth has ~500 families, born <37 wks. (71 <28 wks.)

ITMI has 9,000 whole genome sequences integrated with clinical electronic health record data and study specific information in its data-set

Maternal samples analyzed for RNAseq, methylation, expression

There are 62,700 specimens including 1,427 placenta samples in the ITMI biobank
Network and Data Movement - Research

AWS Research

Outside Network

Inova Research

Inova Clinical
IGL TODAY

• Pharmacogenomics
  – Individual Drug specific tests
    • Example - CLOPIDOGREL
  – Panels
    • MediMap

– Cancer Panels
  – Used for Inova Molecular Tumor Board
Informatics

• Pharmacogenomics
  – Epic Integration
    • Custom Reports
    • Discrete results \ HL7 messaging
    • In process
  – Knowledgebase Vendor
    • Translational Software

• Cancer Panels
  – Cancer Hotspot \ Oncomine
Challenges
Inova Challenges

• Inova - MediMap - https://www.inova.org/itmi/medimap

  – Pharmacogenomics (PGx) Panel
  • Infants at birth – Inova Fairfax Hospital
  • Consent needed from Mother
  • 7 Genes and their alleles (FDA Approved)
  • Large amount of tests (compared to other PGx Tests at Inova)
Return of Results

- Complicated
  - Needed concise summary – first page of report
  - Detailed followed later

Pharmacogenomics is specialized

- Knowledgebase
- Annotations

EHR not ready for Genetic \ Genomic results

Customization needed for:

- EHR, LIS, data processing, data exchange and reporting (just about everything)

Standardization of genetic testing, Allele and Mutation coding is still developing

Others are still using reports with little discrete return of results within EHR

Data sizes small compared to other Next Generations Sequencing (NGS) tests
Challenges – From Research to Clinical Care

Data and Information

What we want it to look like!

Does it look more like?
State of Mind – From Research to Clinical Care

- **Standardization**
  - **Healthcare System**
    - Built for billing and government regulations
    - Can be misleading for research
    - EHRs, still new \ lack maturity for genetics \ genomic results
  - **Research**
    - Love the concept
    - Hard to implement
    - Always something new!
Genomic Testing Matrix – NGS Panels

Pharmacogenomics (Panels)

- Test Ordering: EHR
- Lab Processing: LIMS
- Bio Data QC: Internal Pipeline
- Data Analysis \ Annotation: Software
- Clinical Review Process: Software
- Return of Results: EHR
- Clinical Decision Support: EHR

Cancer (Panels)

- Test Ordering: EHR
- Lab Processing: LIMS, Lab Machine
- Bio Data QC: Internal Pipeline
- Data Analysis \ Annotation: Software
- Clinical Review Process: Software
- Return of Results: EHR
- Clinical Decision Support: EHR

Whole Genome Sequencing …etc

- Test Ordering: EHR
- Lab Processing: LIMS
- Data Analysis \ Annotation: Software
- Return of Results: EHR
- Clinical Decision Support: EHR
Genomic Tests – Additional Functionality

Pharmacogenomics (Panels)

- Reporting \ Analytics
  - Reporting Tool

- Clinical Alerts (PGx, Trials)
  - EHR

- Virtual Tumor Board
  - N/A

- 3rd Party Test Ordering
  - Manual

- Research Data Sharing
  - Build or Buy

- Integration with EHR
  - Build or Buy

Cancer (Panels)

- Reporting \ Analytics
  - Reporting Tool

- Clinical Alerts (PGx, Trials)
  - EHR

- Virtual Tumor Board
  - Build or Buy

- 3rd Party Test Ordering
  - Manual

- Research Data Sharing
  - Build or Buy

- Integration with EHR
  - Build or Buy
Genetic \ Genomic data standards

Next Generation Sequencing
Data Level: Genomic
Defined by:
Genomic Build Version
Chromosome, Genomic Start and Stop
Reference and Observed Allele

Sanger Sequencing
Data Level: DNA
Defined by:
Reference Sequence Version
Mutations Using HGVS standard
Nucleotide Start and Stop
Reference and Observed Allele

Genetic Testing Kits
Data Level: DNA Snippets
Defined by:
HGVS Name and or
Common Name / BioMarker

Source: Variation of LOINC Genomics Standards 2016 Draft
Challenges for Genetic \ Genomic Testing

