

A Trio of Visualization Design Studies

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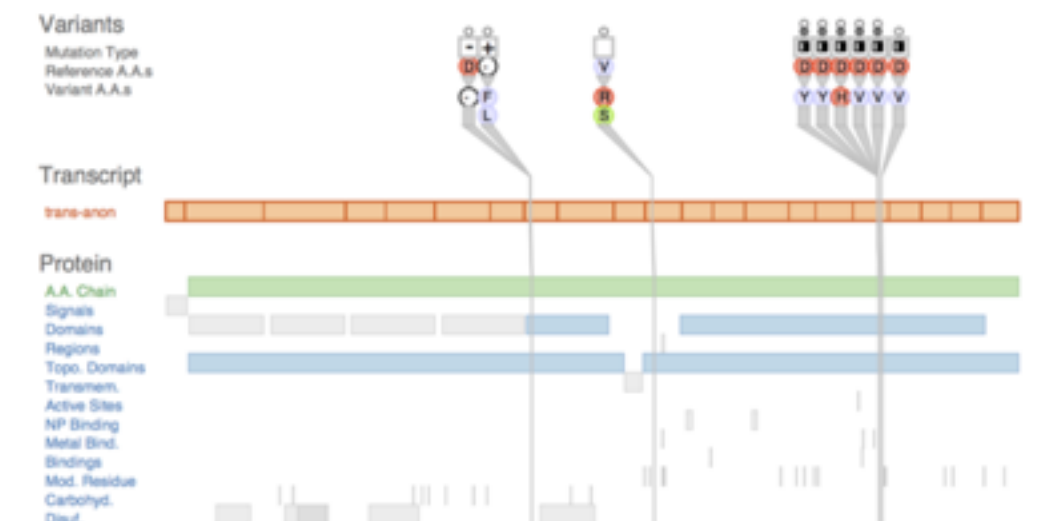
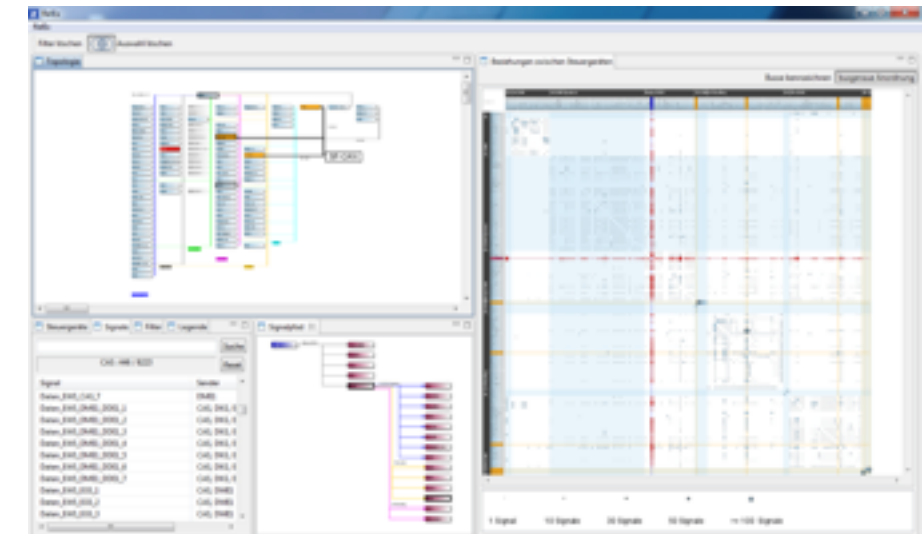
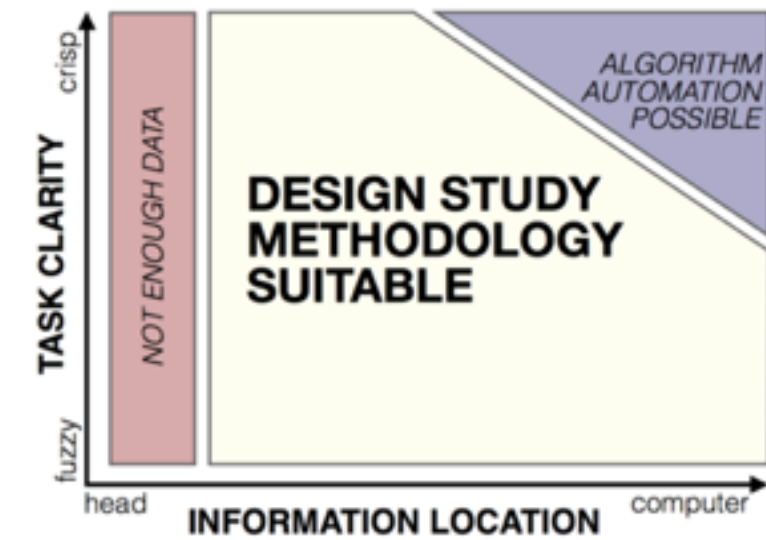
Segal Design Institute, Northwestern University

8 April 2014, Chicago IL

<http://www.cs.ubc.ca/~tmm/talks.html#chicago14>

Trio

- Design Study Methodology
 - meta-paper: how to do design studies
- RelEx
 - overlay network optimization for in-car networks
- Variant View
 - sequence variant analysis in gene context



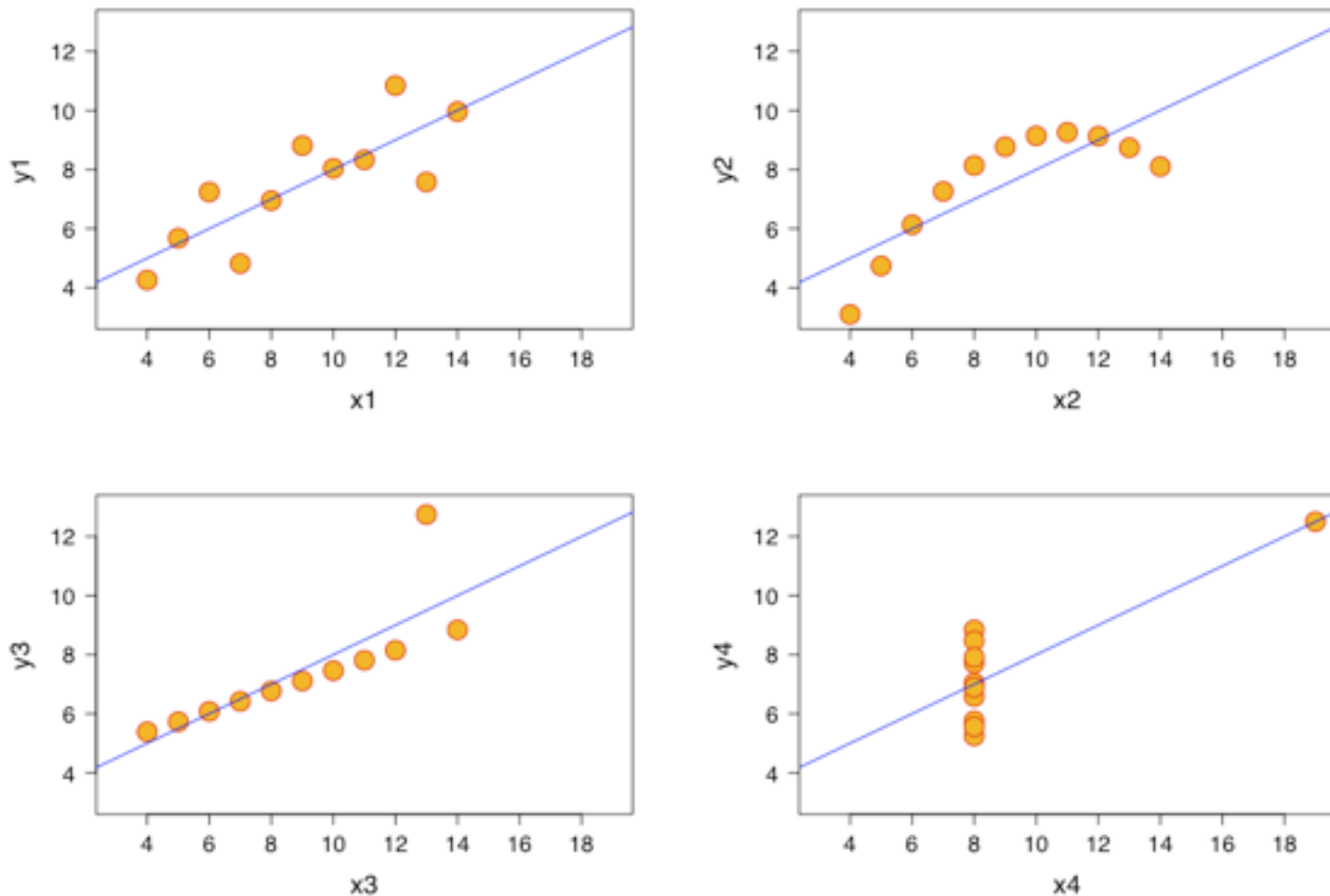
Defining Visualization

Computer-based visualization systems provide visual representations of datasets designed to help people carry out tasks more effectively.

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- human in the loop needs the details
 - doesn't know exactly what questions to ask in advance



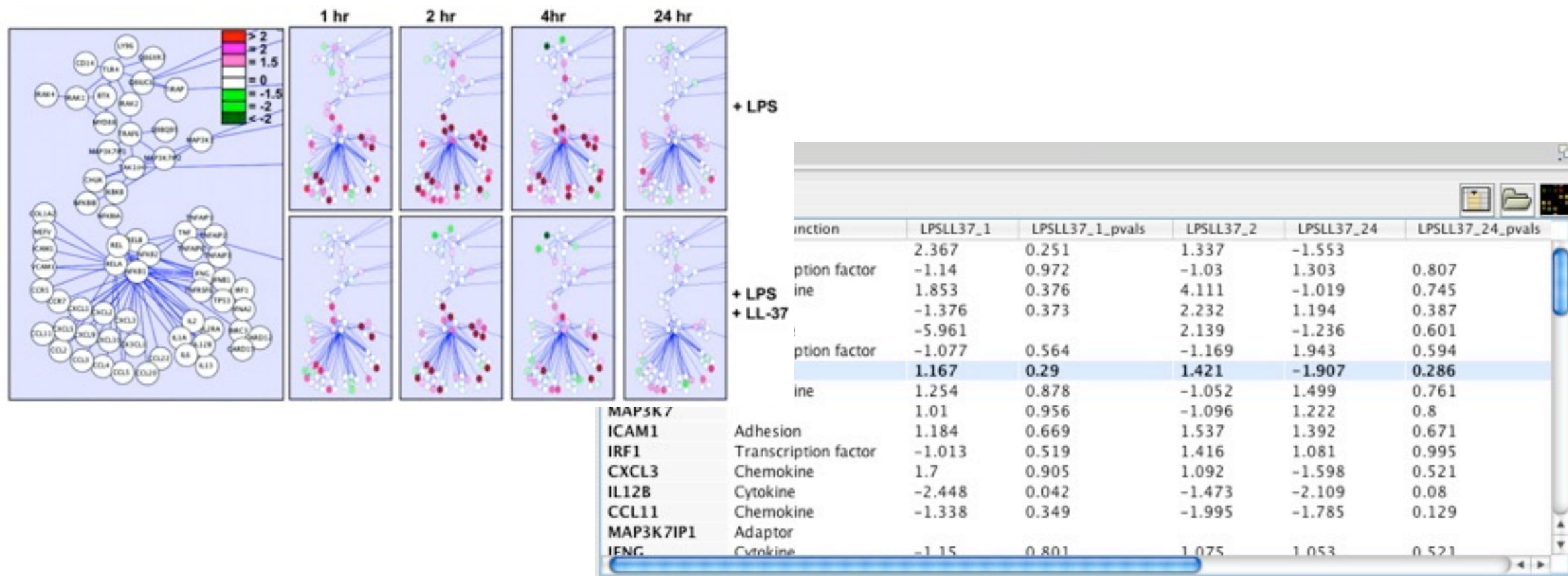
Identical statistics

x mean	9.0
x variance	10.0
y mean	7.50
y variance	3.75
x/y correlation	0.816

Defining Visualization

Computer-based visualization systems provide **visual representations** of datasets designed to help people carry out tasks more effectively.

- human in the loop needs the details
 - doesn't know exactly what questions to ask in advance
- external representation: replace cognition with perception



Defining Visualization

Computer-based visualization systems provide visual representations of datasets designed to help people carry out tasks more effectively.

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 - doesn't know exactly what questions to ask in advance
- external representation: perception vs cognition
- intended task

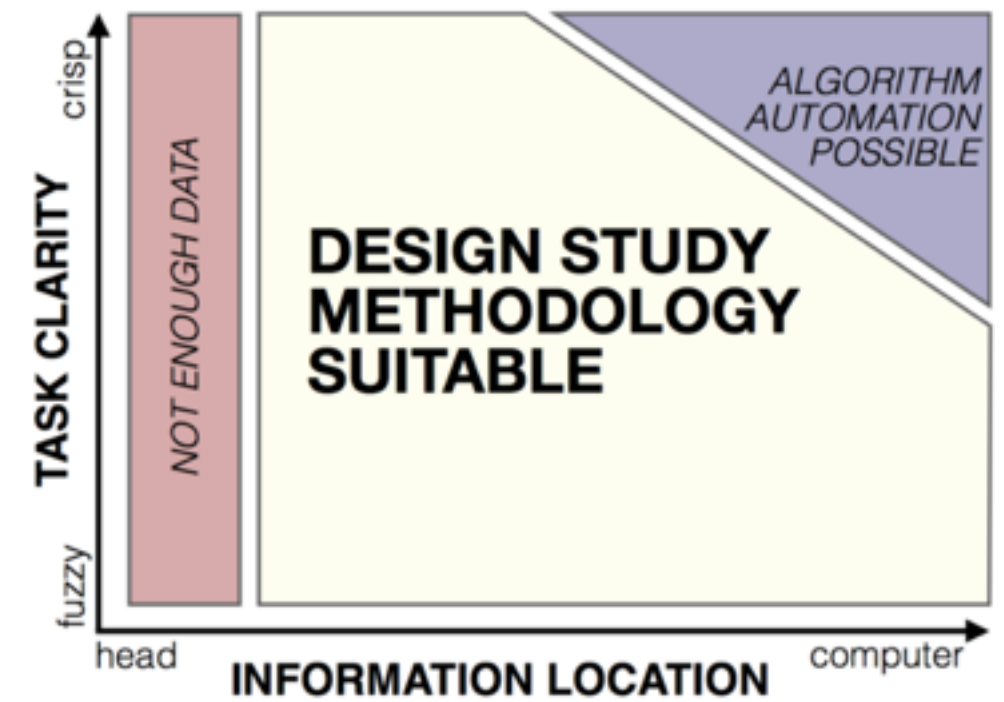
Defining Visualization

Computer-based visualization systems provide visual representations of datasets designed to help people carry out tasks more effectively.

- human in the loop needs the details
 - doesn't know exactly what questions to ask in advance
- external representation: perception vs cognition
- intended task
- measurable definitions of effectiveness

more at:

Visualization Analysis and Design, Chapter 1.
Munzner.AK Peters, 2014, to appear.



Design Study Methodology

Reflections from the Trenches and from the Stacks

joint work with:

Michael Sedlmair, Miriah Meyer

<http://www.cs.ubc.ca/labs/imager/tr/2012/dsm/>

Design Study Methodology: Reflections from the Trenches and from the Stacks.
Sedlmair, Meyer, Munzner. *IEEE TVCG* 18(12): 2431-2440, 2012 (Proc. InfoVis 2012).

Defining Design Study

- a specific **real-world** problem
 - real users and real data,
 - collaboration is (often) fundamental
- **design** a visualization system
 - implications: requirements, multiple ideas
- **validate** the design
 - at appropriate levels
- **reflect** about lessons learned
 - transferable research: improve design guidelines for vis in general
 - confirm, refine, reject, propose

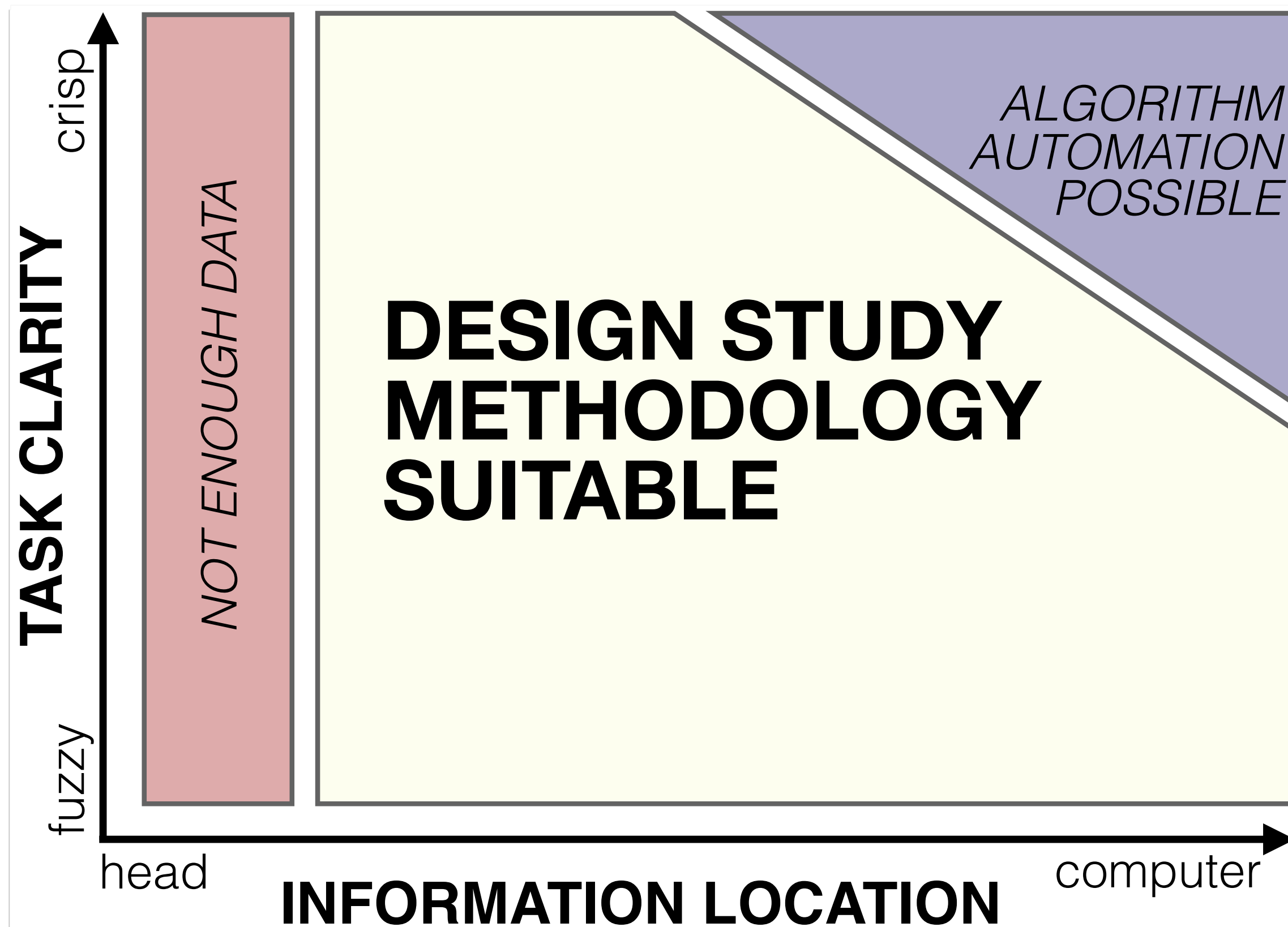
more at:

A Nested Model of Visualization Design and Validation.
Munzner. *IEEE TVCG 15(6):921-928, 2009 (Proc. InfoVis 2009).*

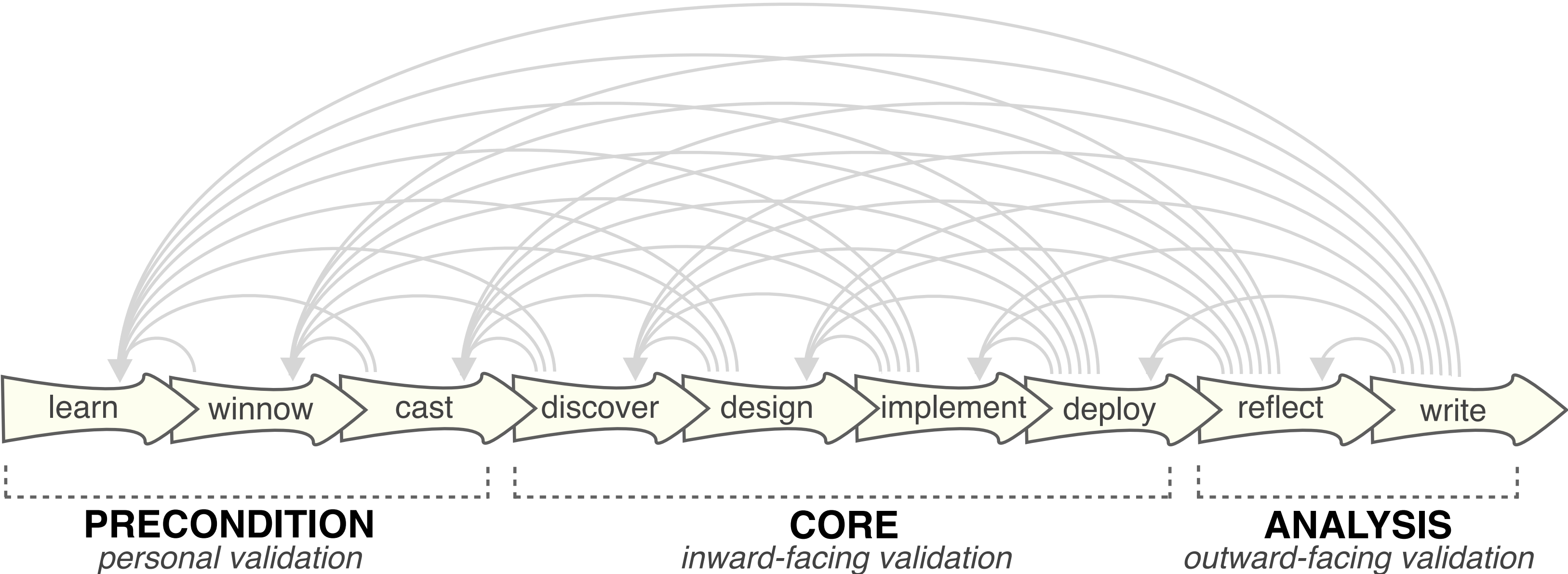
more at:

The Nested Blocks and Guidelines Model.
Meyer, Sedlmair, Quinan, Munzner. *Information Visualization Journal, 2014,*
to appear.