- New tests and constantly changing knowledge
  - Many vendors don't have LOINC codes for their genetic tests
  - Codes inconsistently defined

<table>
<thead>
<tr>
<th>163</th>
<th>02600-3</th>
<th>Cells analyzed</th>
<th>Num</th>
<th>Pt</th>
<th>Bld/Tiss</th>
<th>Qn</th>
<th>Molgen</th>
<th>H,7,CYTOSEN</th>
<th>YH</th>
</tr>
</thead>
<tbody>
<tr>
<td>164</td>
<td>02601-1</td>
<td>Cells counted</td>
<td>Num</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Qn</td>
<td>Molgen</td>
<td>H,7,CYTOSEN</td>
<td>YH</td>
</tr>
<tr>
<td>165</td>
<td>51777-7</td>
<td>CYP gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>166</td>
<td>29396-1</td>
<td>CYP450 gene allele 1</td>
<td>Arb</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>AR</td>
</tr>
<tr>
<td>167</td>
<td>29395-9</td>
<td>CYP450 gene allele 2</td>
<td>Arb</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>AR</td>
</tr>
<tr>
<td>168</td>
<td>66968-0</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Amino Fd</td>
<td>Nar</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>YH</td>
</tr>
<tr>
<td>169</td>
<td>29404-0</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nar</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>170</td>
<td>21177-1</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>QS</td>
</tr>
<tr>
<td>171</td>
<td>29417-9</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Amino Fd</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>172</td>
<td>21054-9</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>QR</td>
</tr>
<tr>
<td>173</td>
<td>21054-4</td>
<td>CYP450 gene mutations tested for</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>QR</td>
</tr>
<tr>
<td>174</td>
<td>20594-4</td>
<td>CYP450 gene mutations tested for</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>GL</td>
</tr>
<tr>
<td>175</td>
<td>38414-9</td>
<td>CYP450 gene c.1078delT</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>176</td>
<td>38415-3</td>
<td>CYP450 gene c.2184delA</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>177</td>
<td>38416-1</td>
<td>CYP450 gene c.2788+50A</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>178</td>
<td>38417-9</td>
<td>CYP450 gene c.3120+10A</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>179</td>
<td>39700-2</td>
<td>CYP450 gene c.3195del6</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>180</td>
<td>38418-7</td>
<td>CYP450 gene c.3659delC</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>181</td>
<td>38419-0</td>
<td>CYP450 gene c.3849+1005A</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>182</td>
<td>38420-2</td>
<td>CYP450 gene c.621+10T</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>183</td>
<td>38421-7</td>
<td>CYP450 gene c.711+10T</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>184</td>
<td>38422-7</td>
<td>CYP450 gene p.A405E</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>185</td>
<td>38423-9</td>
<td>CYP450 gene p.A1152H</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>186</td>
<td>21655-6</td>
<td>CYP450 gene p.S508del</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>GP</td>
</tr>
<tr>
<td>187</td>
<td>38424-9</td>
<td>CYP450 gene p.L698E</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>188</td>
<td>32375-6</td>
<td>CYP450 gene p.V398f</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>189</td>
<td>38426-4</td>
<td>CYP450 gene p.V553f poly 7/9T variant</td>
<td>Arb</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>190</td>
<td>37475-4</td>
<td>CYP450 gene p.R137H+T variant</td>
<td>Pr</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Ord</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>191</td>
<td>37931-8</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nom</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>3N</td>
</tr>
<tr>
<td>192</td>
<td>42242-2</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nar</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>193</td>
<td>37474-9</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nar</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
<tr>
<td>194</td>
<td>40004-4</td>
<td>CYP450 gene mutation analysis</td>
<td>Prtd</td>
<td>Pt</td>
<td>Bld/Tiss</td>
<td>Nar</td>
<td>Molgen</td>
<td>MOLPATH,MUT</td>
<td>PH</td>
</tr>
</tbody>
</table>
### Variant and Allele standards

- Definition of variants still being defined
- Single gene vs multi-gene
- Amplified with complex variants \ structural variants
- Difficult to nail down overall data standardization on genes \ alleles \ interpretation

**An over-simplification**

<table>
<thead>
<tr>
<th>Simple</th>
<th>Complex</th>
<th>Structural (Insert)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A T T G C T</td>
<td>A T T G C T A T T G C A</td>
<td>A T T G C A T A C G C A T T G C</td>
</tr>
<tr>
<td>Blue</td>
<td>Blue + <strong>Yellow</strong></td>
<td><strong>Yellow</strong> ??? Blue</td>
</tr>
</tbody>
</table>

Call it **Green** or (Blue + **Yellow**)?