When To Do Design Studies

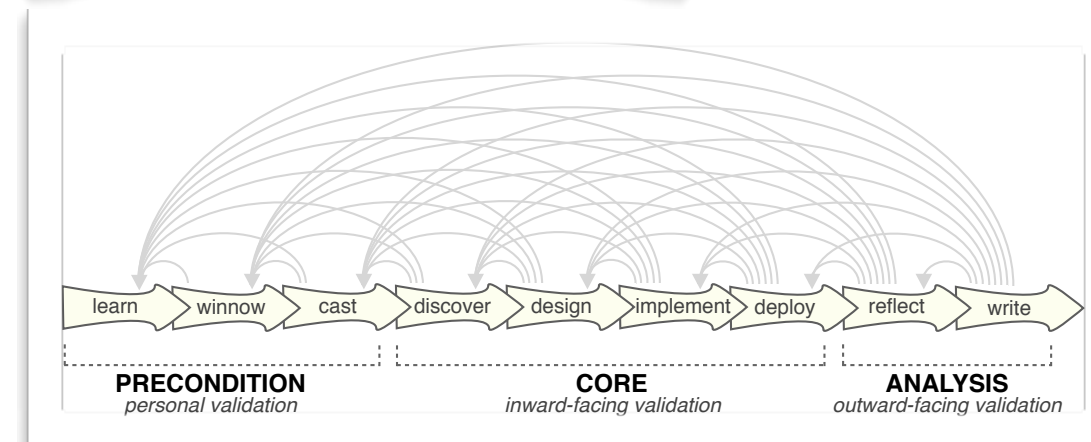
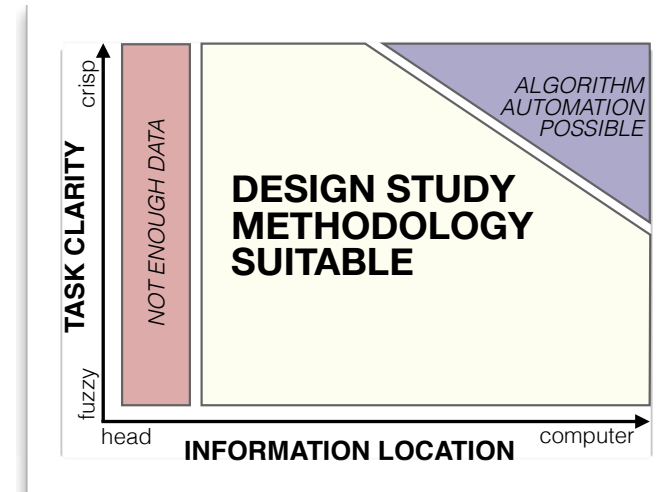


Nine-Stage Framework



How To Do Design Studies

- definitions
- 9-stage framework
- 32 pitfalls and how to avoid them



PF-1	premature advance: jumping forward over stages	general
PF-2	premature start: insufficient knowledge of vis literature	learn
PF-3	premature commitment: collaboration with wrong people	winnow
PF-4	no real data available (yet)	winnow
PF-5	insufficient time available from potential collaborators	winnow
PF-6	no need for visualization: problem can be automated	winnow
PF-7	researcher expertise does not match domain problem	winnow
PF-8	no need for research: engineering vs. research project	winnow
PF-9	no need for change: existing tools are good enough	winnow

Pitfall Example: Premature Publishing

algorithm innovation

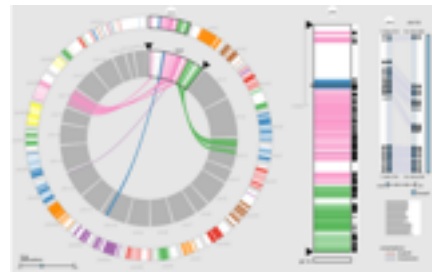
design studies

Must be first!

Am I ready?



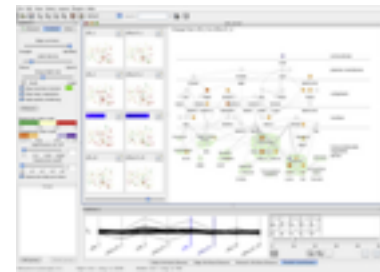
Design Studies: Lessons learned after 21 of them



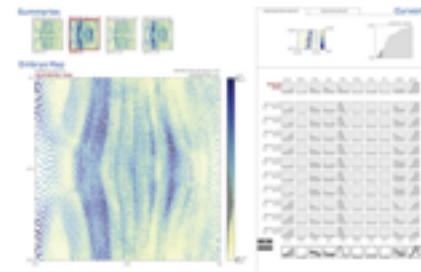
MizBee
genomics



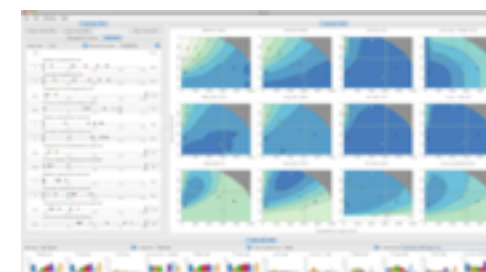
Pathline
genomics



Cerebral
genomics



MulteeSum
genomics



Vismon
fisheries management



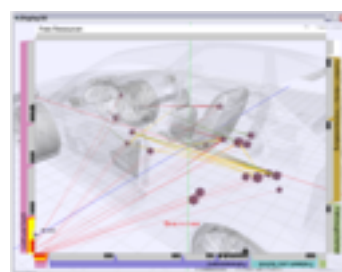
QuestVis
sustainability



WiKeVis
in-car networks



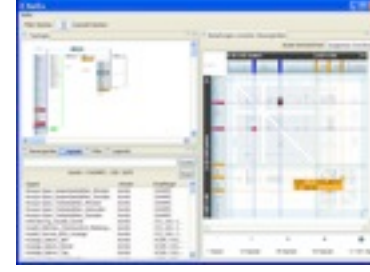
MostVis
in-car networks



Car-X-Ray
in-car networks



ProgSpy2010
in-car networks



ReEx
in-car networks



Cardiogram
in-car networks



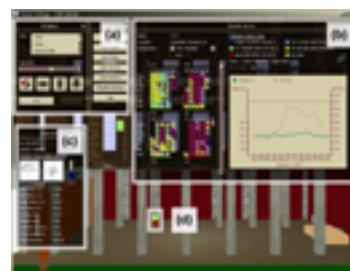
AutobahnVis
in-car networks



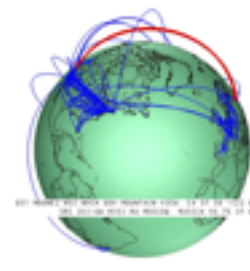
VisTra
in-car networks



Constellation
linguistics



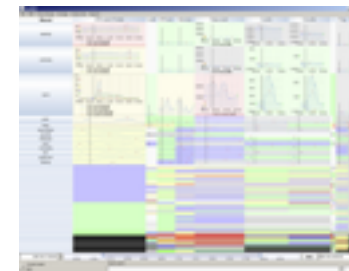
LibVis
cultural heritage



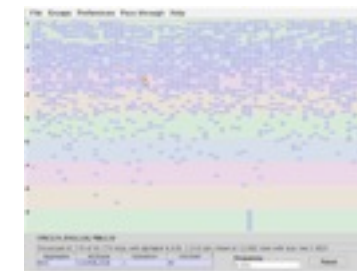
Caidants
multicast



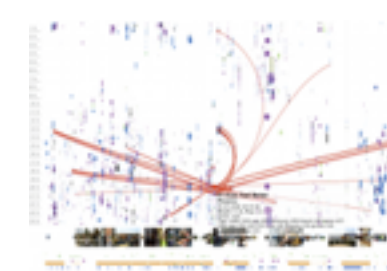
SessionViewer
web log analysis



LiveRAC
server hosting



PowerSetViewer
data mining

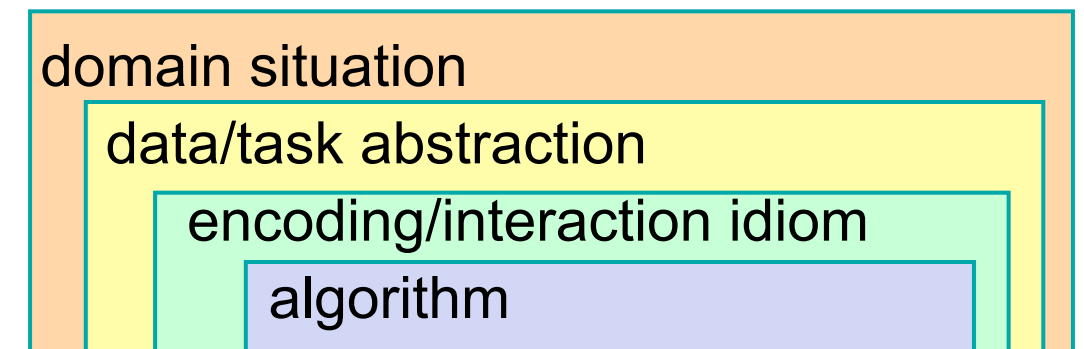


LastHistory
music listening

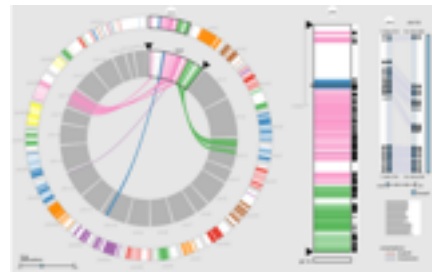
- commonality of representations cross-cuts domains!

Abstractions and Idioms

- abstractions
 - **translate** from specifics of domain to vocabulary of vis
 - task abstraction: **why** they're looking at it
 - data abstraction: **what** to draw
 - **transform** data into form useful for task at hand
 - don't just draw what you're given; decide what is the right thing!
- idioms
 - visual encoding idiom: **how** to draw
 - interaction idiom: **how** to manipulate
- focus today: two mappings
 - from domain to abstraction
 - from abstraction to idiom



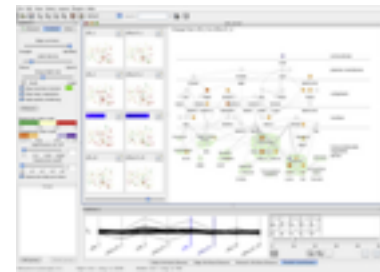
Today's Focus



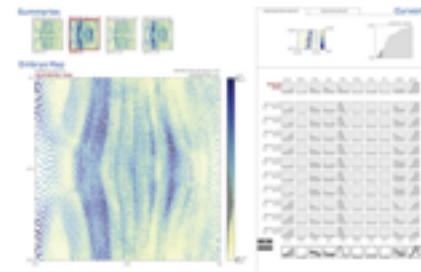
MizBee
genomics



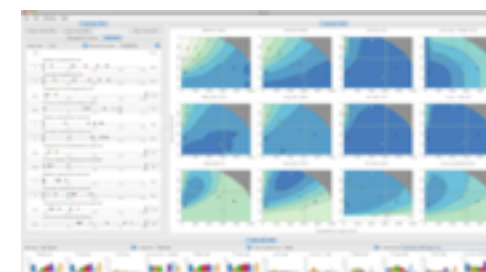
Pathline
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Vismon
fisheries management



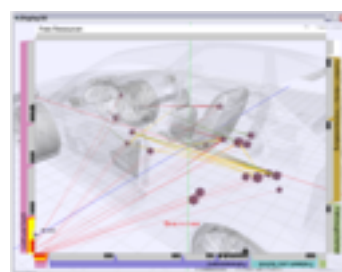
QuestVis
sustainability



WiKeVis
in-car networks



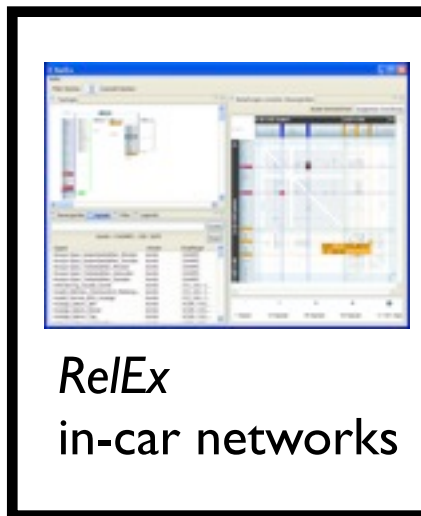
MostVis
in-car networks



Car-X-Ray
in-car networks



ProgSpy2010
in-car networks



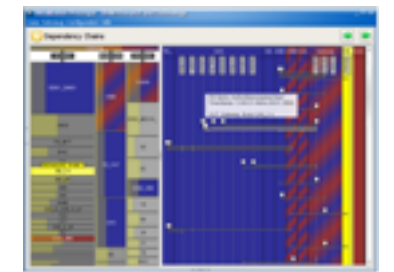
RelEx
in-car networks



Cardiogram
in-car networks



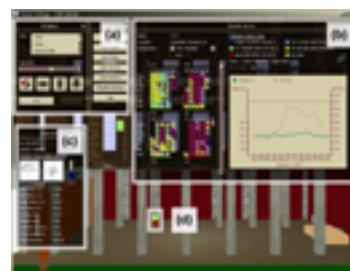
AutobahnVis
in-car networks



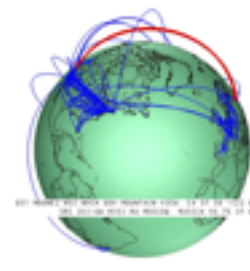
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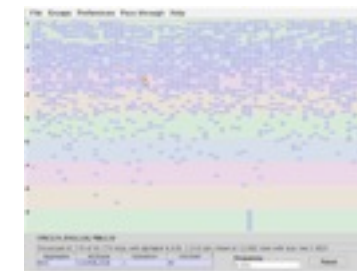
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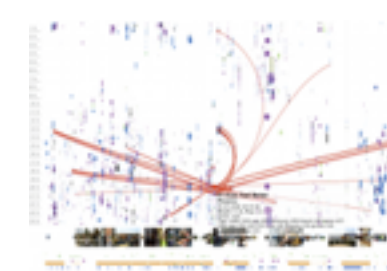
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web log analysis



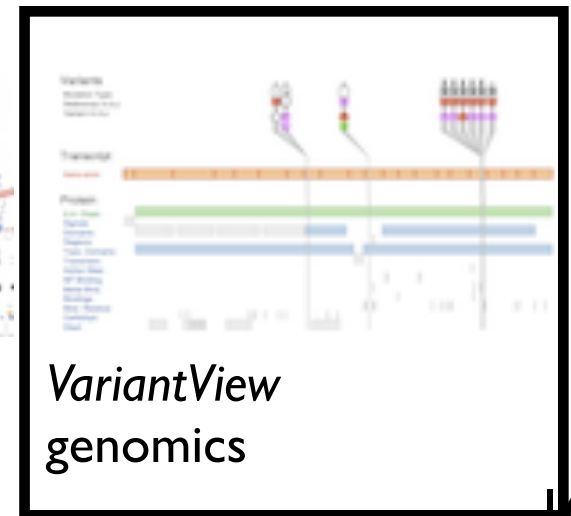
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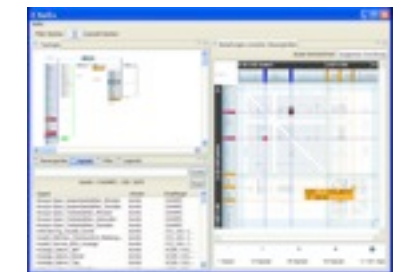
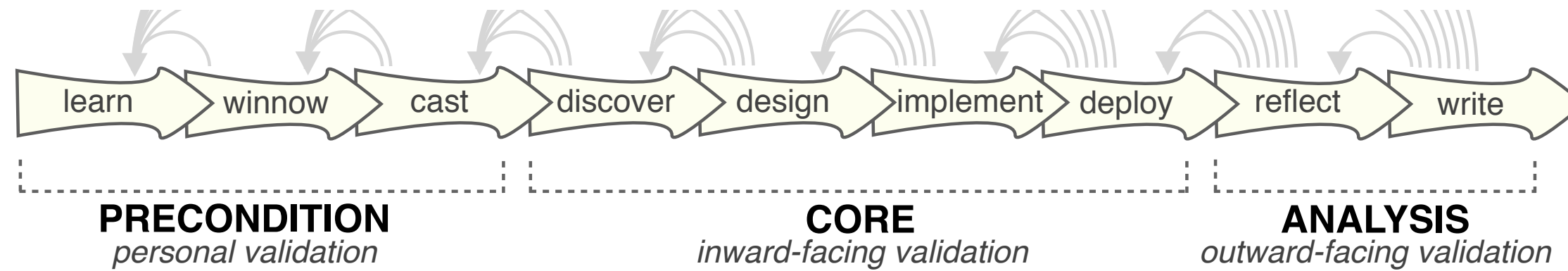
LastHistory
music listening



VariantView
genomics

Themes

- task and data abstraction
 - both cases: complex and tricky
 - clear description in final talk/paper is end of a long, long road
 - writing as research: refine during reflection even after vis tool is finalized...



RelEx
in-car networks

- visual encoding and interaction idioms
 - RelEx: reduce memory load with interaction
 - Variant View: reduce interaction load with better visual encoding



VariantView
genomics

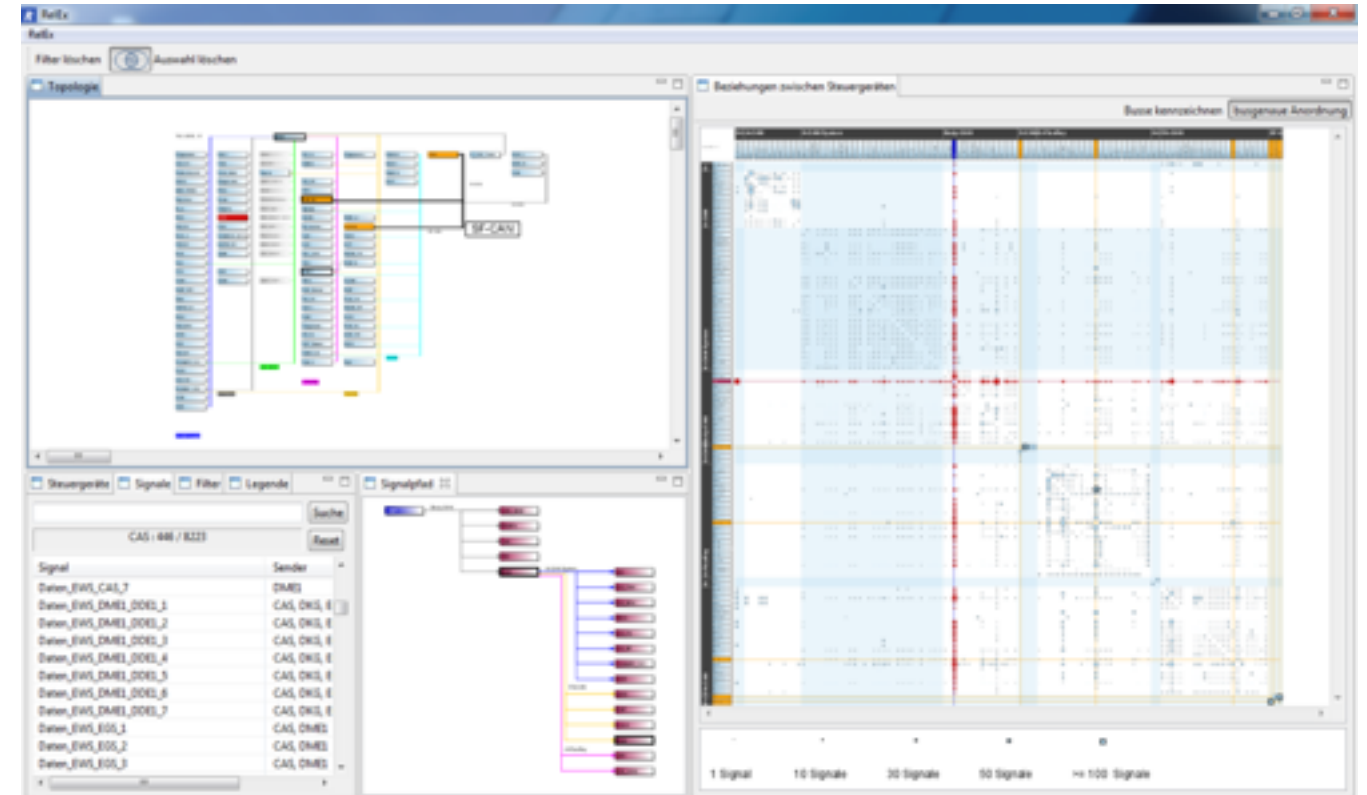
RelEx

Visualization for Actively Changing Overlay Network Specifications

joint work with:

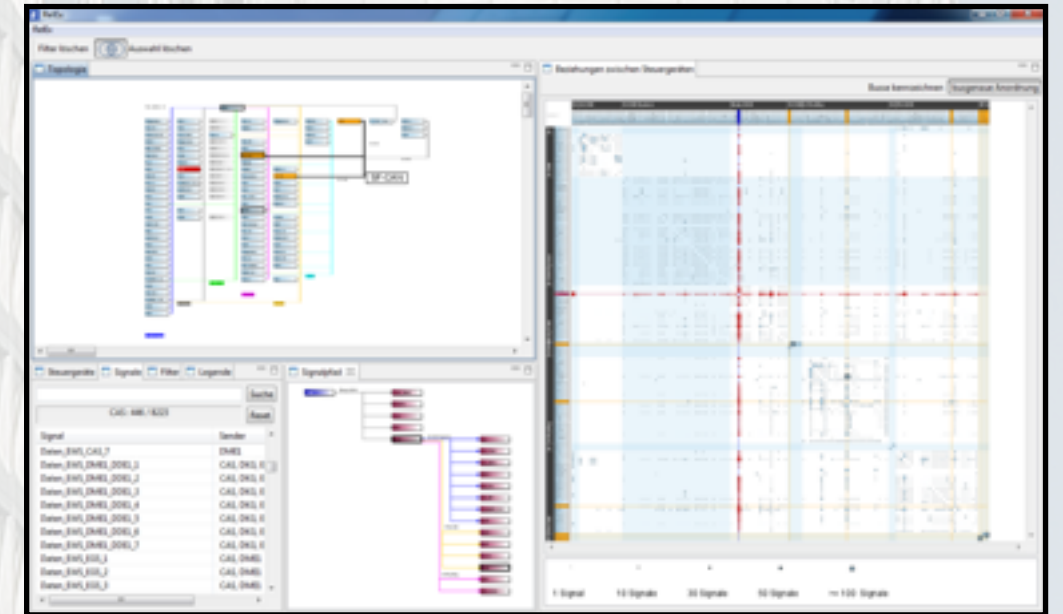
Michael Sedlmair, Annika Frank, Andreas Butz

<http://www.cs.ubc.ca/labs/imager/tr/2012/relex/>



RelEx: Visualization for Actively Changing Overlay Network Specifications.
Sedlmair, Frank, Butz, Munzner. *IEEE TVCG* 18(12): 2729-2738, 2012 (Proc. InfoVis 2012).

Domain: **In-car network engineering**



Abstractions

DATA

In-car Electronics



Data Abstraction: 3 Networks

- **physical** network

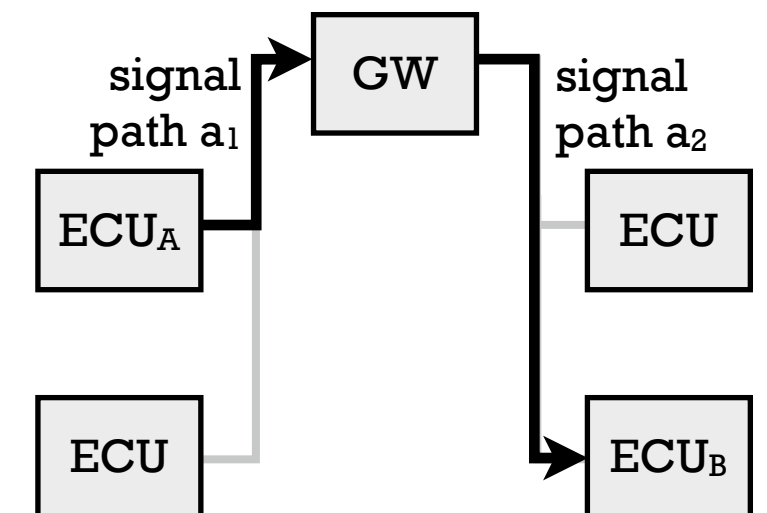
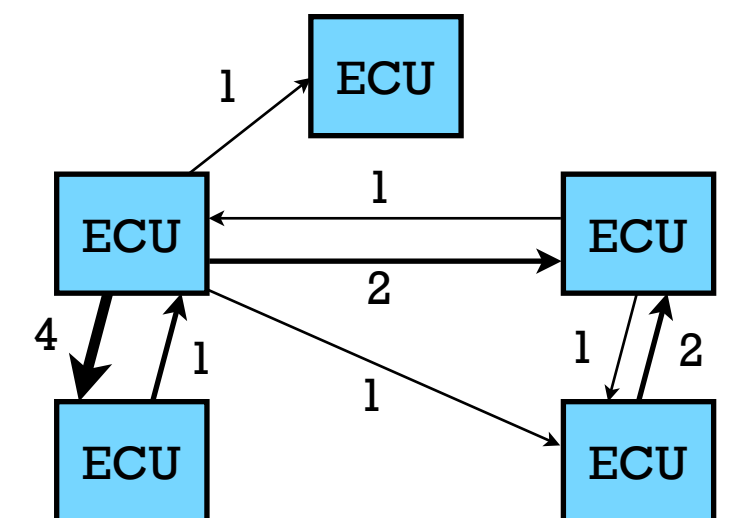
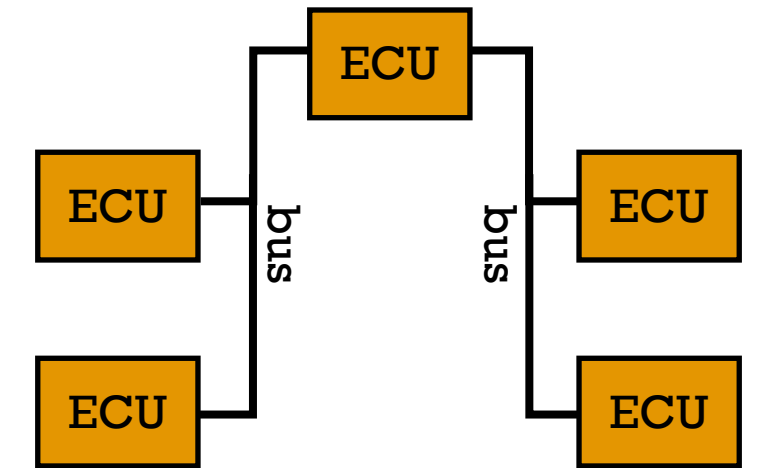
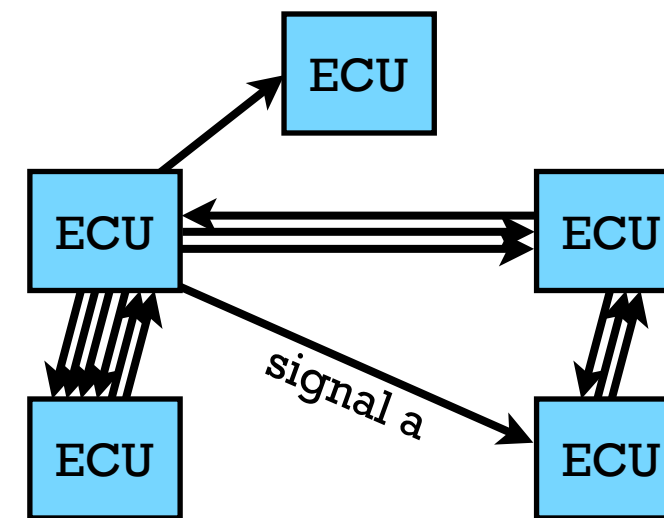
- 100 nodes: *Electronic Control Units*
- 10-15 hyperedges: *bus systems*
- hardware engineers

- **logical** network

- same nodes
- 10,000 multigraph edges: *signals*
- 1,000 weighted edges: *signal counts*
- software engineers

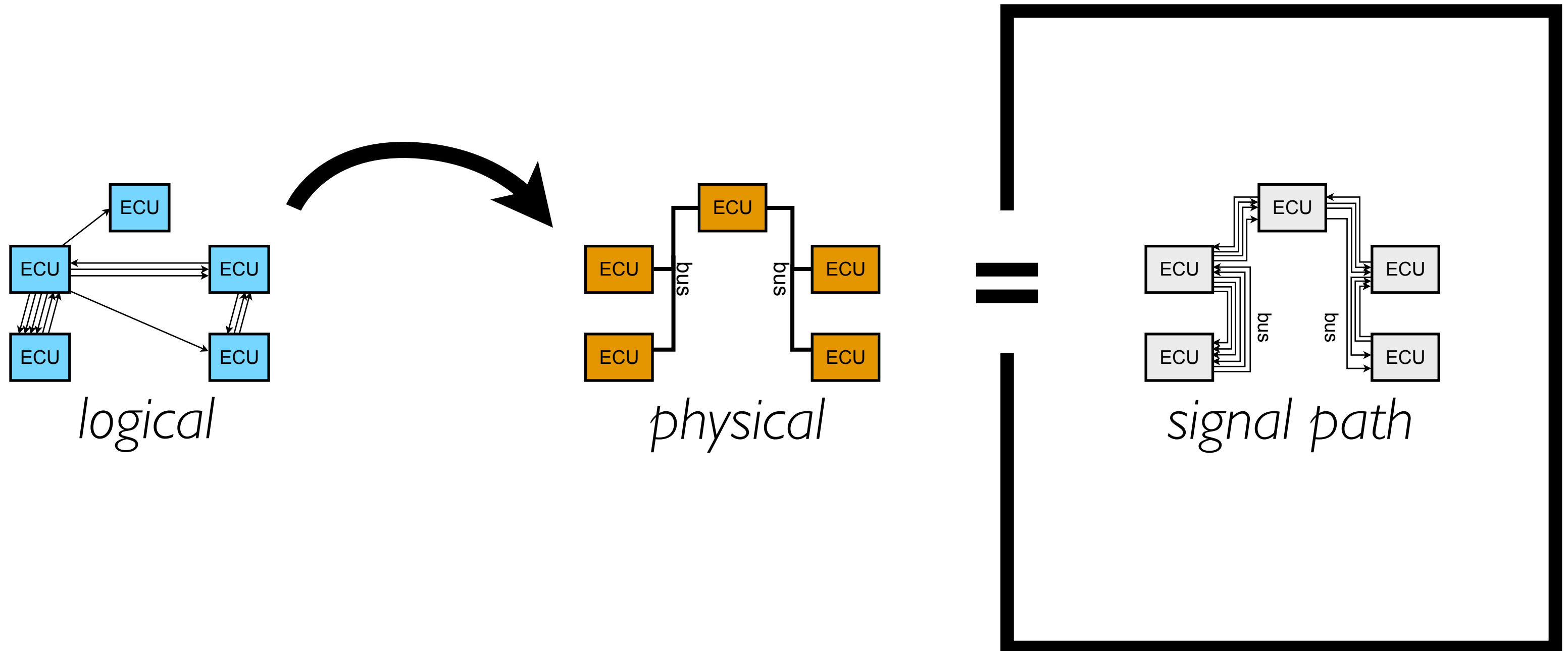
- **overlay** network

- maps logical onto physical
- 30,000 edges: *signal paths*
- target engineers



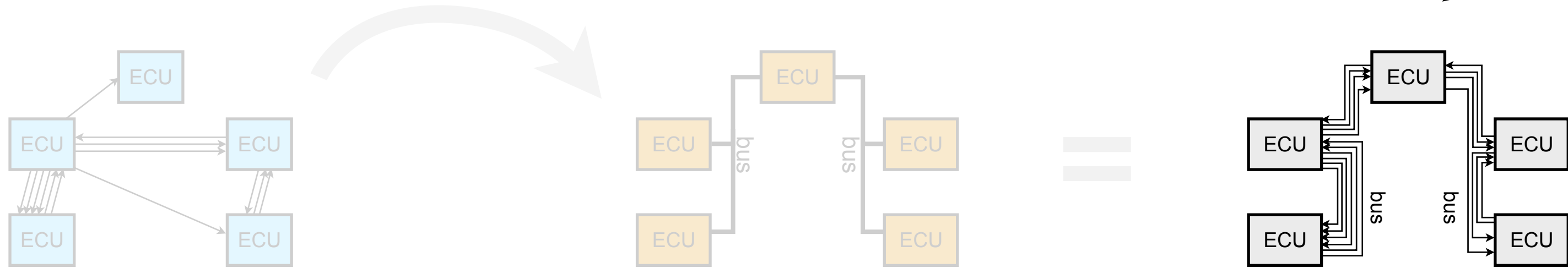
Task Abstraction: Mapping

- specify overlay network that maps logical onto physical



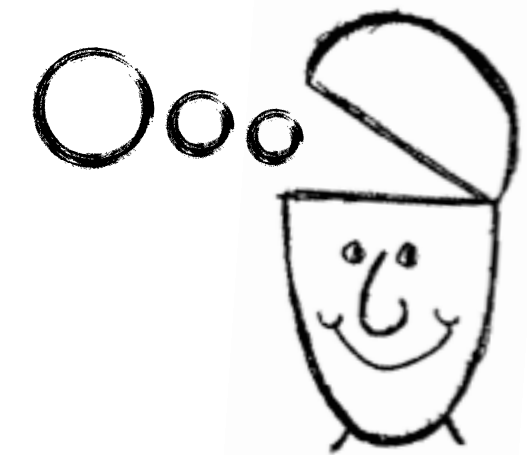
Task Abstraction: Optimizing

- traffic optimization



Many constraints

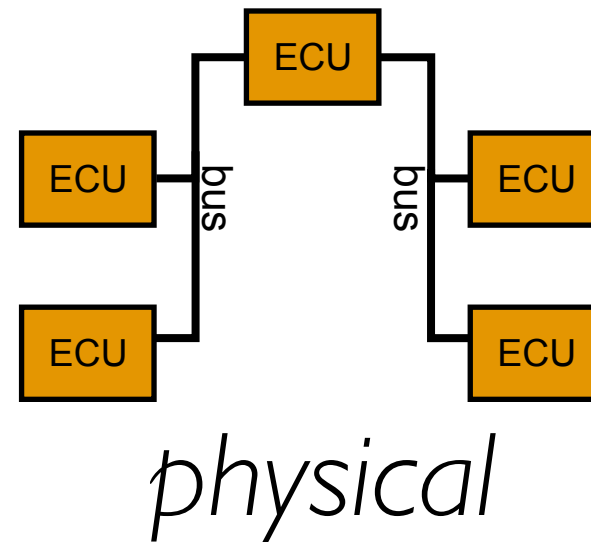
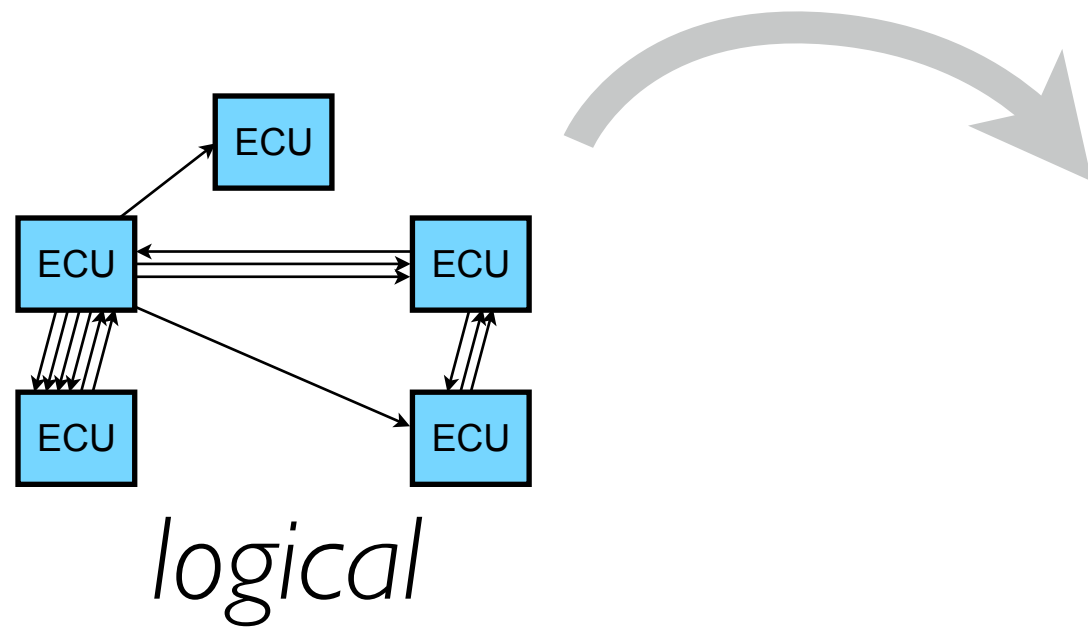
bandwidth ... delay/real time ...
path length ... load balance ...
reliability ... money ...



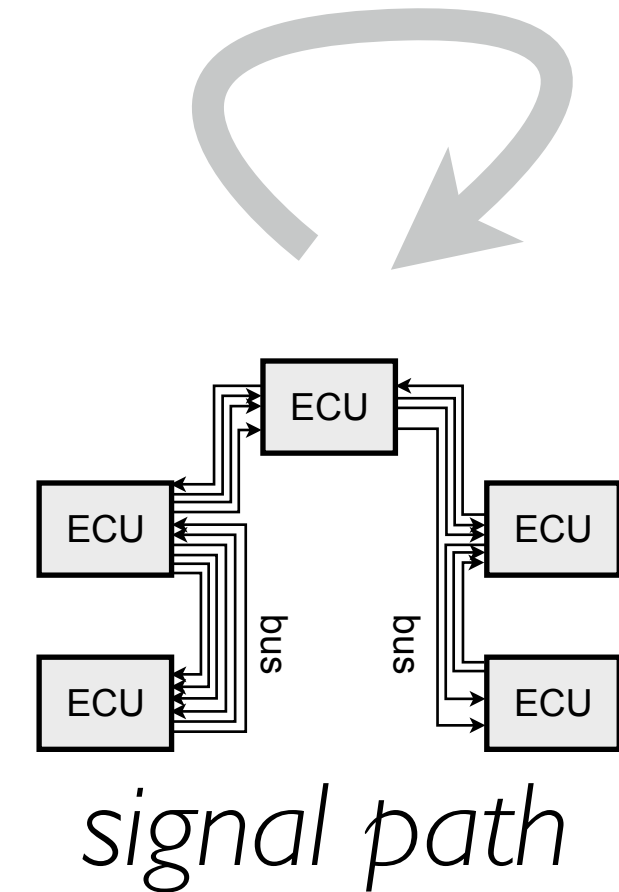
-- engineer, BMW --

Task Abstraction: Changing

- external change requests



=

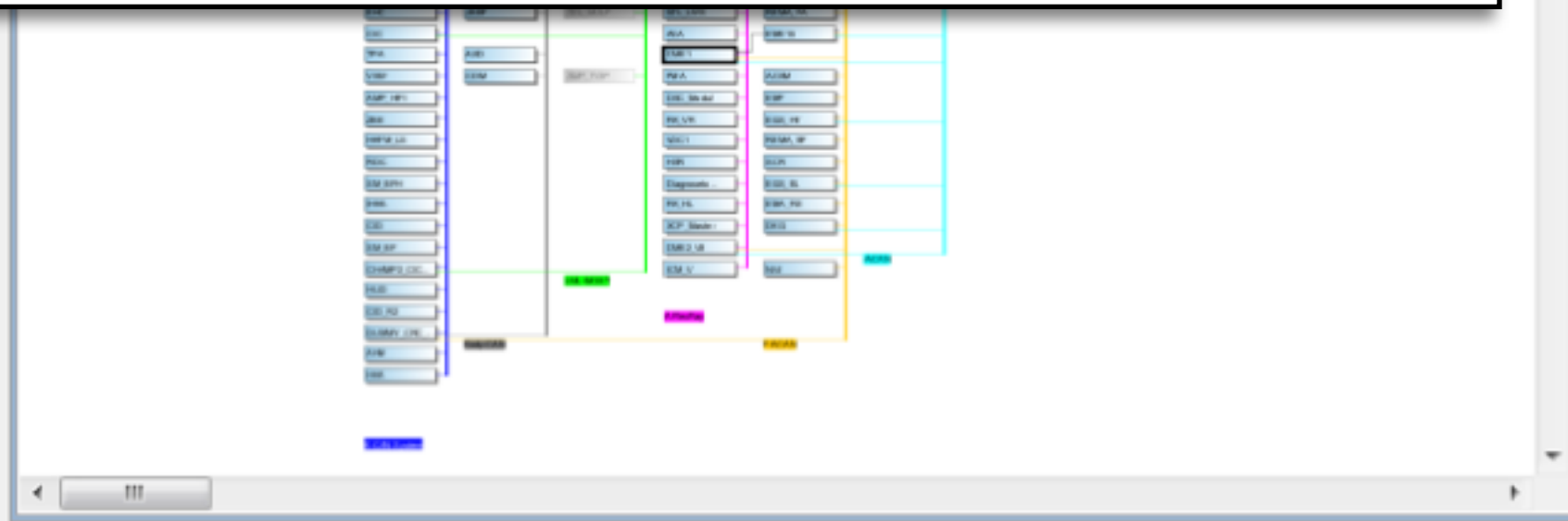


Change
(trivial requests might lead to complex changes)



Idioms

RELEX: Relation Explorer



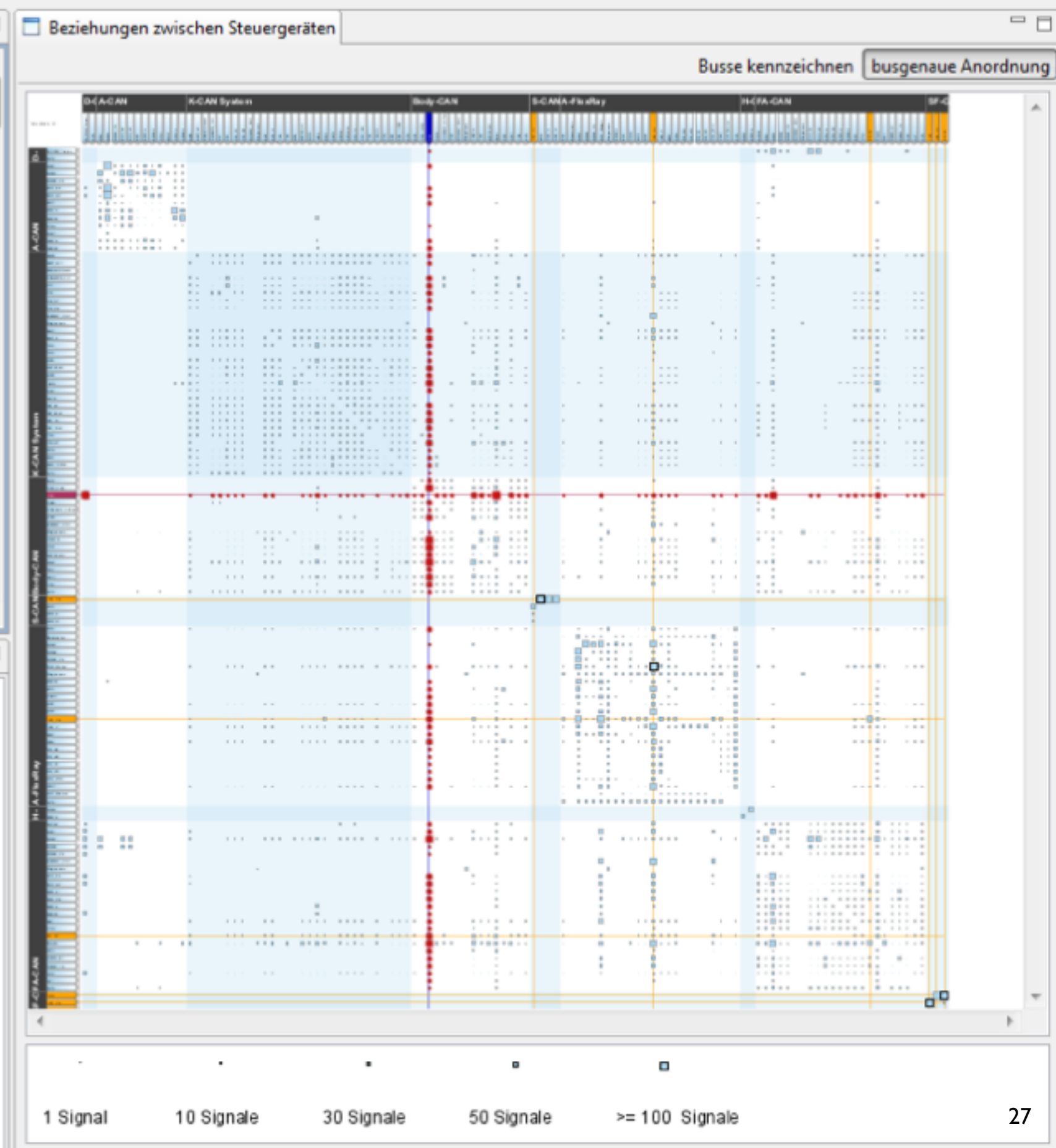
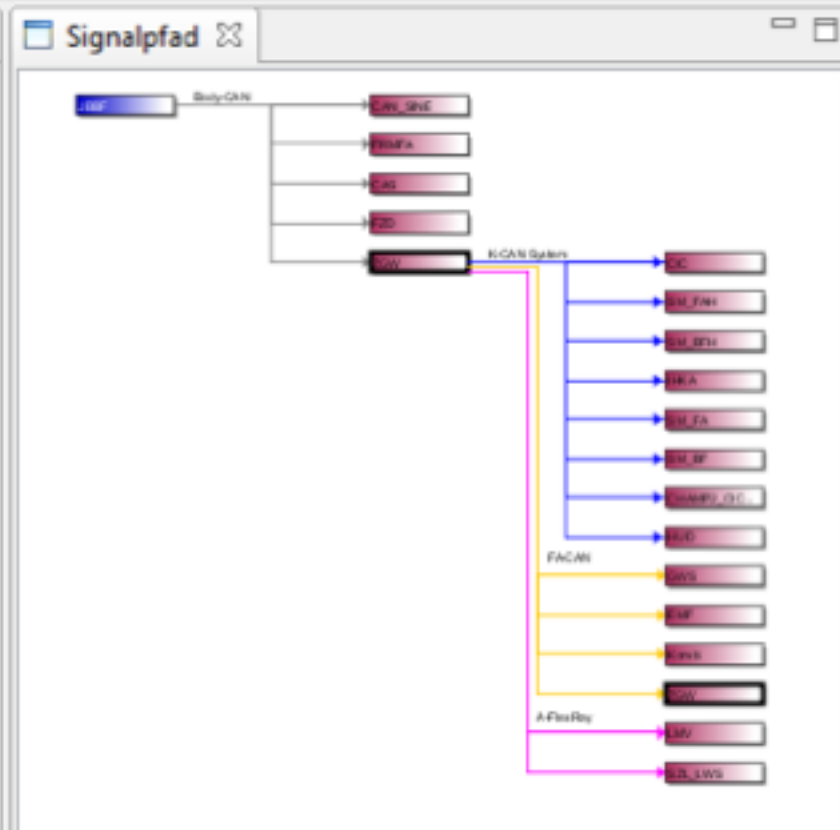
Steuergeräte Signale Filter Legende