What if there is a 3rd \ 4th or \ 5th color?

What do you call this?

What if there is 10 digits between these sequences? Do we change what we call it?
Different Interpretations

Vendor and Platform differences

- **Standardization of Metadata**
  - Platforms
    - NGS \ Microarray and other
    - Depth, quality
  - Annotation
    - Lack of standard knowledgebase
    - Open Source vs. Proprietary
  - Lack of Vendor Incentive
    - To conform to standard
    - Or provide standard messaging
  - Analysis Software
    - Output differences
    - Differences in interpretation (quality and refresh rate of knowledgebase)
    - Filtering \ Versioning
Genomic Data Standards

- Output differences – examples -> Whole Genome Sequencing
More Variation – Variant Count Differences

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Variant Count</th>
<th>Sample ID</th>
<th>Variant Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-101-782</td>
<td>30,852,475</td>
<td>M-101-860</td>
<td>21,730,706</td>
</tr>
<tr>
<td>M-101-745</td>
<td>30,042,376</td>
<td>M-101-859</td>
<td>22,608,801</td>
</tr>
<tr>
<td>M-101-739</td>
<td>26,707,715</td>
<td>M-101-857</td>
<td>21,799,979</td>
</tr>
<tr>
<td>M-101-725</td>
<td>29,824,009</td>
<td>M-101-852</td>
<td>21,716,404</td>
</tr>
<tr>
<td>M-101-564</td>
<td>31,643,799</td>
<td>M-101-844</td>
<td>23,669,638</td>
</tr>
<tr>
<td>M-101-563</td>
<td>29,468,614</td>
<td>M-101-841</td>
<td>22,096,639</td>
</tr>
<tr>
<td>M-101-551</td>
<td>42,026,951</td>
<td>M-101-831</td>
<td>24,763,282</td>
</tr>
<tr>
<td>M-101-545</td>
<td>37,007,718</td>
<td>M-101-822</td>
<td>22,556,401</td>
</tr>
<tr>
<td>M-101-541</td>
<td>31,025,564</td>
<td>M-101-809</td>
<td>24,125,102</td>
</tr>
<tr>
<td>M-101-533</td>
<td>28,782,119</td>
<td>M-101-807</td>
<td>23,856,995</td>
</tr>
<tr>
<td>M-101-527</td>
<td>26,249,287</td>
<td>M-101-798</td>
<td>23,277,692</td>
</tr>
<tr>
<td>M-101-521</td>
<td>27,790,222</td>
<td>M-101-797</td>
<td>24,547,830</td>
</tr>
<tr>
<td>M-101-520</td>
<td>36,558,146</td>
<td>M-101-792</td>
<td>22,992,333</td>
</tr>
<tr>
<td>M-101-514</td>
<td>29,651,471</td>
<td>M-101-783</td>
<td>22,395,499</td>
</tr>
<tr>
<td>M-101-511</td>
<td>31,727,054</td>
<td>M-101-768</td>
<td>24,125,402</td>
</tr>
</tbody>
</table>

**Variant Rows\Variant File**

<table>
<thead>
<tr>
<th>Avg Illumina</th>
<th>Avg Complete Genomics</th>
<th>Pct Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>37,891,953</td>
<td>22,983,258</td>
<td>39%</td>
</tr>
</tbody>
</table>

```
<table>
<thead>
<tr>
<th>Genome Numbers</th>
<th>Variant Rows</th>
<th>Variant Row Columns</th>
<th>Total Data Points Tracked</th>
</tr>
</thead>
<tbody>
<tr>
<td>5,501</td>
<td>208,443,630,919</td>
<td>27</td>
<td>5,627,978,034,812</td>
</tr>
<tr>
<td>2774</td>
<td>63,755,558,741</td>
<td>27</td>
<td>1,721,400,085,999</td>
</tr>
<tr>
<td>8,275</td>
<td>272,199,189,660</td>
<td>54</td>
<td>7,349,378,120,811</td>
</tr>
</tbody>
</table>
```
Considerations

• Constantly new and updated information on current genes \ molecular markers
  – Standardization is crucial for constantly updating knowledge base
  – In order to realize value, providers and vendors need to keep knowledge updated
  – Mechanisms to alert patients of new information
    • Legal and ethical considerations
    • Business \ how long to keep data?
  – What results to return?
    • Clinically Actionable
    • Variants of unknown significance
    • Other?