Suche

CAS: 446 / 8223

Reset

Signal	Sender
Daten_EWS_CAS_7	DME1
Daten_EWS_DME1_DDE1_1	CAS, DKG, E
Daten_EWS_DME1_DDE1_2	CAS, DKG, E
Daten_EWS_DME1_DDE1_3	CAS, DKG, E
Daten_EWS_DME1_DDE1_4	CAS, DKG, E
Daten_EWS_DME1_DDE1_5	CAS, DKG, E
Daten_EWS_DME1_DDE1_6	CAS, DKG, E
Daten_EWS_DME1_DDE1_7	CAS, DKG, E
Daten_EWS_EGS_1	CAS, DME1
Daten_EWS_EGS_2	CAS, DME1
Daten_EWS_EGS_3	CAS, DME1

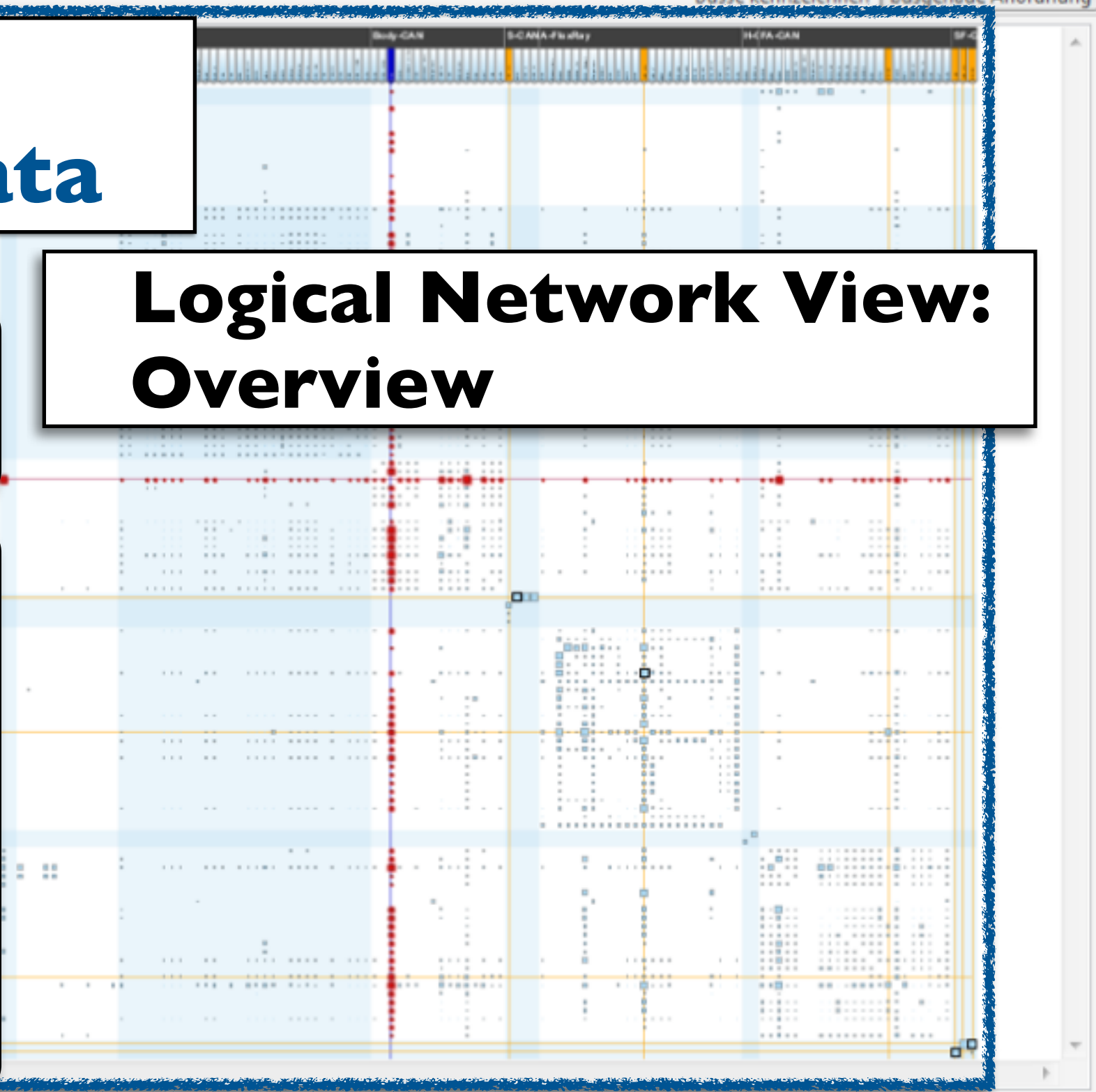
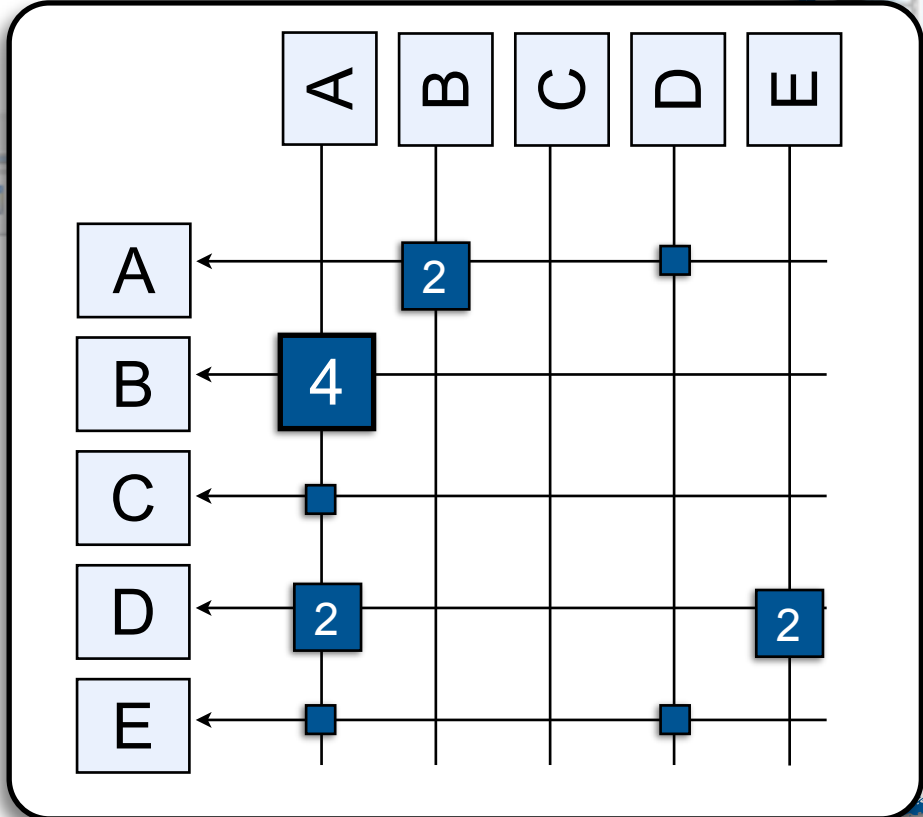
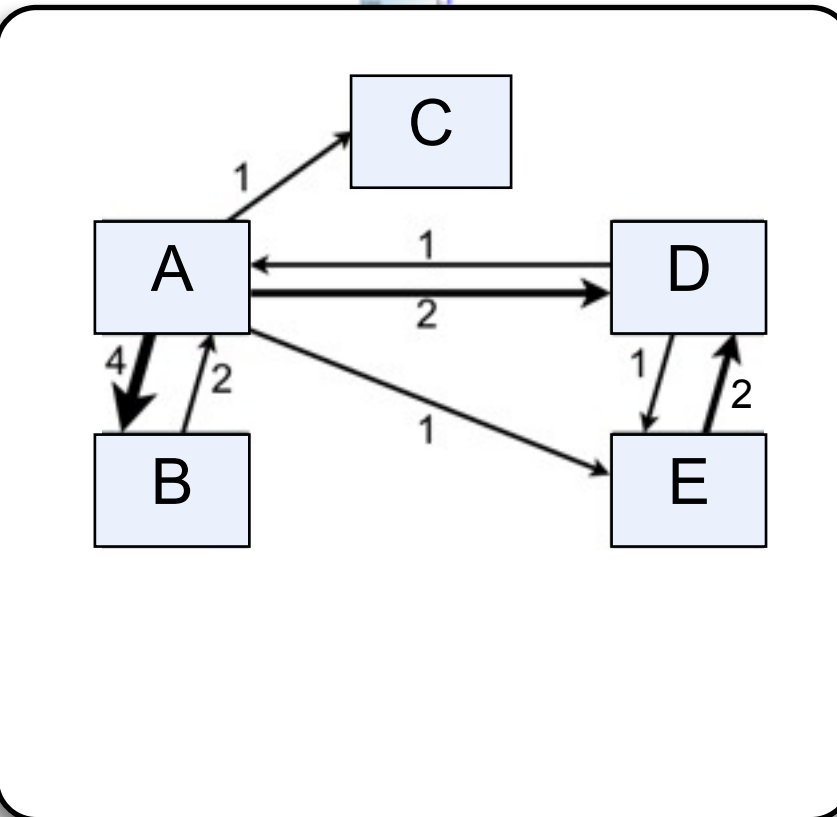


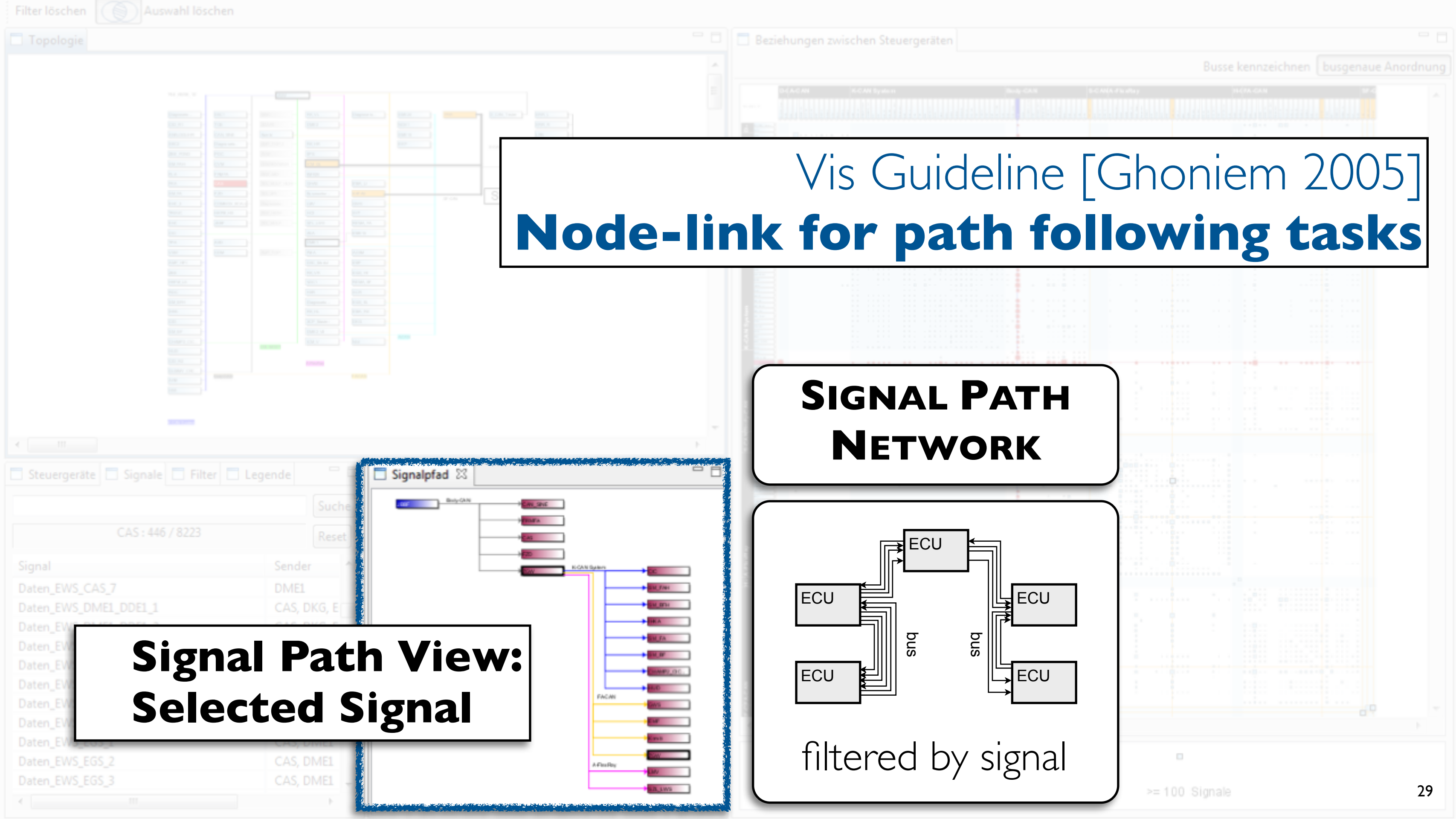
Vis Guideline [Ghoniem 2005] Matrix for dense network data

Logical Network View: Overview

SIGNAL COUNT NETWORK

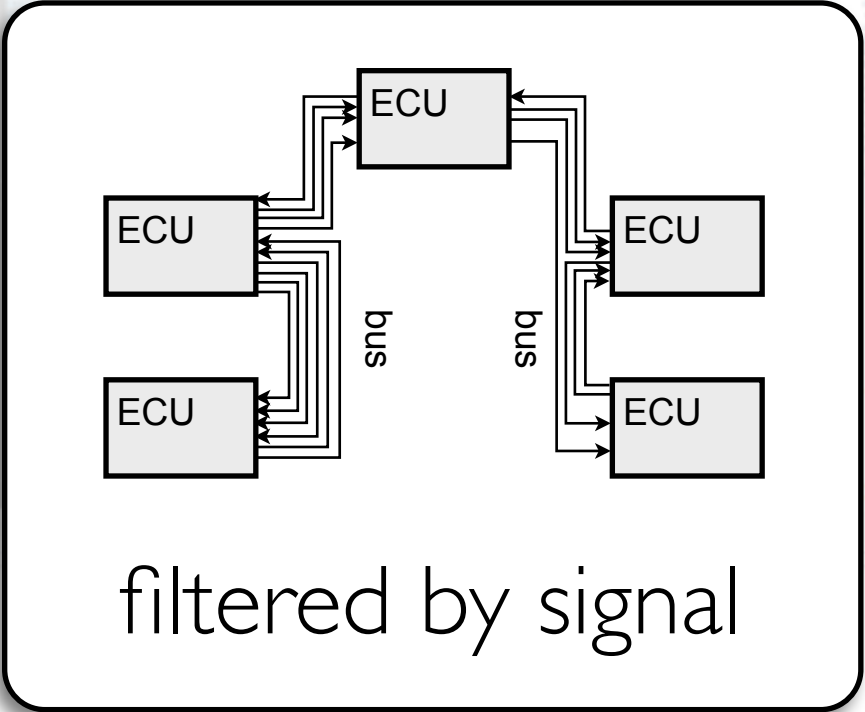
visual encoding:
size-coded matrix





Vis Guideline [Ghoniem 2005]
Node-link for path following tasks

SIGNAL PATH NETWORK



**Signal Path View:
Selected Signal**

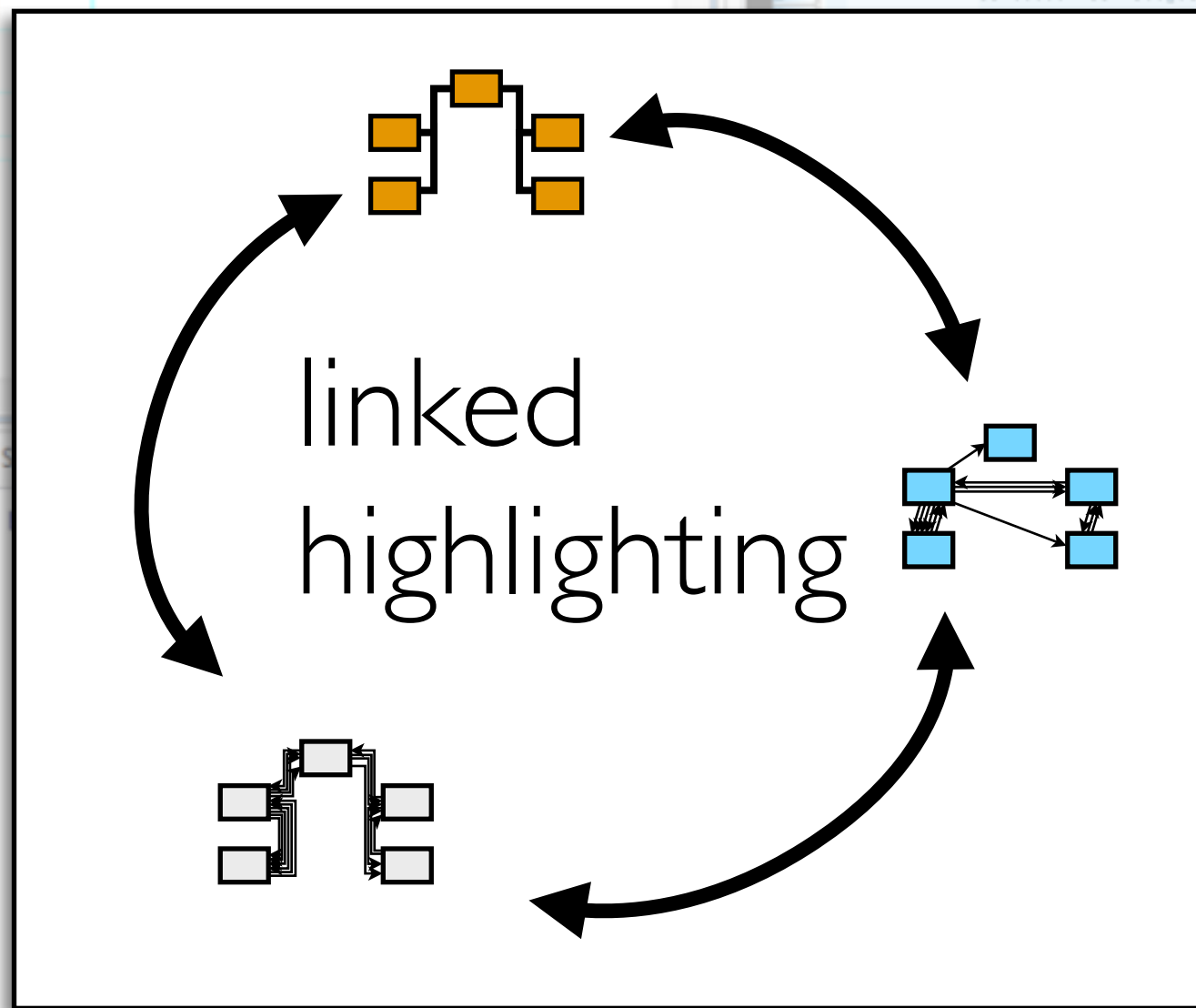
Signal	Sender
Daten_EWS_CAS_7	DME1
Daten_EWS_DME1_DDE1_1	CAS, DKG, E
Daten_EWS_DME1_DDE1_2	CAS, DKG, E
Daten_EWS_DME1_DDE1_3	CAS, DKG, E
Daten_EWS_DME1_DDE1_4	CAS, DKG, E
Daten_EWS_DME1_DDE1_5	CAS, DKG, E
Daten_EWS_DME1_DDE1_6	CAS, DKG, E
Daten_EWS_DME1_DDE1_7	CAS, DKG, E
Daten_EWS_DME1_DDE1_8	CAS, DKG, E
Daten_EWS_DME1_DDE1_9	CAS, DKG, E
Daten_EWS_DME1_DDE1_10	CAS, DKG, E
Daten_EWS_DME1_DDE1_11	CAS, DKG, E
Daten_EWS_DME1_DDE1_12	CAS, DKG, E
Daten_EWS_DME1_DDE1_13	CAS, DKG, E
Daten_EWS_DME1_DDE1_14	CAS, DKG, E
Daten_EWS_DME1_DDE1_15	CAS, DKG, E
Daten_EWS_DME1_DDE1_16	CAS, DKG, E
Daten_EWS_DME1_DDE1_17	CAS, DKG, E
Daten_EWS_DME1_DDE1_18	CAS, DKG, E
Daten_EWS_DME1_DDE1_19	CAS, DKG, E
Daten_EWS_DME1_DDE1_20	CAS, DKG, E
Daten_EWS_DME1_DDE1_21	CAS, DKG, E
Daten_EWS_DME1_DDE1_22	CAS, DKG, E
Daten_EWS_DME1_DDE1_23	CAS, DKG, E
Daten_EWS_DME1_DDE1_24	CAS, DKG, E
Daten_EWS_DME1_DDE1_25	CAS, DKG, E
Daten_EWS_DME1_DDE1_26	CAS, DKG, E
Daten_EWS_DME1_DDE1_27	CAS, DKG, E
Daten_EWS_DME1_DDE1_28	CAS, DKG, E
Daten_EWS_DME1_DDE1_29	CAS, DKG, E
Daten_EWS_DME1_DDE1_30	CAS, DKG, E
Daten_EWS_DME1_DDE1_31	CAS, DKG, E
Daten_EWS_DME1_DDE1_32	CAS, DKG, E
Daten_EWS_DME1_DDE1_33	CAS, DKG, E
Daten_EWS_DME1_DDE1_34	CAS, DKG, E
Daten_EWS_DME1_DDE1_35	CAS, DKG, E
Daten_EWS_DME1_DDE1_36	CAS, DKG, E
Daten_EWS_DME1_DDE1_37	CAS, DKG, E
Daten_EWS_DME1_DDE1_38	CAS, DKG, E
Daten_EWS_DME1_DDE1_39	CAS, DKG, E
Daten_EWS_DME1_DDE1_40	CAS, DKG, E
Daten_EWS_DME1_DDE1_41	CAS, DKG, E
Daten_EWS_DME1_DDE1_42	CAS, DKG, E
Daten_EWS_DME1_DDE1_43	CAS, DKG, E
Daten_EWS_DME1_DDE1_44	CAS, DKG, E
Daten_EWS_DME1_DDE1_45	CAS, DKG, E
Daten_EWS_DME1_DDE1_46	CAS, DKG, E
Daten_EWS_DME1_DDE1_47	CAS, DKG, E
Daten_EWS_DME1_DDE1_48	CAS, DKG, E
Daten_EWS_DME1_DDE1_49	CAS, DKG, E
Daten_EWS_DME1_DDE1_50	CAS, DKG, E
Daten_EWS_DME1_DDE1_51	CAS, DKG, E
Daten_EWS_DME1_DDE1_52	CAS, DKG, E
Daten_EWS_DME1_DDE1_53	CAS, DKG, E
Daten_EWS_DME1_DDE1_54	CAS, DKG, E
Daten_EWS_DME1_DDE1_55	CAS, DKG, E
Daten_EWS_DME1_DDE1_56	CAS, DKG, E
Daten_EWS_DME1_DDE1_57	CAS, DKG, E
Daten_EWS_DME1_DDE1_58	CAS, DKG, E
Daten_EWS_DME1_DDE1_59	CAS, DKG, E
Daten_EWS_DME1_DDE1_60	CAS, DKG, E
Daten_EWS_DME1_DDE1_61	CAS, DKG, E
Daten_EWS_DME1_DDE1_62	CAS, DKG, E
Daten_EWS_DME1_DDE1_63	CAS, DKG, E
Daten_EWS_DME1_DDE1_64	CAS, DKG, E
Daten_EWS_DME1_DDE1_65	CAS, DKG, E
Daten_EWS_DME1_DDE1_66	CAS, DKG, E
Daten_EWS_DME1_DDE1_67	CAS, DKG, E
Daten_EWS_DME1_DDE1_68	CAS, DKG, E
Daten_EWS_DME1_DDE1_69	CAS, DKG, E
Daten_EWS_DME1_DDE1_70	CAS, DKG, E
Daten_EWS_DME1_DDE1_71	CAS, DKG, E
Daten_EWS_DME1_DDE1_72	CAS, DKG, E
Daten_EWS_DME1_DDE1_73	CAS, DKG, E
Daten_EWS_DME1_DDE1_74	CAS, DKG, E
Daten_EWS_DME1_DDE1_75	CAS, DKG, E
Daten_EWS_DME1_DDE1_76	CAS, DKG, E
Daten_EWS_DME1_DDE1_77	CAS, DKG, E
Daten_EWS_DME1_DDE1_78	CAS, DKG, E
Daten_EWS_DME1_DDE1_79	CAS, DKG, E
Daten_EWS_DME1_DDE1_80	CAS, DKG, E
Daten_EWS_DME1_DDE1_81	CAS, DKG, E
Daten_EWS_DME1_DDE1_82	CAS, DKG, E
Daten_EWS_DME1_DDE1_83	CAS, DKG, E
Daten_EWS_DME1_DDE1_84	CAS, DKG, E
Daten_EWS_DME1_DDE1_85	CAS, DKG, E
Daten_EWS_DME1_DDE1_86	CAS, DKG, E
Daten_EWS_DME1_DDE1_87	CAS, DKG, E
Daten_EWS_DME1_DDE1_88	CAS, DKG, E
Daten_EWS_DME1_DDE1_89	CAS, DKG, E
Daten_EWS_DME1_DDE1_90	CAS, DKG, E
Daten_EWS_DME1_DDE1_91	CAS, DKG, E
Daten_EWS_DME1_DDE1_92	CAS, DKG, E
Daten_EWS_DME1_DDE1_93	CAS, DKG, E
Daten_EWS_DME1_DDE1_94	CAS, DKG, E
Daten_EWS_DME1_DDE1_95	CAS, DKG, E
Daten_EWS_DME1_DDE1_96	CAS, DKG, E
Daten_EWS_DME1_DDE1_97	CAS, DKG, E
Daten_EWS_DME1_DDE1_98	CAS, DKG, E
Daten_EWS_DME1_DDE1_99	CAS, DKG, E
Daten_EWS_DME1_DDE1_100	CAS, DKG, E

INTERACTION IDIOM: Cross-Network Relations

Steuergeräte Signale Filter Legende

CAS: 446 / 8223

Signal	Sender
Daten_EWS_CAS_7	DME1
Daten_EWS_DME1_DDE1_1	CAS, DKG, E
Daten_EWS_DME1_DDE1_2	CAS, DKG, E
Daten_EWS_DME1_DDE1_3	CAS, DKG, E
Daten_EWS_DME1_DDE1_4	CAS, DKG, E
Daten_EWS_DME1_DDE1_5	CAS, DKG, E
Daten_EWS_DME1_DDE1_6	CAS, DKG, E
Daten_EWS_DME1_DDE1_7	CAS, DKG, E
Daten_EWS_EGS_1	CAS, DME1
Daten_EWS_EGS_2	CAS, DME1
Daten_EWS_EGS_3	CAS, DME1



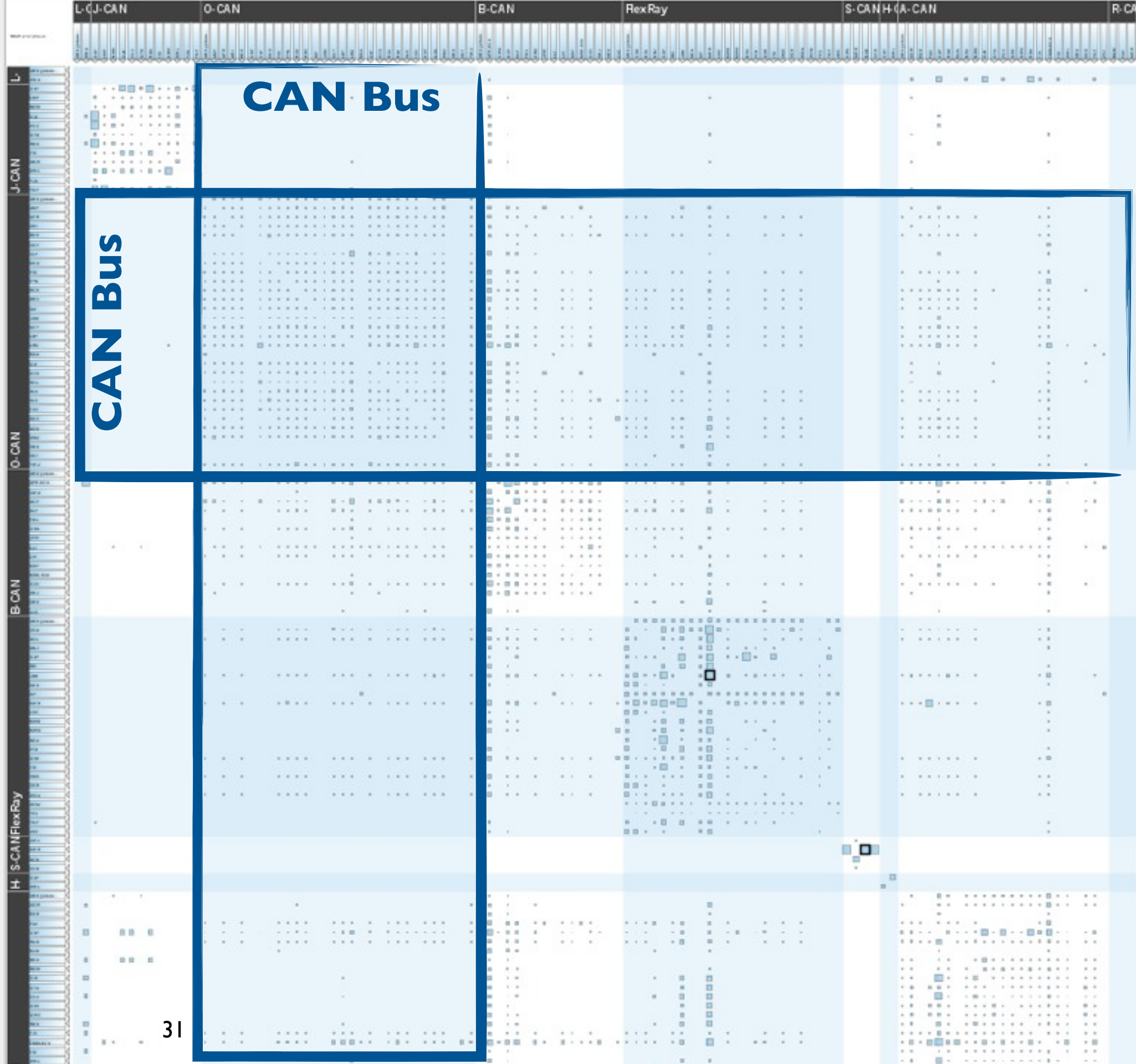
Busse kennzeichnen busgenaue Anordnung

1 Signal 10 Signale 30 Signale 50 Signale >= 100 Signale

VIDEO

INTERESTS

Bus communication patterns

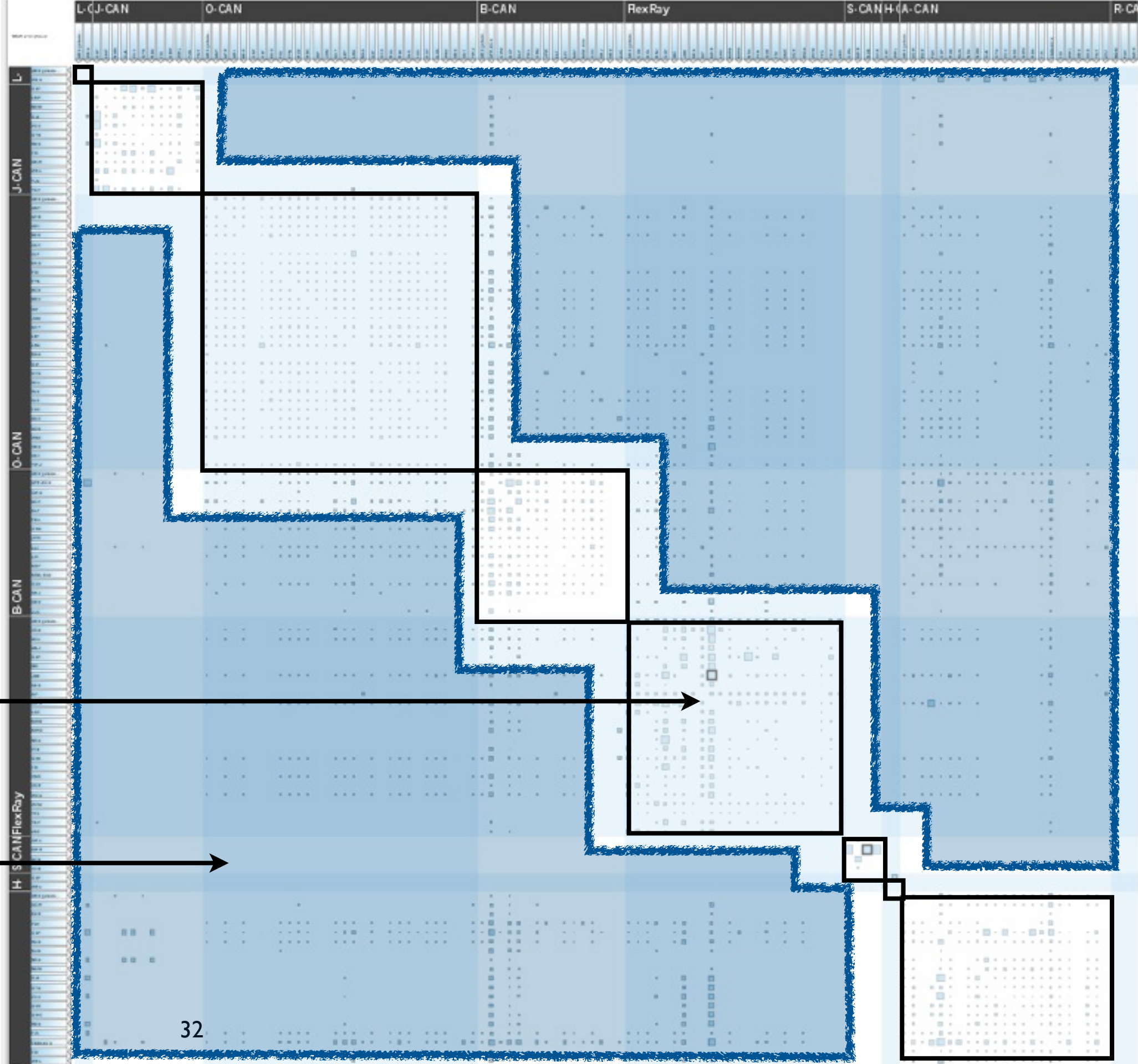


INTERESTS

Bus communication patterns

Within-bus

Between-bus



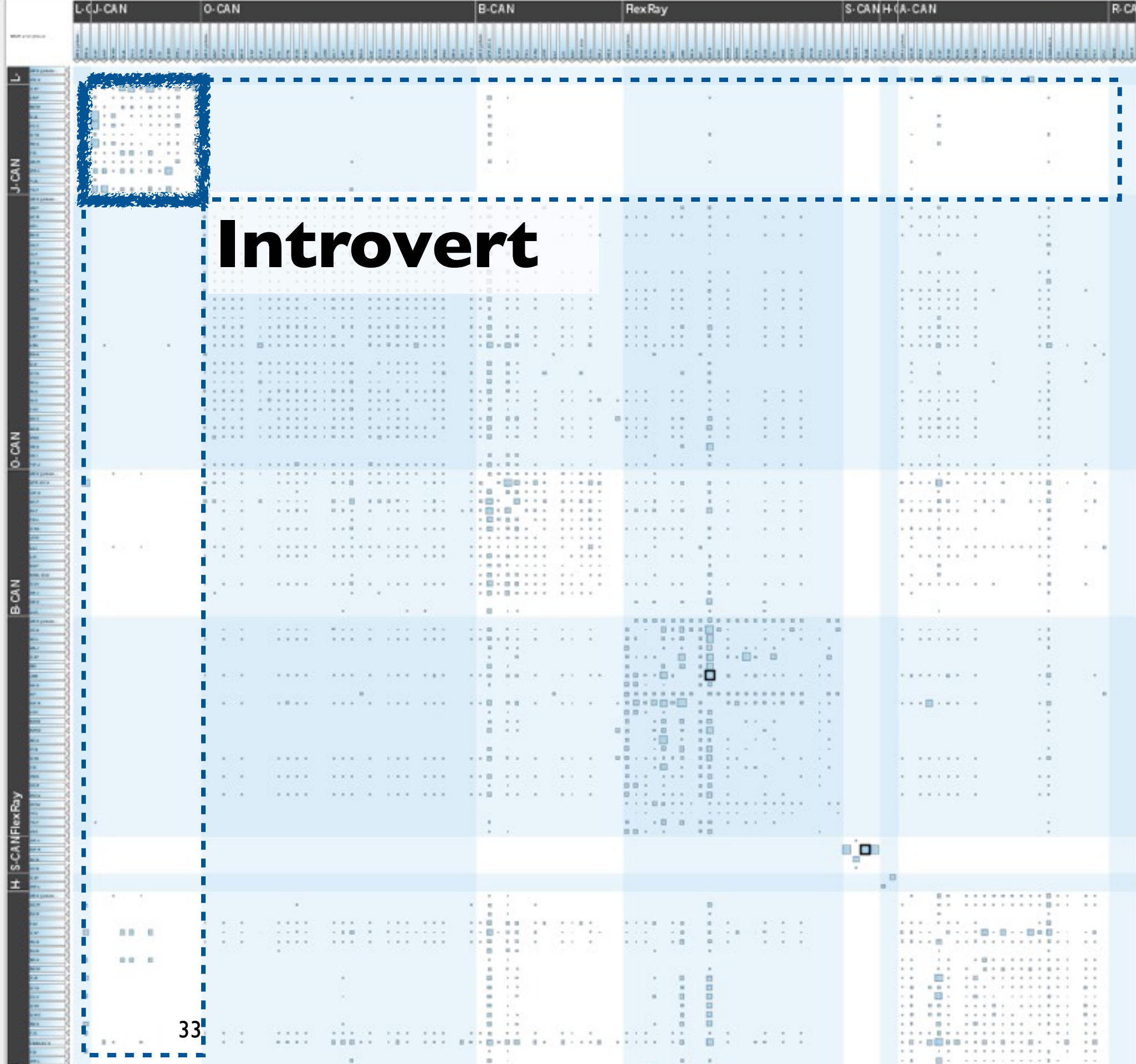
INTERESTS

Bus communication patterns

introvert

vs.

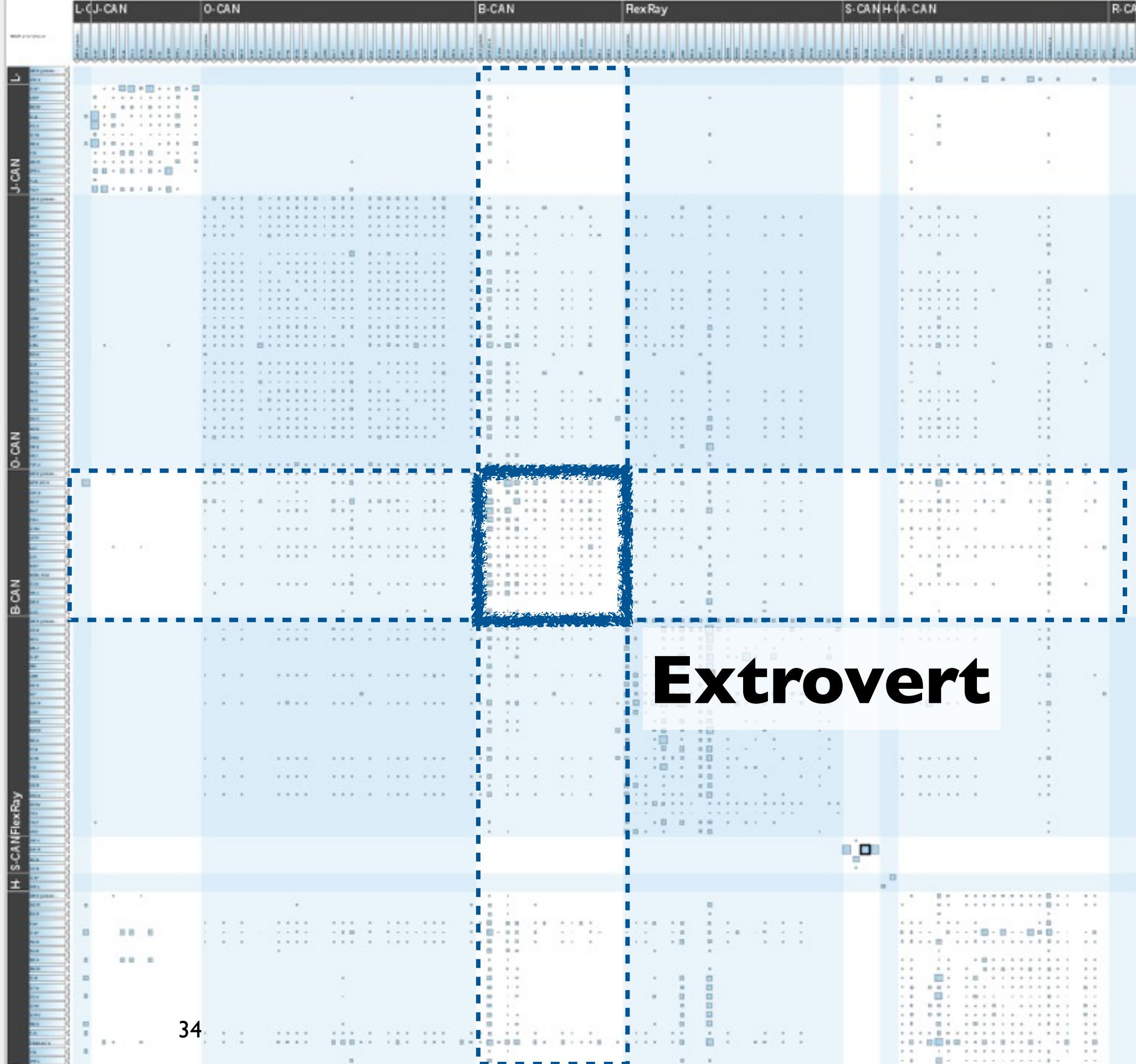
extrovert



INTERESTS

Bus communication patterns

introvert
vs.
extrovert



Extrovert

Methods

Phase I: Discover

3 months



- embedded within BMW
 - phases 1, 2, 3
- contextual inquiry
- abstracting
- deriving design requirements

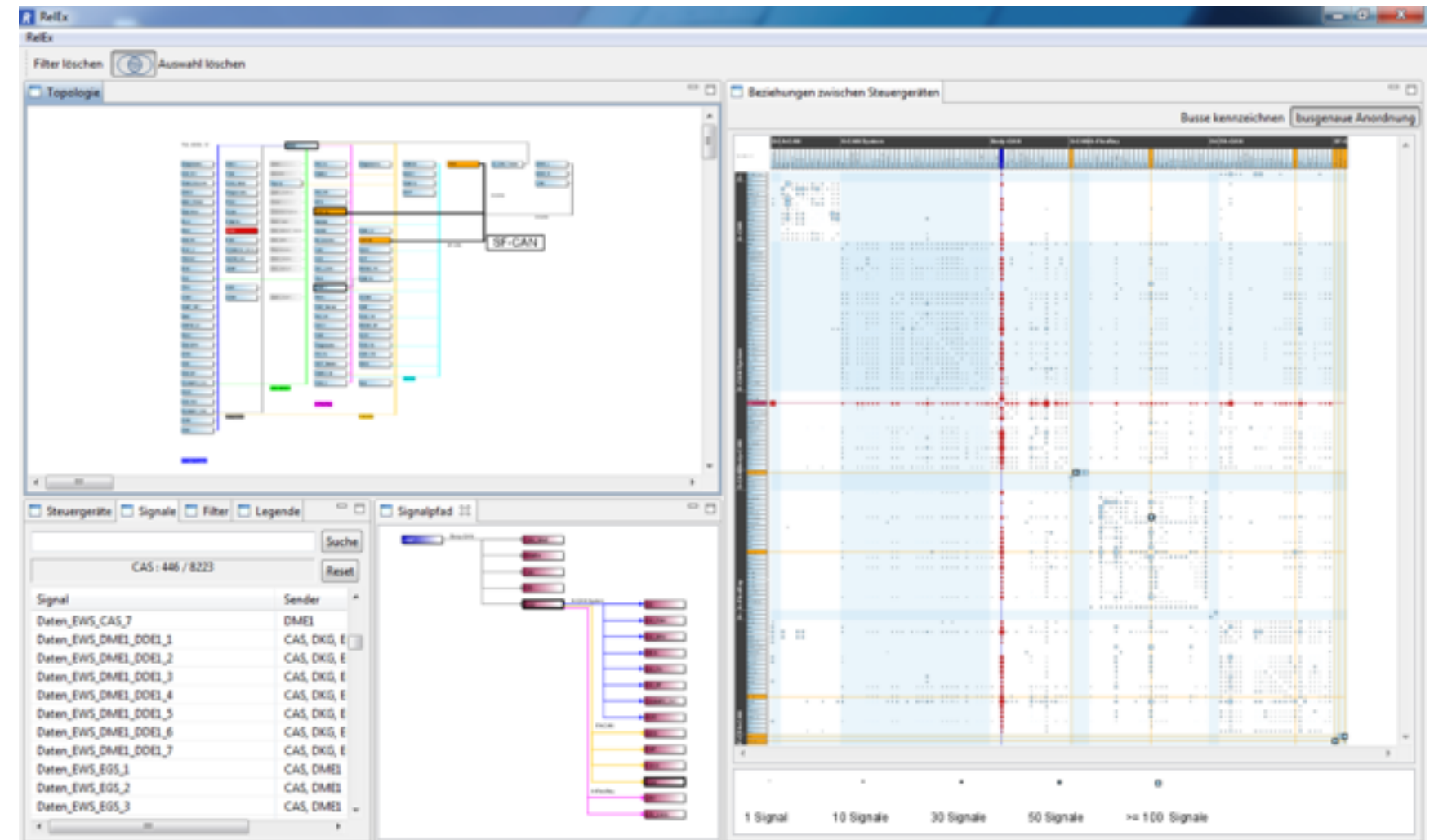


Phase 2: Design, implement, deploy

4 months



- iterative paper prototyping
- agile software development
 - 3 lead users (engineers)
 - 6 deployed releases
- usability engineering
 - domain experts
 - HCI students