• Other items to consider
  – How long to store raw and intermediate results? Which results? Costs?
  – How often should we update the knowledge base? Upon request, will it be a billable service?
  – Should we scan records when there is a major adverse discovery found?
LOINC coding – current state – PGx Example

Genetic \ Genomic Test

- PGx Panel test example
  - LOINC code: **55208-3** - DNA analysis discrete sequence variation panel

- Gene:
  - LOINC code: **48018-6** - Gene Identifier

- Human Genome Organization Nomenclature Committee Identifier for a Genes)

- Allele
  - LOINC code: **53034-5** - Allelic state
  - Heteroplasmic: LA6703-8
  - Homoplasmic: LA6704-6
  - Homozygous: LA6705-3
  - Heterozygous: LA6706-1
  - Hemizygous: LA6707-9

- Interpretation
  - LOINC code: **53040-2** - Drug metabolism sequence variation interpretation
  - Ultrarapid metabolizer: LA10315-2
  - Extensive metabolizer: LA10316-0
  - Intermediate metabolizer: LA10317-8
  - Poor metabolizer: LA9657-3
Single Gene vs Panel

Genetic \ Genomic Test

- Gene
- Variant \ Allele
- Interpretation

Genetic \ Genomic Test Panel

- Gene
- Variant \ Allele
- Interpretation
- Gene
- Variant \ Allele
- Interpretation
- Gene
- Variant \ Allele
- Interpretation
Complex Panel

Genetic \ Genomic Test Panel

Gene 1

Variant \ Allele 1

Gene 2

Variant \ Allele 2

Interpretation

Gene

Variant \ Allele

Interpretation
Genetic Test Panel Variants

Genes Tested
- Ranges
- Gene Name (coded)
- Disease Assessed (coded)
- Interpretation (coded)
- Source (coded)
- HGVS Version

Variant

Transcript Specification
- Type
- Gene
- DNA Change
- Amino Acid Change

Genomic Specification
- Reference Sequence
- Reference Allele
- Allele Location
- Alternate Allele

Optional Coding systems (test specific)
- dbSNP ID
- COSMIC (Cancer)
- CiGAR

Allele Specifications
- Allelic State
- Clinical Significance
- Assoc. Phenotype
Genetic Test Panel Variants

Genes Tested

Simple Variant
- Transcript Specification
- Genomic Specification
- Optional Coding systems (test specific)
- Allele Specifications

Complex Variant
- Simple Variant
  - Transcript Specification
  - Genomic Specification
  - Optional Coding systems (test specific)
  - Allele Specifications
  - Simple Variant
    - Transcript Specification
    - Genomic Specification
    - Optional Coding systems (test specific)
    - Allele Specifications
  - Structural Variant
    - Transcript Specification
    - Genomic Specification
    - Optional Coding systems (test specific)
    - Allele Specifications

All Can Repeat
Opportunities
• Consumer demand
  
  Consumers are demanding genetic and genomic interpretations
Transient Population - Example
• Movement to Proactive Health Management
  – Personalized, Preventive, and Precise
  – Focus on specific risks in specific patients
  – Increase surveillance of high-risk individuals
  – Able to use high-risk medications for targeted individuals
  – Reduce adverse events in high-risk individuals

• Improved Clinical Decision Support
  – Timely application of new genomic knowledge in delivery of healthcare

• Reduced Health Care Costs
  – Reduced adverse events
  – Decrease potential liability

How does the U.S. rank internationally?

Benefits

- Cost savings
  - Tests can be run once
  - Save costs to reinterpret vs new test and analysis
  - Computer and staff time savings
- Further savings if this data can be securely exchanged between institutions
- Utility grows exponentially as more data and information is gathered
- Create standardized methodology for Return on Investment (ROI)
  - Benchmark for institutions who are evaluating tests
  - Used to help drive reimbursement from Government and Private Insurance
Virginia Leadership Advantages

– Become US leader in genetic \ genomic testing standards
  • Attractive to partnerships and opportunities both inside \ outside of Virginia

– Research
  • Consortium of Virginia institutions and collaborators can produce high quality, consistent and large datasets for research and collaboration
  • Population Health – genetic \ genomics results combined with other healthcare datasets
  • Collaborations for research and technology development
  • Private \ Public partnerships and investment

– Virginia can attract and keep people and families who value the best healthcare

– Attract health, scientific and technology talent to work in Virginia
  • Work with software and data companies for mutual benefit

– Venture Capital and Philanthropy

– Advise other State and Federal Agencies
Why now?