Phase 3: Summative evaluation

2 months



- field study
 - 7 engineers
 - 5 weeks
- think aloud study
 - 10 engineers
 - ~1 hour each session
- adoption
 - 15+ users, 3 months post-study

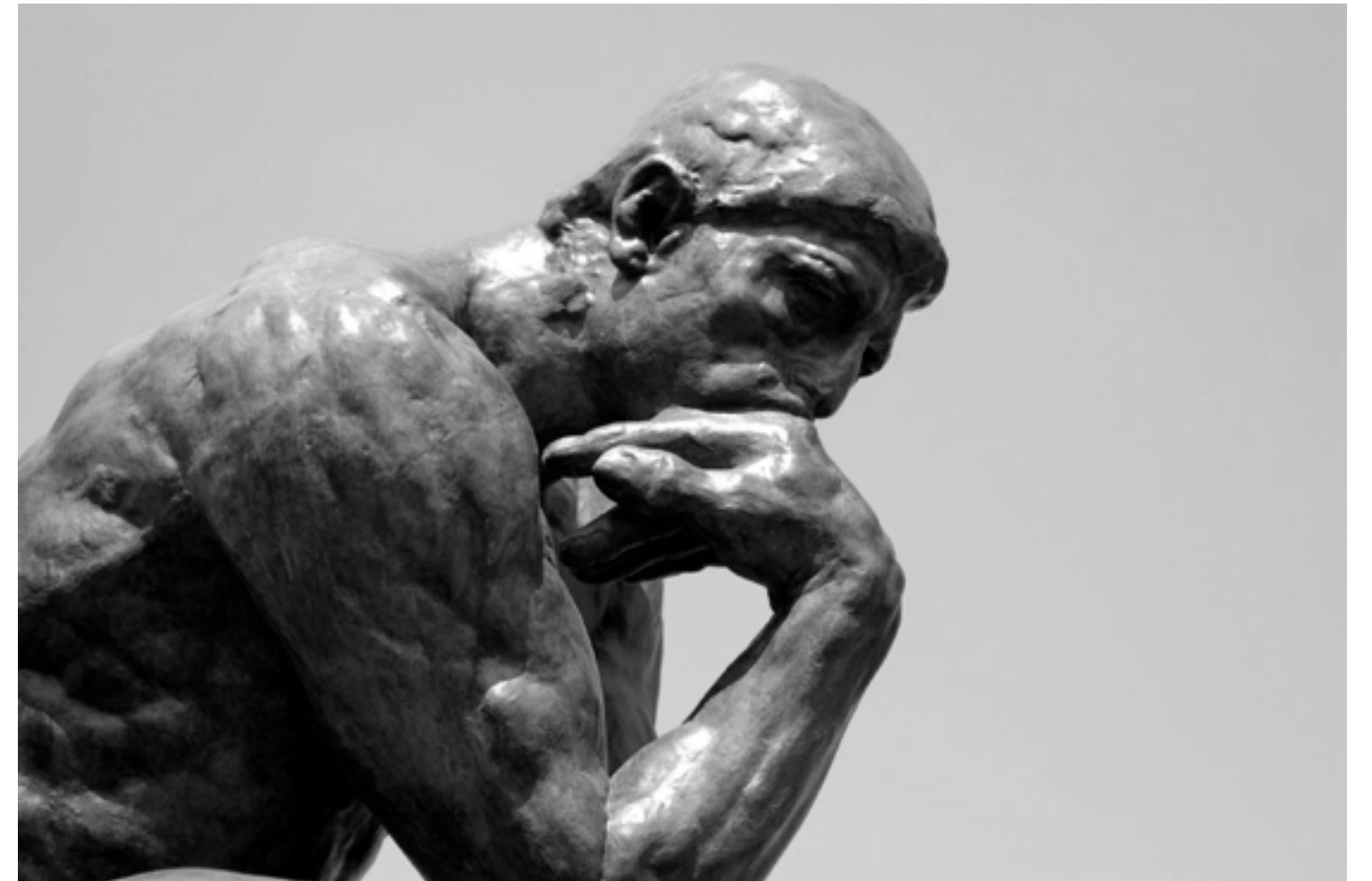


Phase 4: Reflect and write

3 months



- revisit abstractions
- relate to other design studies
- write up

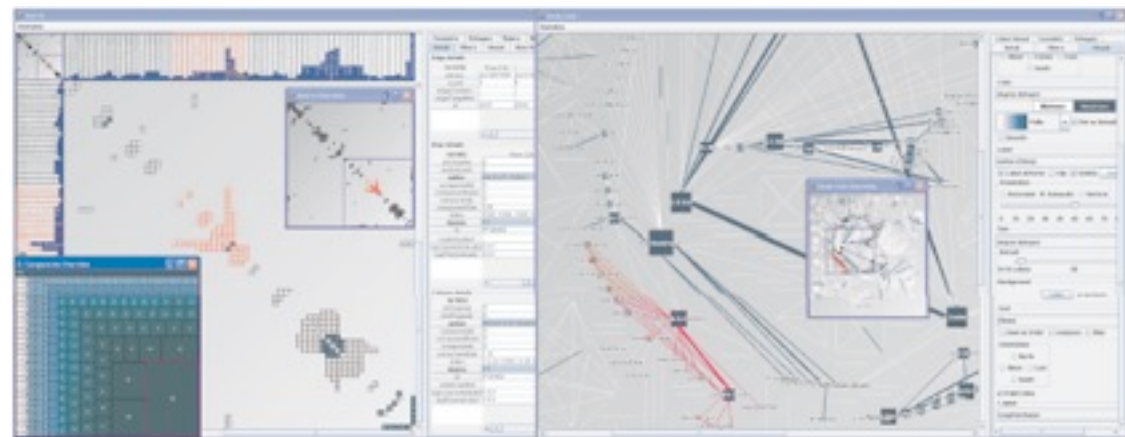


Abstraction Innovation

Previous Work

Focus on social network analysis

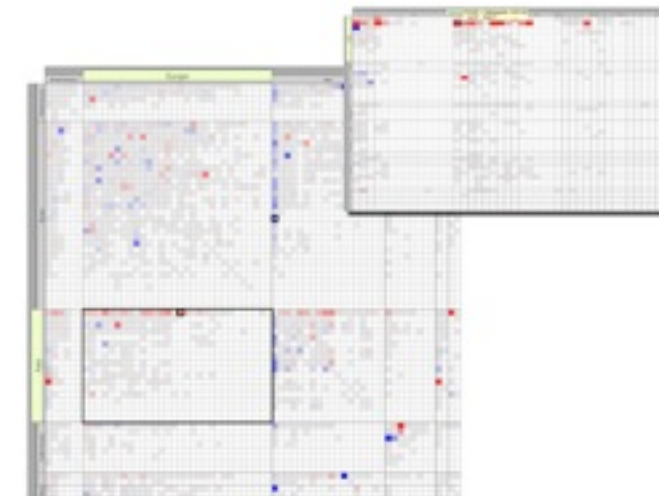
- radically different task and data abstractions



MatrixExplorer



SocialAction



Honeycomb



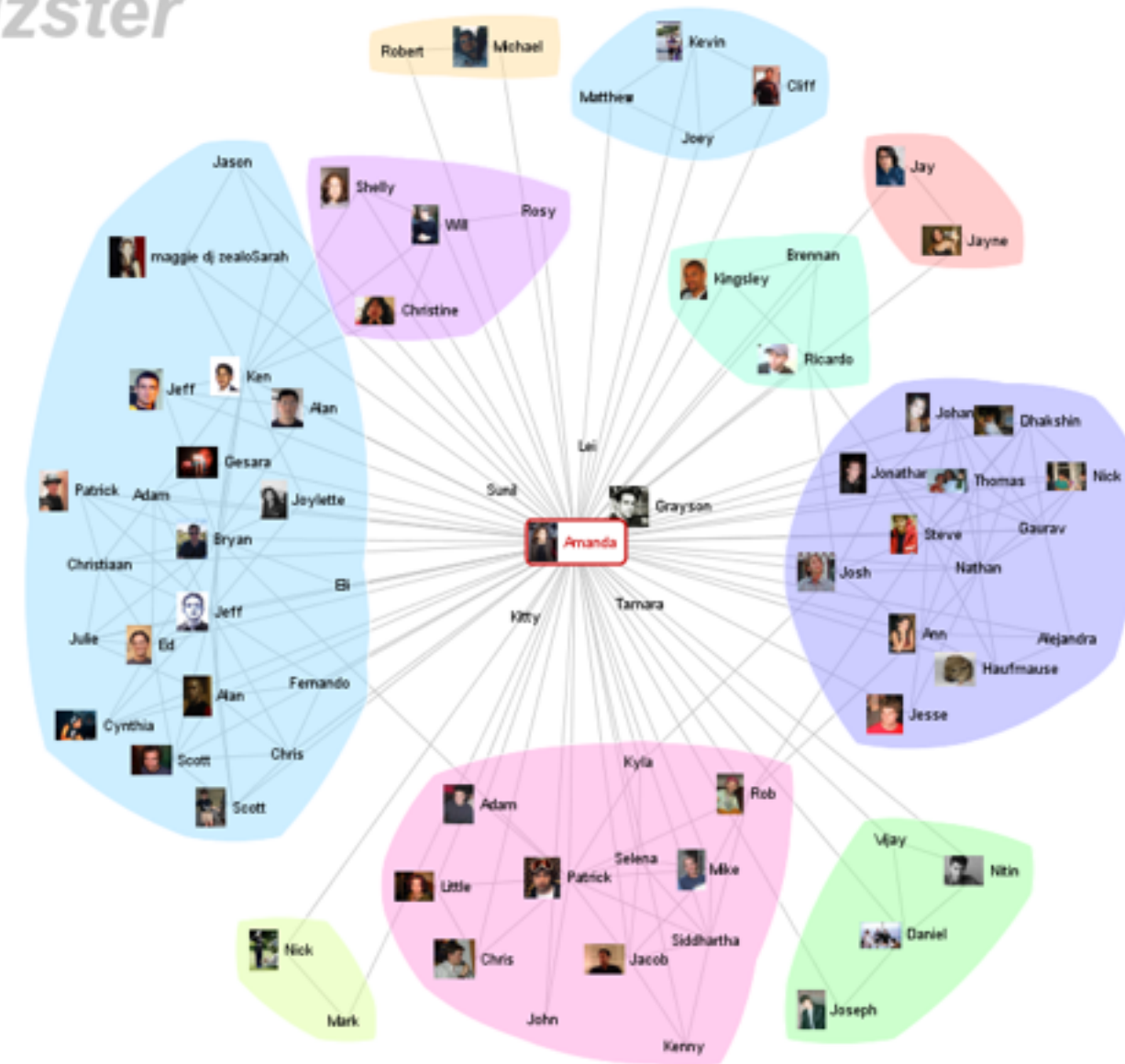
vizster

Task Abstraction

Social Network Analysis Domain

- find clusters

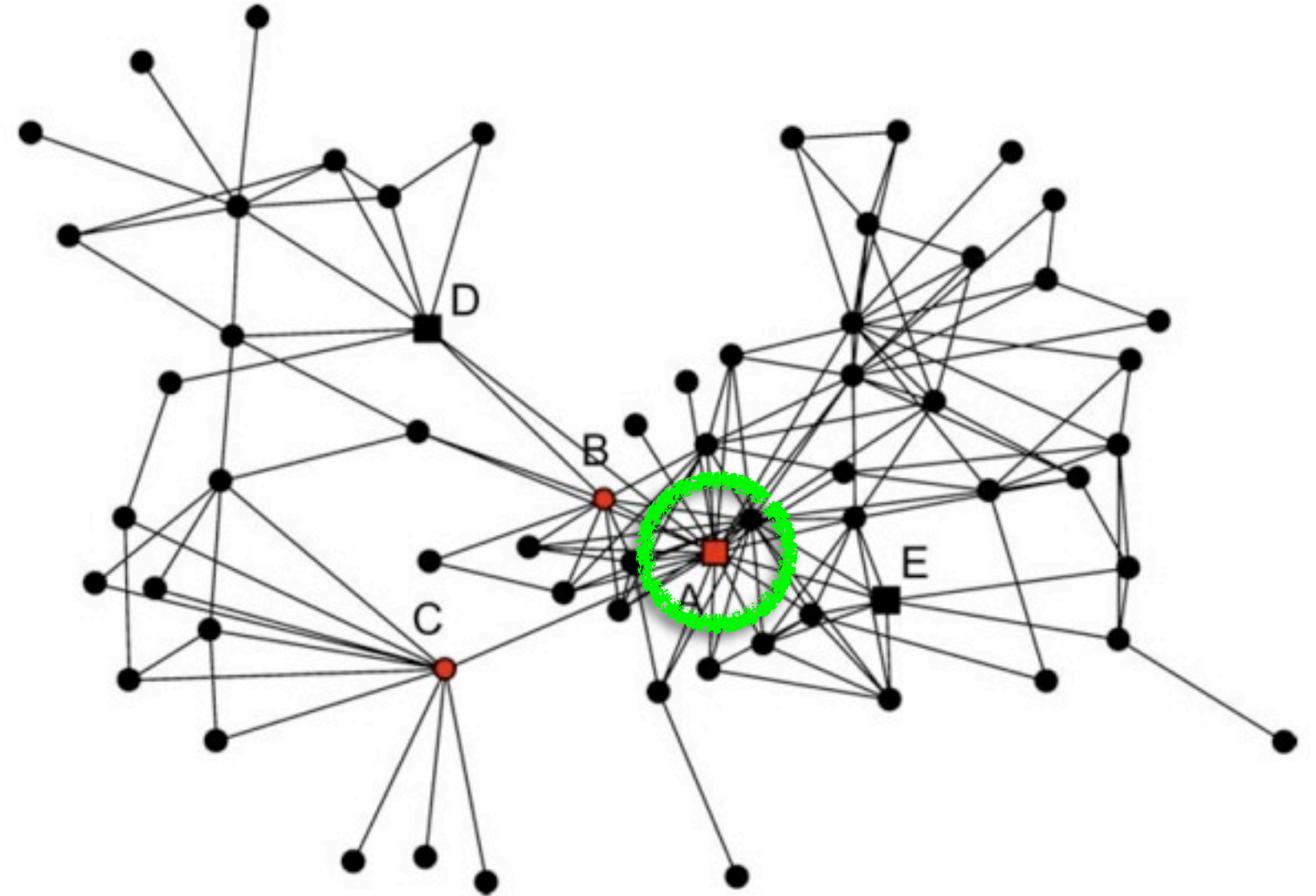
vizster



Task Abstraction

Social Network Analysis Domain

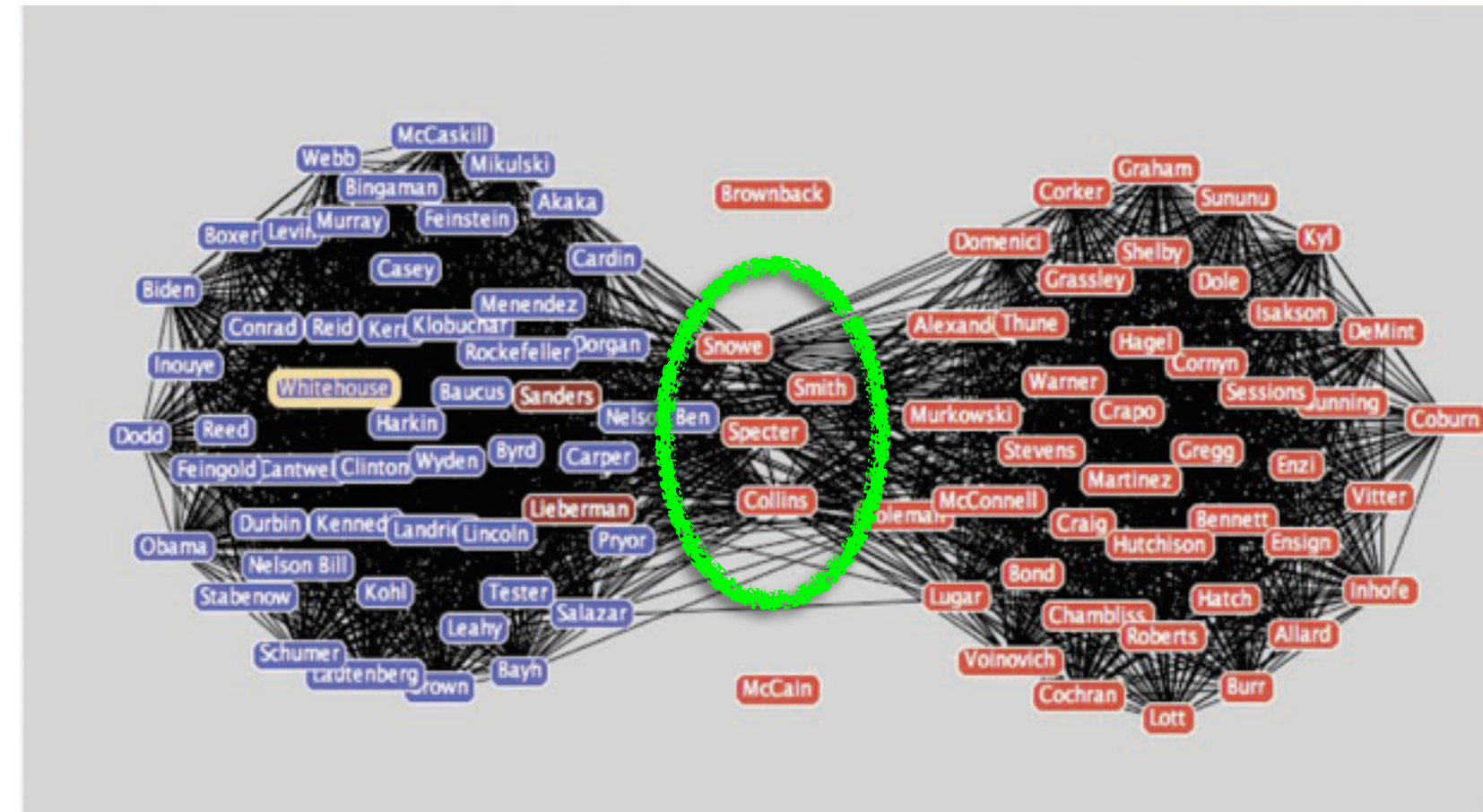
- find clusters
- find high-degree nodes



Task Abstraction

Social Network Analysis Domain

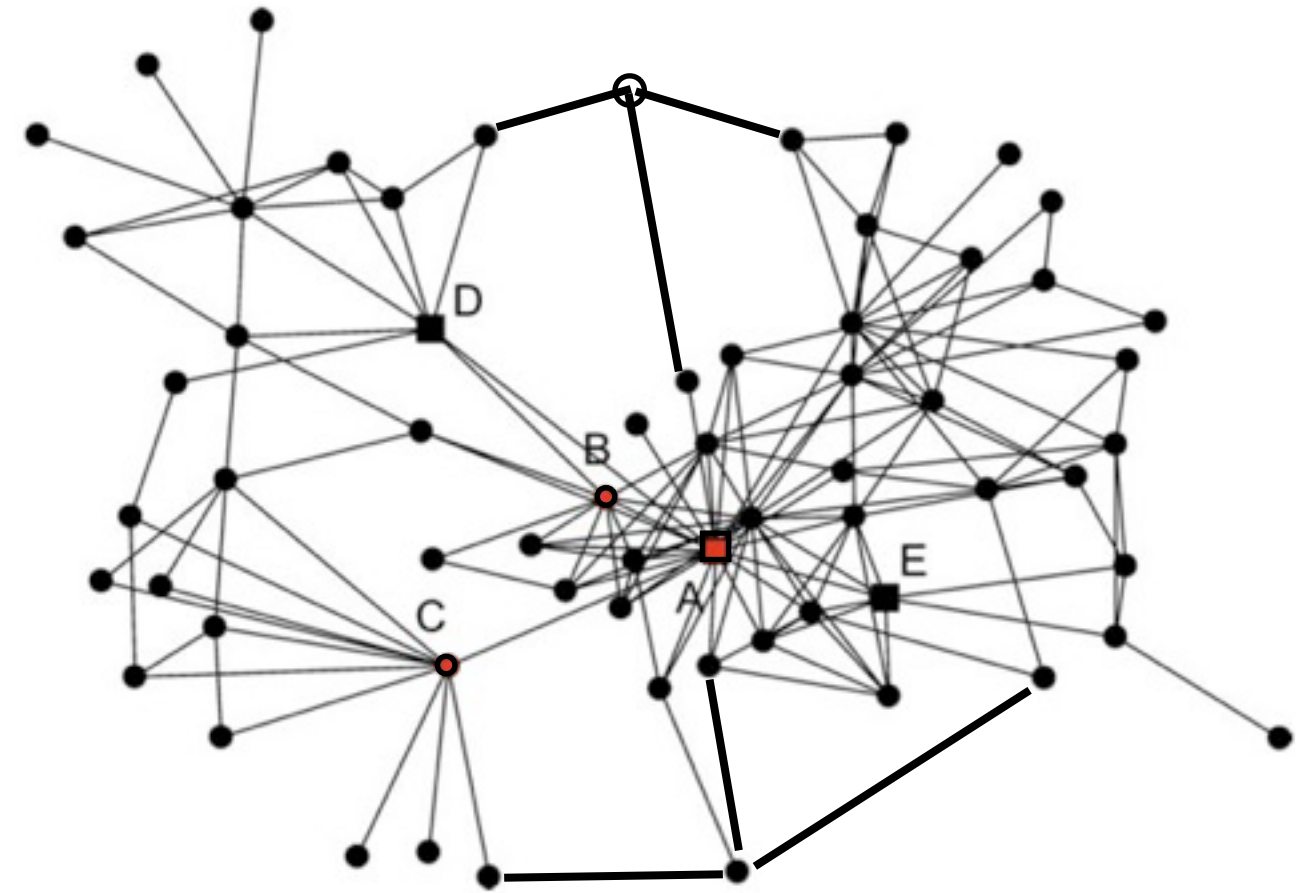
- find clusters
- find high-degree nodes
- find bridge nodes



Task Abstraction

Social Network Analysis Domain

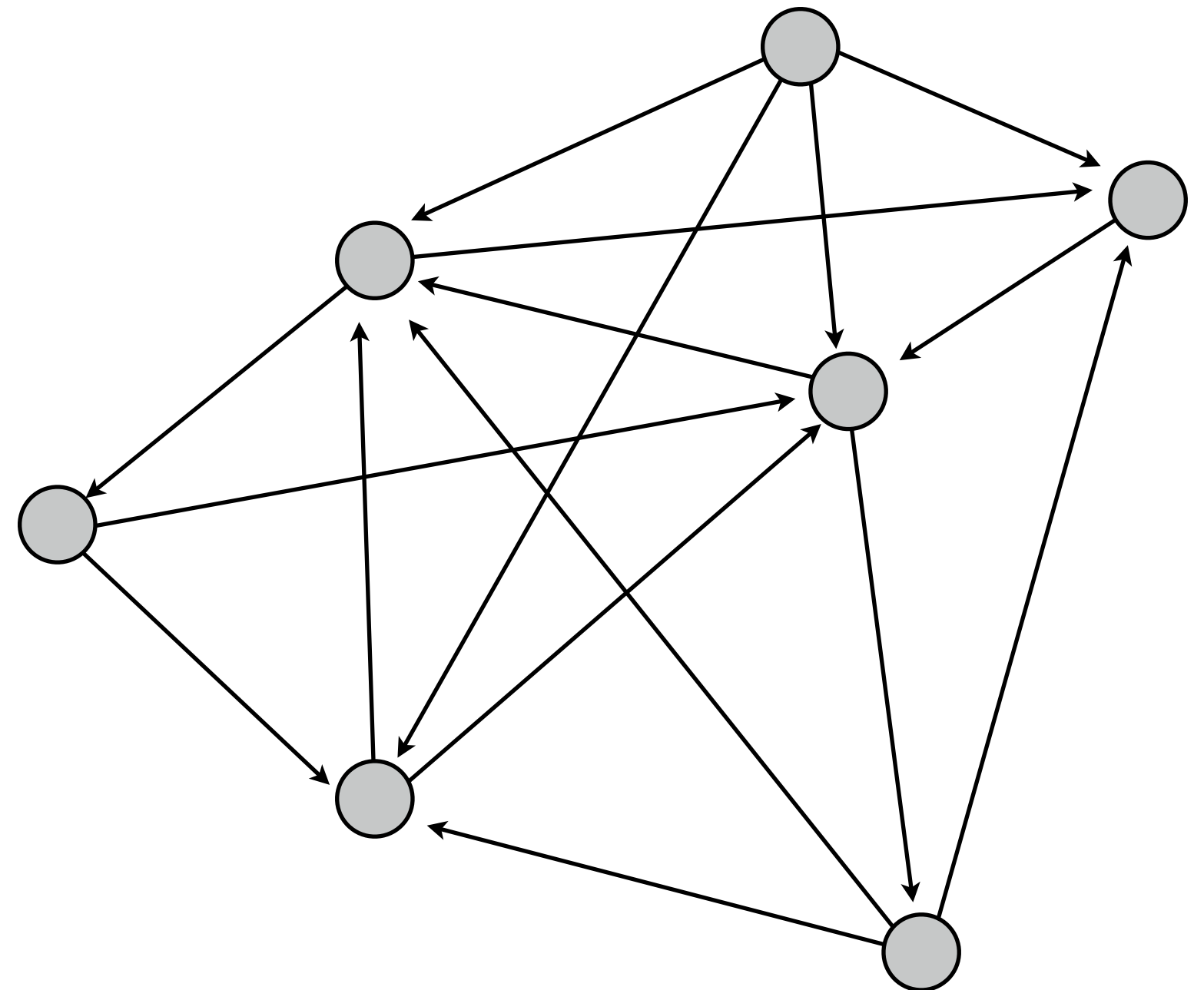
- find clusters
- find high-degree nodes
- find bridge nodes
- understand temporal dynamics
 - passively notice changes



Data Abstraction

Social Network Analysis Domain

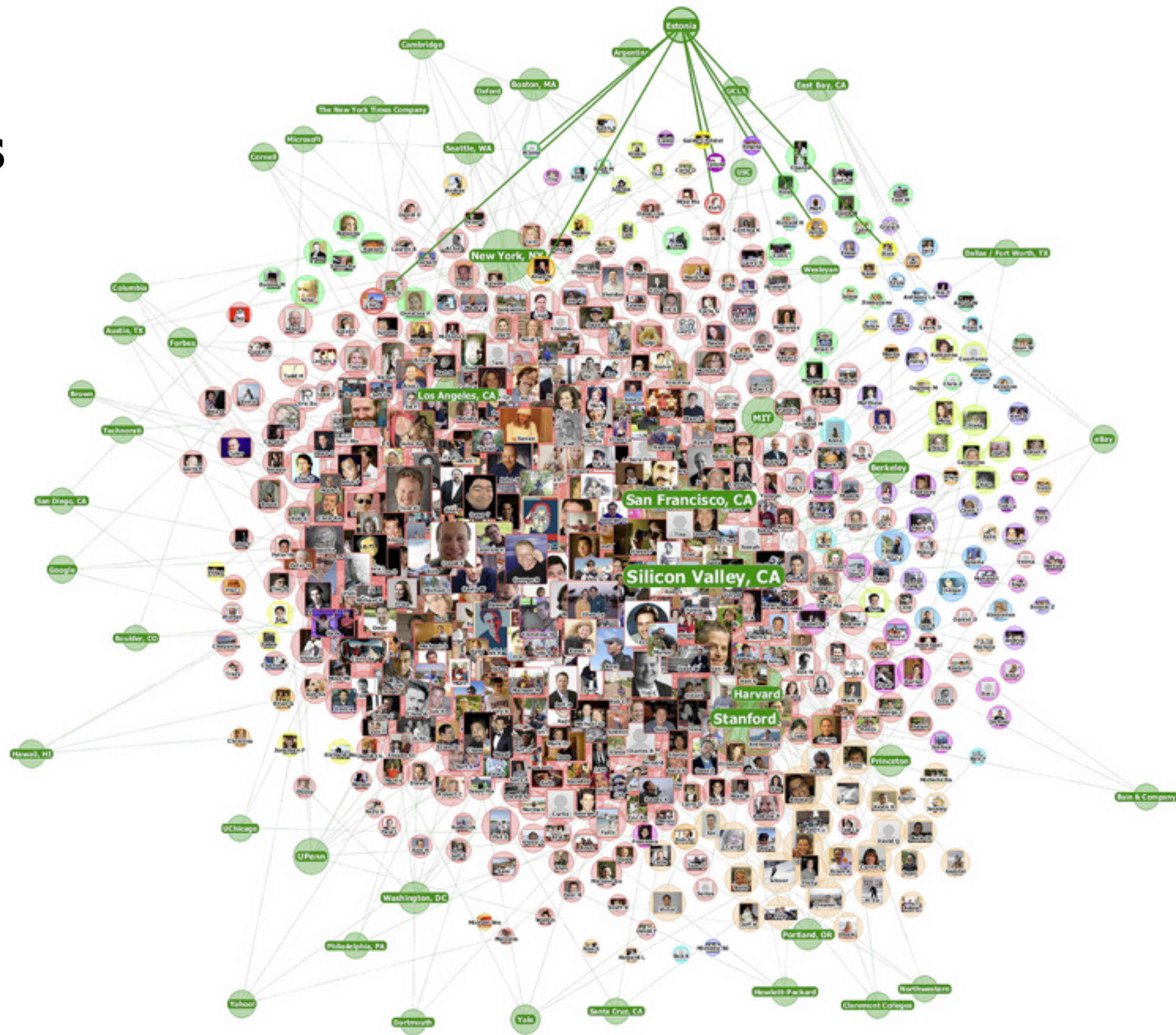
- single graph



Data Abstraction

Social Network Analysis


- single graph
- scalability challenge: nodes




Abstraction Differences

Social Network Analysis vs Overlay Network Optimization



- data
 - single network
 - node scalability
 - sparse edges
- task
 - find clusters, high-degree nodes, bridge nodes
 - passive changes 



- data
 - three related networks
 - physical, logical, overlay
 - path scalability
 - dense edges, few nodes
- task
 - traffic optimization
 - active changes 

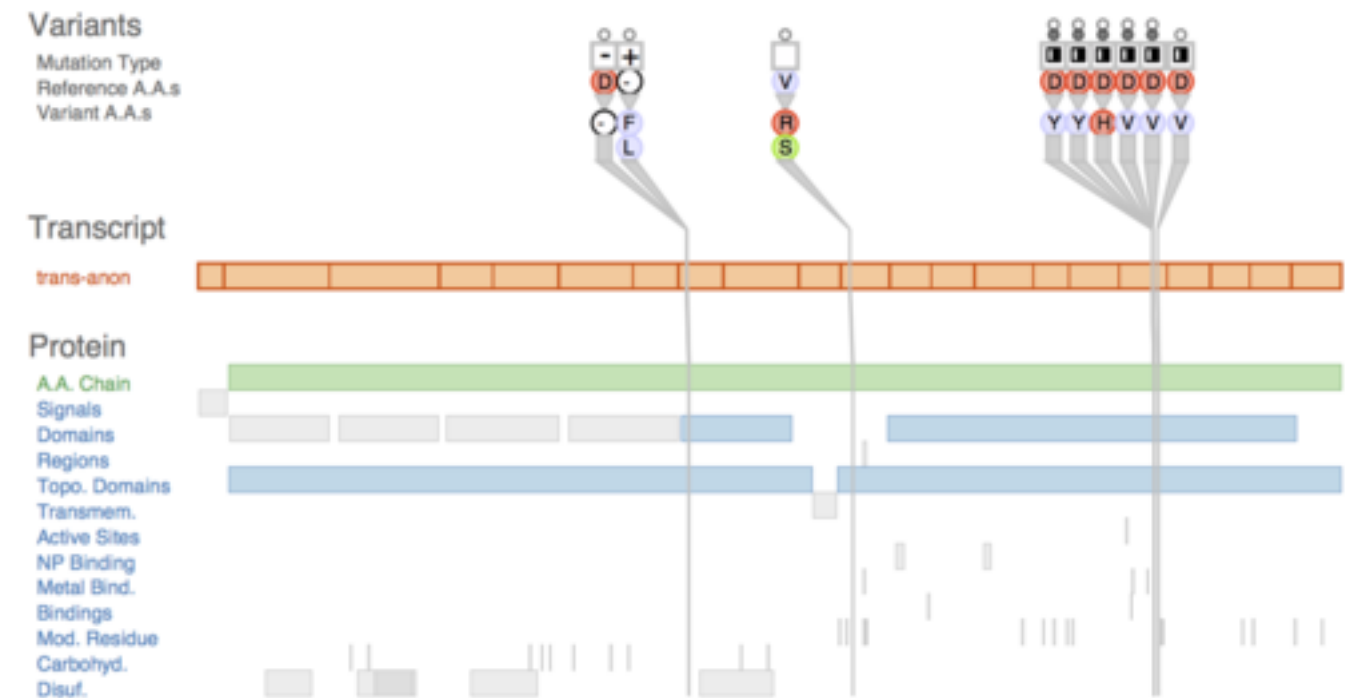
Variant View

Visualizing Sequence Variants in their Gene Context

joint work with:

Joel Ferstay, Cydney Nielsen

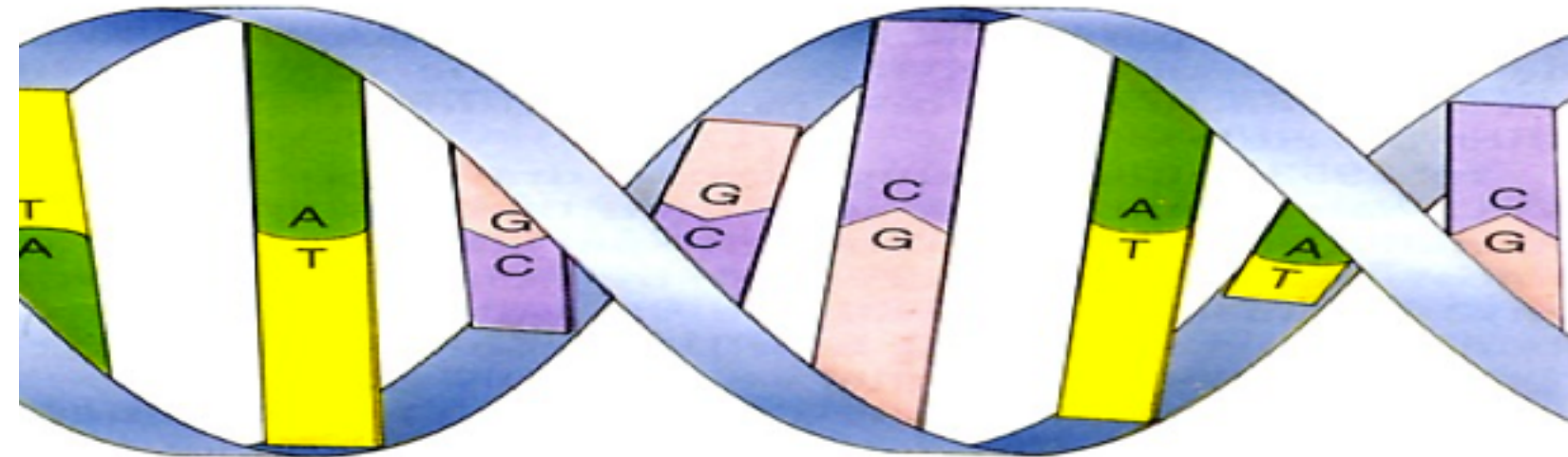
<http://www.cs.ubc.ca/labs/imager/tr/2012/VariantView/>



Variant View: Visualizing Sequence Variants in their Gene Context.
Ferstay, Nielsen, Munzner. *IEEE TVCG* 19(12): 2546-2555, 2013 (Proc. InfoVis 2013).

Sequence Variant Definition

- Sequence variants
 - Difference between reference and given genome



Reference Genome DNA: ATA TGA TCA ACA CTT

Sample 1 Genome DNA: ATA TG**G** TCA **ATA** CTT

Sample 2 Genome DNA: ATA TGA **TGA** ACA **CCT**

Harmful?

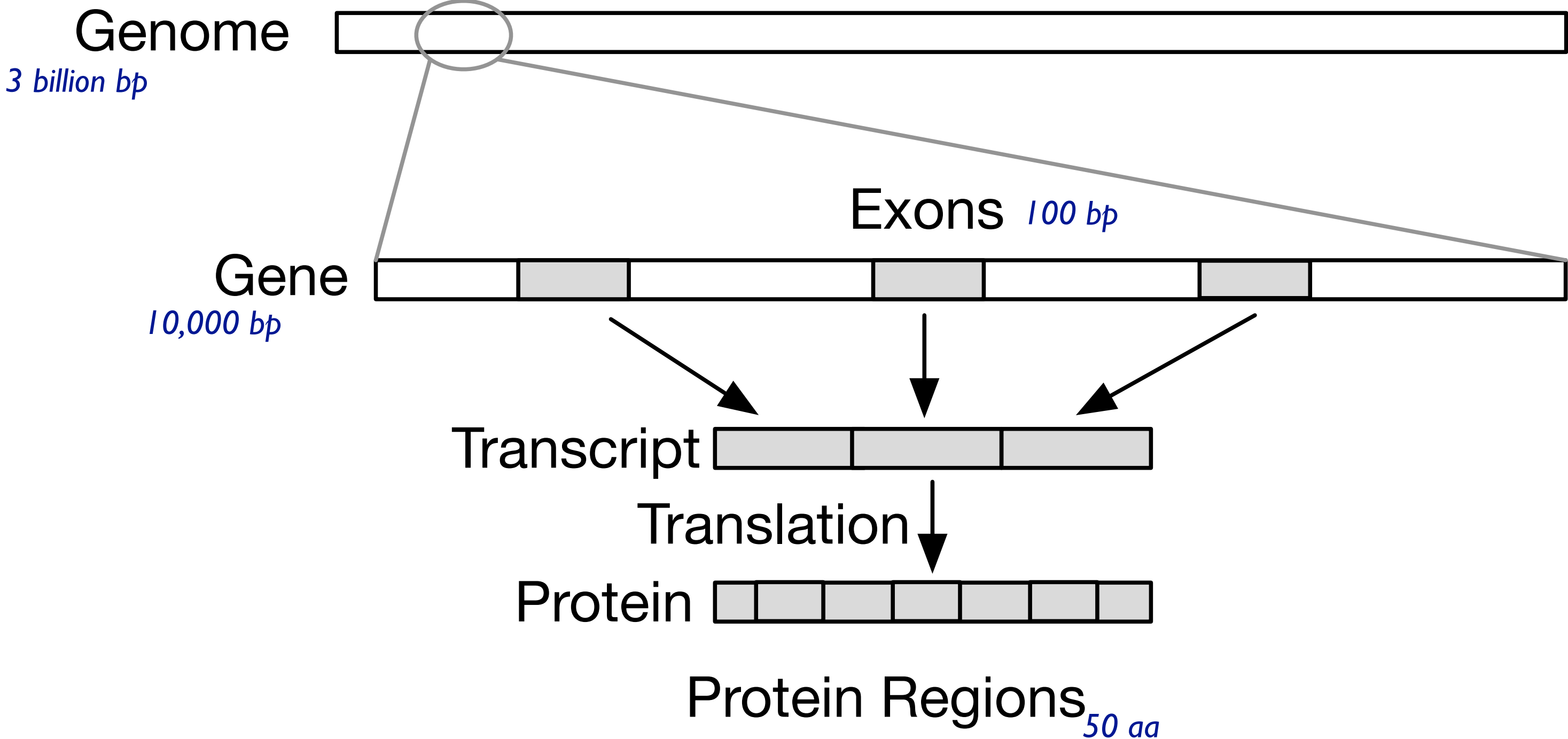
Harmless?

Cancer Research

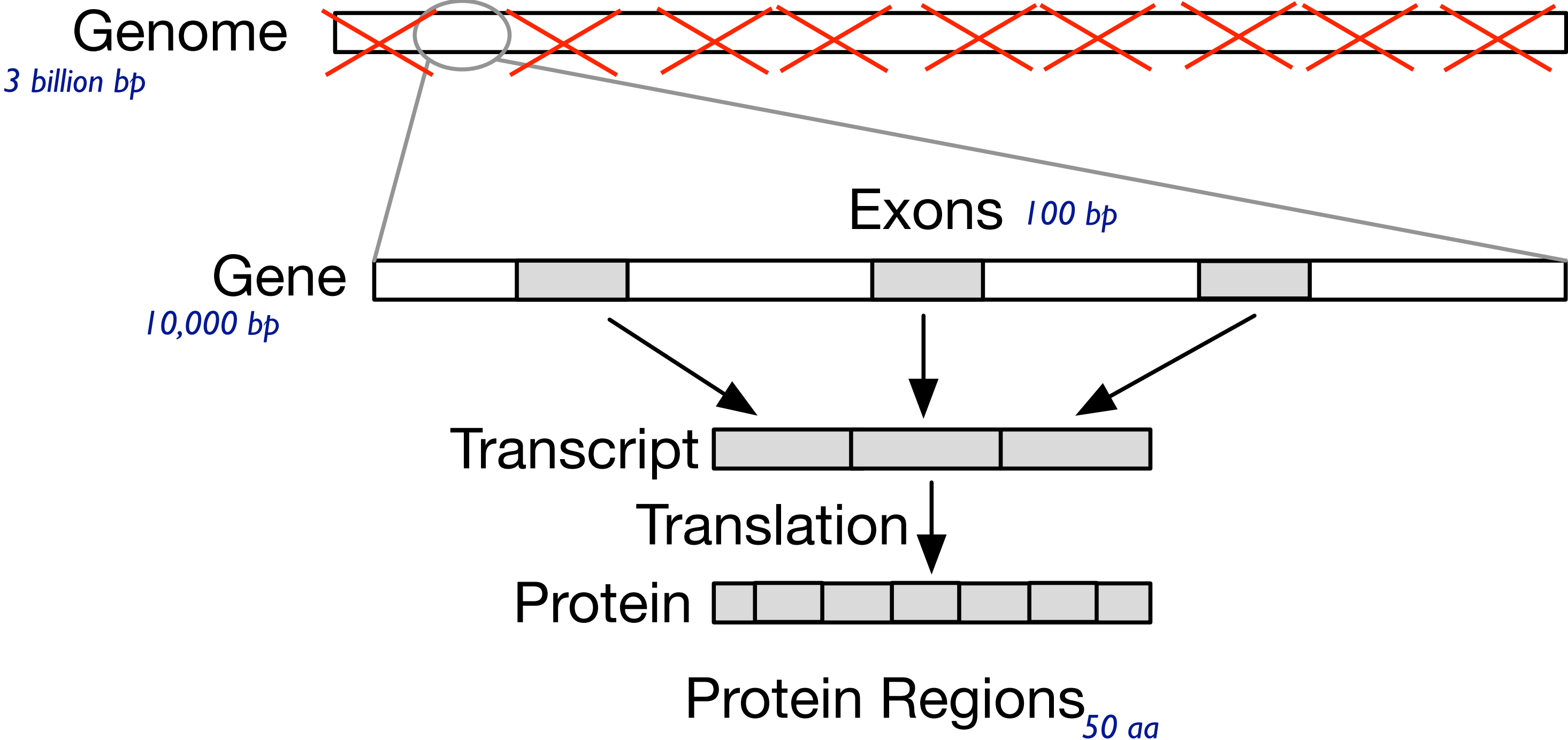
- collaboration with analysts at BC Genome Sciences Center
 - studying genetic basis of leukemia
- driving task
 - discover new candidate genes with harmful variants
- two big questions
 - what to show
 - data abstraction
 - challenge: enormous range of scales in the data
 - how to show it
 - visual encoding idiom

Abstractions

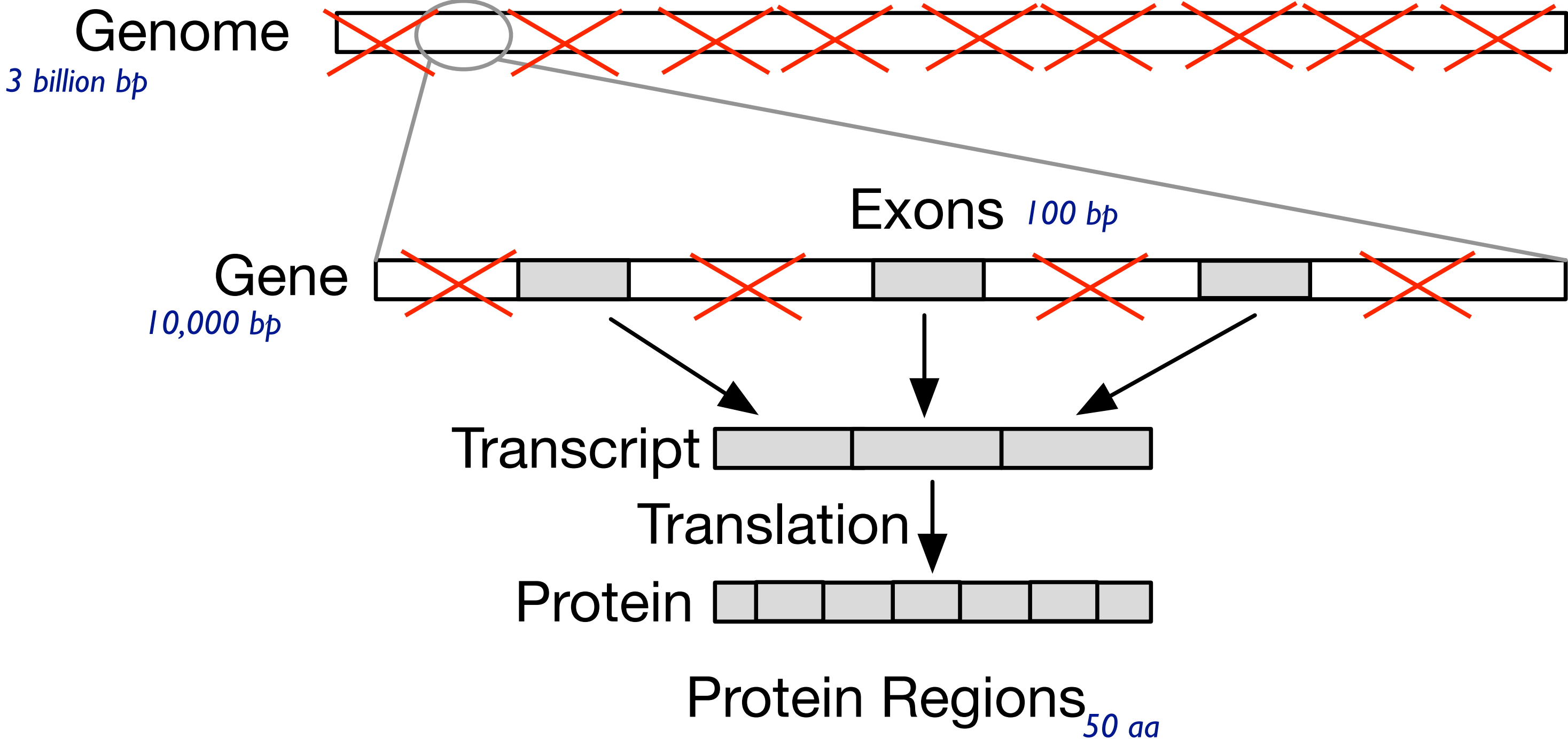
Data: Filtering to relevant biological levels and scales