- **Momentum**
  - Large push from Government, Academia, Venture and Philanthropy

- **Consortium**
  - Group think, others are pushing forward and provide valuable information.

- **Optimizations**
  - More knowledge of costs and performance metrics for better evaluations of studies and clinical testing.
Opportunities

• Vendor Maturity in Healthcare and Life Sciences
  – Many more valid options, more understanding and less ramp-up time.
Proposed Process for Genetic \ Genomic Standards
Current Implementation Roadmap Recommendations (used by several pilot organizations)

1. Incorporate design in databases
2. Implement design standard in laboratory reports and/or data files
3. Validate utility of information model through active use in business
4. Iterate on information model incorporating lessons learned
5. Formally develop HL7 interfaces for fully codified/qualified data when business is ready

Proposed process

1. Organize cross functional team to build methodology on data specifications for Genetic and Genomic tests

Who?

- Hospitals \ State Labs (2-3 distinct institutions)
  - Criteria
    - Have or will offer genetic \ genomic tests
    - Lab \ Genetic Experts (humans, microbes, animals)
    - Dedicate Clinical, Genomic and EHR expertise
    - Informatics experts

- Virginia Government
- External informatics experts (HL7 and LOINC)
- Software vendor(s)
– (2) Goal for cross functional team
  • Create standards recommendations to Virginia for at least 2 genetic tests
  • Select:
    – One simple test
    – One slightly more complex
  • An example would be Pharmacogenomics (PGx)
    – Simple → Individual Gene \ Drug test (ie Plavix)
    – More complex → Set of PGx genes and alleles
(3) For those tests, the team would present specification to HITSAC recommendations on, but not limited to the following:

- Coding and messaging standards (LOINC, HGVS, COSMIC..)
- Data exchange standards between like institutions (LOINC..)
- Reporting standards
  - Return of results to EHR (Formats and exchange \ LOINC, HL7)
  - Impact of tests
    » Patient care improvement (short and medium term)
    » ROI
    » Overall Efficiencies gained
– (3) Present roadmap for future tests to evaluate standards for more complex and diverse tests.
  • To support clinical use cases like:
    – Newborn screening
    – Prenatal screening
    – Cancer treatment \ Clinical trials \ Cancer Registry
    – Rare disease
    – Public Health Reporting \ Virginia Health Information Exchange
  • Type of tests \ technologies
    – Panels - NGS \ Array and others
    – Whole Exome and Genome
    – Proteomics \ Cytogenetic testing
Rationale for Process

- Complex standards need experts from multiple disciplines
- Agility will be key, as tests and national standards adopted will change
- Start with simple tests. The standards are better defined for the simple tests
- Application of these standards in one or more institutions will help filter out real world issues and create momentum.
- This is needed (period).
Inova Translational Medicine Institute
John Niederhuber MD
Joe Vockley PhD
Ben Solomon MD
Greg Eley, PhD
Kathi Huddleston, PhD
Ram Iyer, PhD
Dale Bodian, PhD
Wendy Wong, PhD
Alina Khromykh, MD
Dan Stauffer, PhD
and teams

ITMI Informatics
Lin Smith
Sakthi Madhappan
Quang Tran
Prachi Kothiyal PhD
Nick Plaussiou
Shan Gao
Deacon Sweeney PhD
Xinyue Liu
Mehul Shah
Christopher Miller MD
Suriah Shams
Igor Karbovsky
Radhika Hastak
Stuart Young PhD
Anatoly Ulyanov PhD
Michael Soh
James Tallant
Wesley Romero
Anna Chu
Matthew Mares
and teams

Inova IT \ Informatics
Dr. Marshall Ruffin
Dr. Ryan Bosch and Team
Jeannie Brooke and Team
Maggie Cornett
Nikole Raimondo
IT Networking and Infrastructure Teams