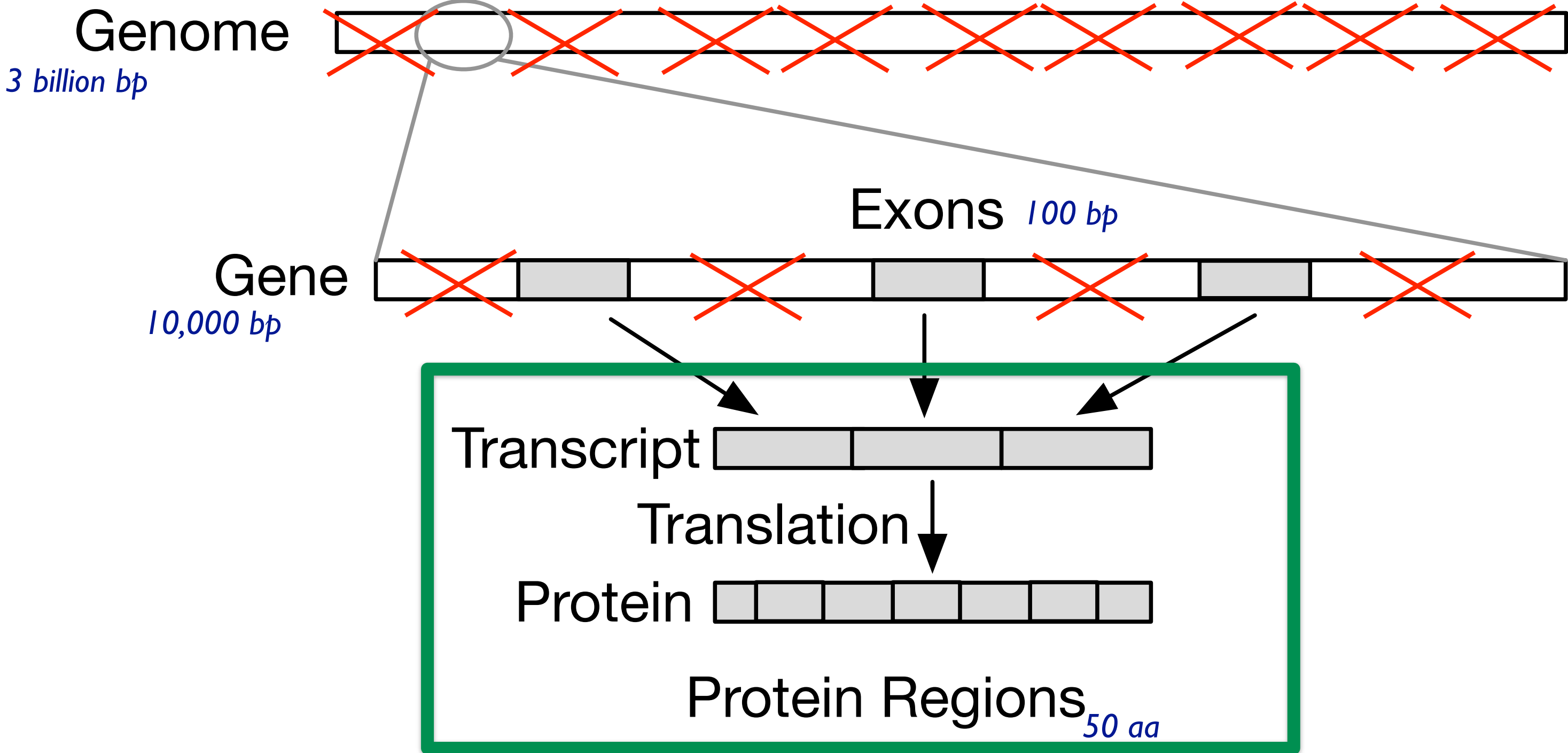
Filter out whole genome; keep genes



Filter out non-exon regions

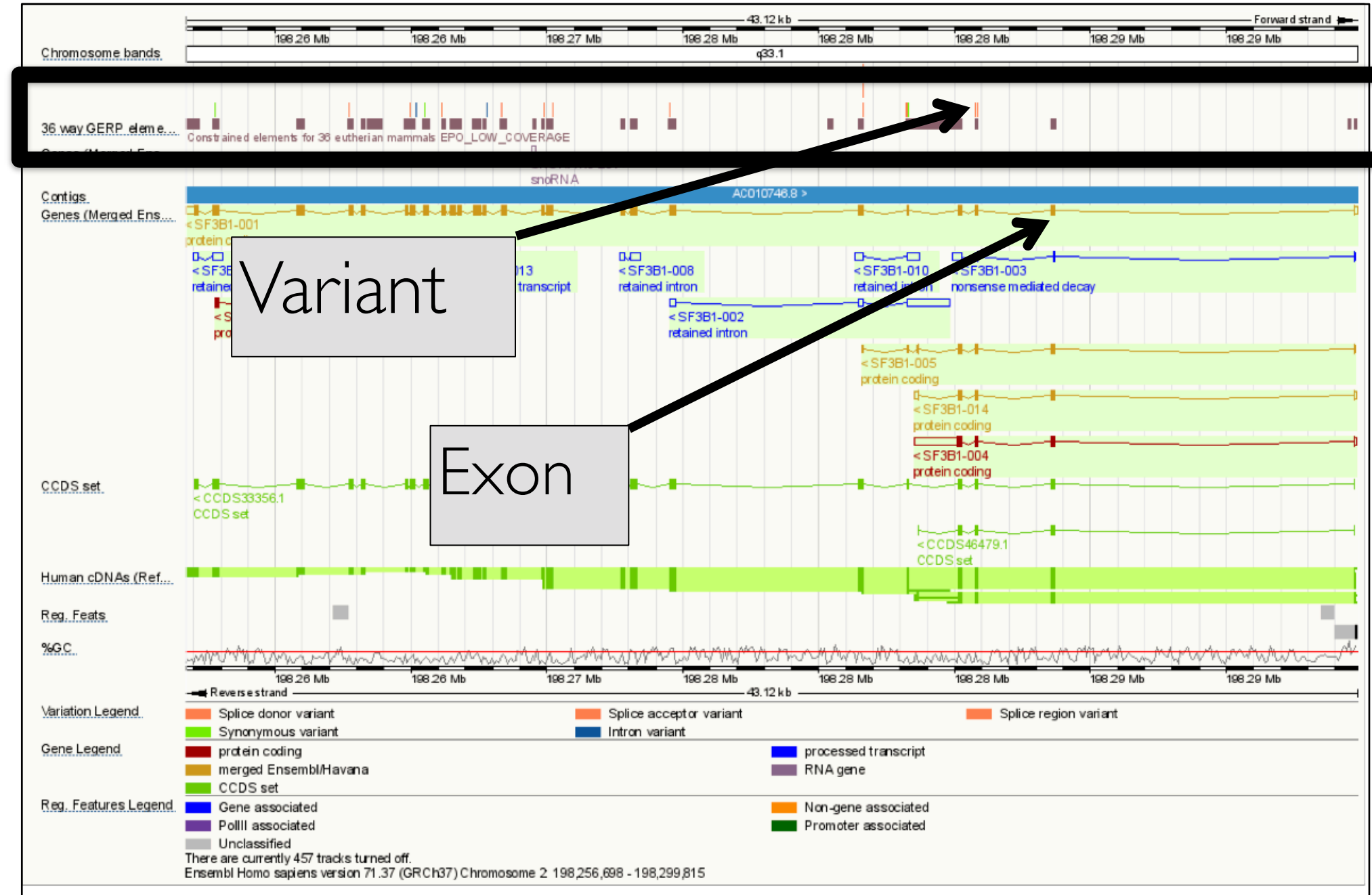


Data abstraction: highly filtered scope of *transcript coordinates*



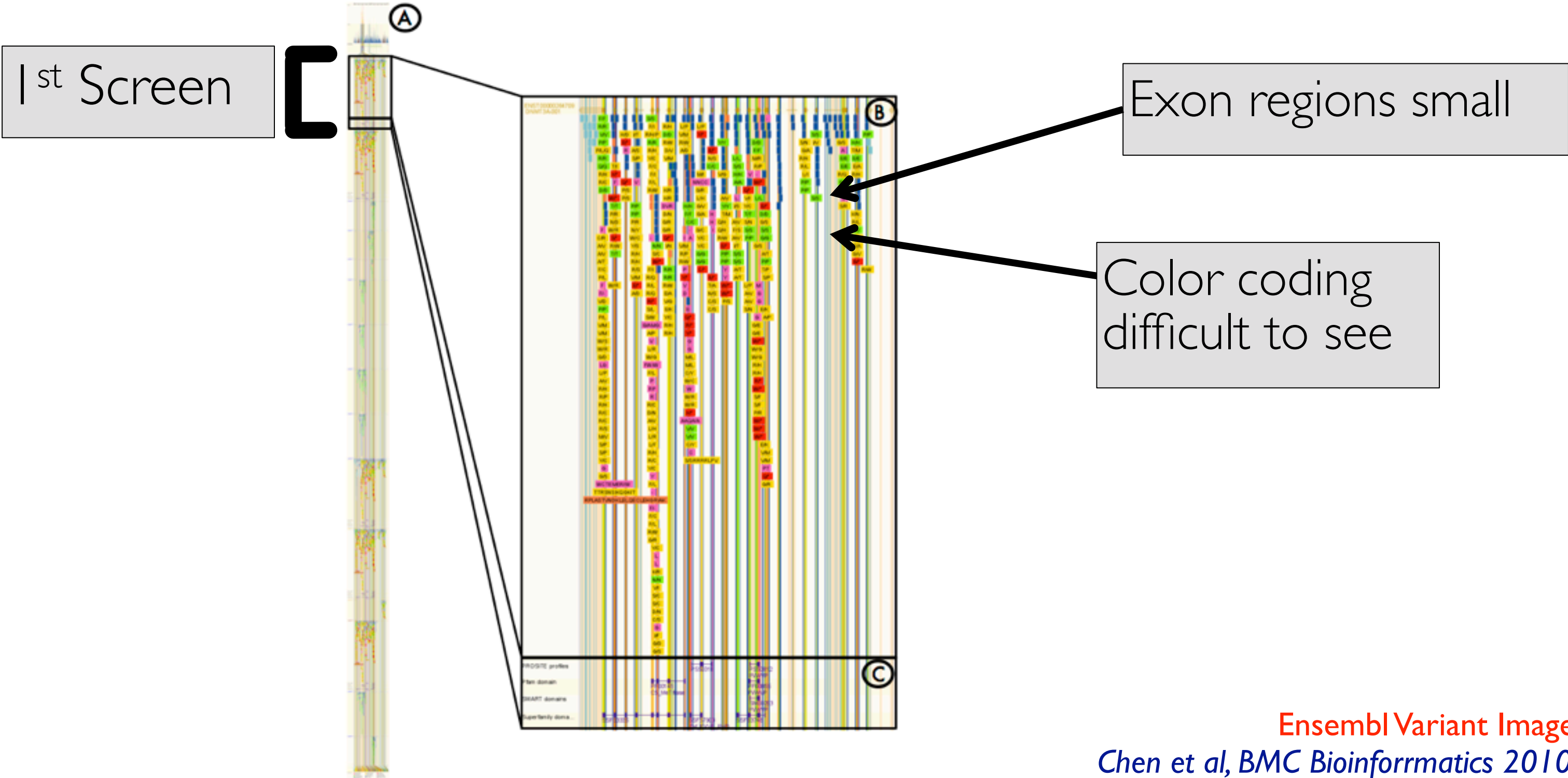
Dominant paradigm: genome browsers

- strengths: flexible and powerful
 - horizontal tracks: user data
 - shared coordinate system: genome coordinates (bp)
- problems
 - tiny features of interest spread out across large extent
 - must zoom far in to inspect known feature, then zoom out and pan to locate next
 - high cognitive load for interaction
 - must already know where to look



representative example: Ensembl
Chen et al, BMC Bioinformatics 2010.

Features of interest small even in variant-specific view



Idioms

Variant View

Gene Search:

Alternative Transcripts:

Variants

Mutation Type
Reference A.A.s
Variant A.A.s

Transcript

trans-anon

Protein

A.A. Chain
Domains
Regions
Active Sites
Bindings
Mod. Residue

(A)

Sort By Gene:

Alpha Cluster Score **Variant Count**

(C)

- DNMT3A (NM_022552)
- IDH2 (NM_002168)
- FLT3 (NM_004119)
- ANKRD36 (NM_001164315)
- ARID1B (NM_017519)
- STAG2 (NM_001042749)
- TNRC18 (NM_001080495)
- WT1 (NM_000378)
- ABCA13 (NM_152701)
- CEBPA (NM_004364)
- TET2 (NM_001127208)
- DNAH10 (NM_207437)
- GPSM1 (NM_015597)
- ASXL1 (NM_015338)
- DNAH1 (NM_015512)
- DNAH6 (NM_001370)
- FAT1 (NM_005245)
- MDN1 (NM_014611)
- PTPN11 (NM_002834)
- SYNE1 (NM_033071)
- ALMS1 (NM_015120)
- C10orf68 (NM_024688)
- CCDC88C (NM_001080414)
- DNAH11 (NM_003777)
- DNAH3 (NM_017539)
- DNAH9 (NM_001372)

Variant Data

Patient ID	Chr. Coord.	Ref Base	Var Base	dbSNP129	dbSNP135	dbSNP137	COSMIC	A.A. Chng.	Gene	Ref. Gene
pid-anon	11288816	G	T	.	.	.	*13028,	G60V	gene-anon	trans-anon
pid-anon	11288816	G	T	.	.	.	*13012,	D61Y	gene-anon	trans-anon
pid-anon	11288819	G	T	.	rs121918	.	13014	A72S	gene-anon	trans-anon
pid-anon	11288819	C	T	.	.	.	*13035,	A72V	gene-anon	trans-anon
pid-anon	11288821	G	C	.	.	.	*13016,	E76Q	gene-anon	trans-anon
pid-anon	11288821	A	G	.	rs121918	.	*13017,	E76G	gene-anon	trans-anon
pid-anon	11288821	G	T	E76D	gene-anon	trans-anon
pid-anon	11292688	T	A	.	rs121918	.	*13020,	S502T	gene-anon	trans-anon
pid-anon	11292688	T	G	.	.	.	*13020,	S502A	gene-anon	trans-anon
pid-anon	11292688	C	T	.	.	.	13023	S502L	gene-anon	trans-anon

(B)

Variant View

Information-dense single gene view

Gene Search:

Alternative Transcripts:

Variants
 Mutation Type
 Reference A.A.s
 Variant A.A.s

Transcript
 trans-anon

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pid-anon	11288816	G	T	.	.	.	*13012,	D61Y	gene-anon	trans-anon
pid-anon	11288819	G	T	.	rs121918	.	13014	A72S	gene-anon	trans-anon
pid-anon	11288819	C	T	.	.	.	*13035,	A72V	gene-anon	trans-anon
pid-anon	11288821	G	C	.	.	.	*13016,	E76Q	gene-anon	trans-anon
pid-anon	11288821	A	G	.	rs121918	.	*13017,	E76G	gene-anon	trans-anon
pid-anon	11288821	G	T	E76D	gene-anon	trans-anon
pid-anon	11292688	T	A	.	rs121918	.	*13020,	S502T	gene-anon	trans-anon
pid-anon	11292688	T	G	.	.	.	*13020,	S502A	gene-anon	trans-anon
pid-anon	11292688	C	T	.	.	.	13023	S502L	gene-anon	trans-anon

Sort By Gene:

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- IDH2 (NM_002168)
- FLT3 (NM_004119)
- ANKRD36 (NM_001164315)
- ARID1B (NM_017519)
- STAG2 (NM_001042749)
- TNRC18 (NM_001080495)
- WT1 (NM_000378)
- ABCA13 (NM_152701)
- CEBPA (NM_004364)
- TET2 (NM_001127208)
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- GPSM1 (NM_015597)
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- DNAH6 (NM_001370)
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- SYNE1 (NM_033071)
- ALMS1 (NM_015120)
- C10orf68 (NM_024688)
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- DNAH11 (NM_003777)
- DNAH3 (NM_017539)
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Variant View

Gene Search:

Alternative Transcripts:

Information-dense single gene view

Variants
Mutation Type
Reference A.A.s
Variant A.A.s

Transcript
trans-anon

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Variant Data

Patient ID	Chr.	Coord.	Ref Base	Var Base	dbSNP129	dbSNP135	dbSNP137	COSMIC	A.A. Ch.	Transcript	Transcript
pid-anon	11	288816	G	T	.	.	.	*13028,	G60V	gene-anon	trans-anon
pid-anon	11	288816	G	T	.	.	.	*13012,	D61Y	gene-anon	trans-anon
pid-anon	11	288819	G	T	.	rs121918	.	13014	A72S	gene-anon	trans-anon
pid-anon	11	288819	C	T	.	.	.	*13035,	A72V	gene-anon	trans-anon
pid-anon	11	288821	G	C	.	.	.	*13016,	E76Q	gene-anon	trans-anon
pid-anon	11	288821	A	G	.	rs121918	.	*13017,	E76G	gene-anon	trans-anon
pid-anon	11	288821	G	T	E76D	gene-anon	trans-anon
pid-anon	11	292688	T	A	.	rs121918	.	*13020,	S502T	gene-anon	trans-anon
pid-anon	11	292688	T	G	.	.	.	*13020,	S502A	gene-anon	trans-anon
pid-anon	11	292688	C	T	.	.	.	13023	S502L	gene-anon	trans-anon

No need for pan and zoom

Variant View

Sorting metrics guide gene navigation

Alternative Transcripts: gene-anon (trans-anon)

Variants

Mutation Type
Reference A.A.s
Variant A.A.s

Transcript

trans-anon

Protein

A.A. Chain
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Variant Data

Patient ID	Chr. Coord.	Ref Base	Var Base	dbSNP129	dbSNP135	dbSNP137	COSMIC	A.A. Chng.	Gene	Ref. Gene
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pid-anon	11288816	G	T	.	.	.	*13012,	D61Y	gene-anon	trans-anon
pid-anon	11288819	G	T	.	rs121918	.	13014	A72S	gene-anon	trans-anon
pid-anon	11288819	C	T	.	.	.	*13035,	A72V	gene-anon	trans-anon
pid-anon	11288821	G	C	.	.	.	*13016,	E76Q	gene-anon	trans-anon
pid-anon	11288821	A	G	.	rs121918	.	*13017,	E76G	gene-anon	trans-anon
pid-anon	11288821	G	T	E76D	gene-anon	trans-anon
pid-anon	11292688	T	A	.	rs121918	.	*13020,	S502T	gene-anon	trans-anon
pid-anon	11292688	T	G	.	.	.	*13020,	S502A	gene-anon	trans-anon
pid-anon	11292688	C	T	.	.	.	13023	S502L	gene-anon	trans-anon

Sort By Gene: Alpha | Cluster Score | Variant Count

- DNMT3A (NM_022552)
- IDH2 (NM_002168)
- FLT3 (NM_004119)
- ANKRD36 (NM_001164315)
- ARID1B (NM_017519)
- STAG2 (NM_001042749)
- TNRC18 (NM_001080495)
- WT1 (NM_000378)
- ABCA13 (NM_152701)
- CEBPA (NM_004364)
- TET2 (NM_001127208)
- DNAH10 (NM_207437)
- GPSM1 (NM_015597)
- ASXL1 (NM_015338)
- DNAH1 (NM_015512)
- DNAH6 (NM_001370)
- FAT1 (NM_005245)
- MDN1 (NM_014611)
- PTPN11 (NM_002834)
- SYNE1 (NM_033071)
- ALMS1 (NM_015120)
- C10orf68 (NM_024688)
- CCDC88C (NM_001080414)
- DNAH11 (NM_003777)
- DNAH3 (NM_017539)
- DNAH9 (NM_001372)

Variant View

Sorting metrics guide gene navigation

Alternative Transcripts: gene-anon (trans-anon)

Variants

Mutation Type
Reference A.A.s
Variant A.A.s

Transcript

trans-anon

Protein

A.A. Chain
Domains
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Variant Data

Gene	RefSeq ID	Position	Ref	Alt	dbSNP	COSMIC	A.A. Chng.	Gene	RefSeq ID
gene-anon	trans-anon	1128819	C	T		*13028,	G60V	gene-anon	trans-anon
gene-anon	trans-anon	1128821	G	C		*13012,	D61Y	gene-anon	trans-anon
gene-anon	trans-anon	1128821	A	G	rs121918	13014	A72S	gene-anon	trans-anon
gene-anon	trans-anon	1128821	G	T		*13035,	A72V	gene-anon	trans-anon
gene-anon	trans-anon	11292688	T	A		*13016,	E76Q	gene-anon	trans-anon
gene-anon	trans-anon	11292688	T	G		*13017,	E76G	gene-anon	trans-anon
gene-anon	trans-anon	11292688	C	T		.	E76D	gene-anon	trans-anon
gene-anon	trans-anon					*13020,	S502T	gene-anon	trans-anon
gene-anon	trans-anon					*13020,	S502A	gene-anon	trans-anon
gene-anon	trans-anon					13023	S502L	gene-anon	trans-anon

Sort By Gene: Alpha | **Cluster Score** | Variant Count

- DNMT3A (NM_022552)
- IDH2 (NM_002168)
- FLT3 (NM_004119)
- ANKRD36 (NM_001164315)
- ARID1B (NM_017519)
- STAG2 (NM_001042749)
- TNRC18 (NM_001080495)
- WT1 (NM_000378)
- ABCA13 (NM_152701)
- CEBPA (NM_004364)
- TET2 (NM_001127208)
- DNAH10 (NM_207437)
- GPSM1 (NM_015597)
- ASXL1 (NM_015338)
- DNAH1 (NM_015512)
- DNAH6 (NM_001370)
- FAT1 (NM_005245)
- MDN1 (NM_014611)
- PTPN11 (NM_002834)
- SYNE1 (NM_033071)
- ALMS1 (NM_015120)
- C10orf68 (NM_024688)
- CCDC88C (NM_001080414)
- DNAH11 (NM_003777)
- DNAH3 (NM_017539)
- DNAH9 (NM_001372)

Callouts: A (Sort By Gene), B (Variant Data table), C (Gene list)

Control what shows up here

Variant View

Gene Search:

Alternative Transcripts:

A

Variants

Mutation Type
Reference A.A.s
Variant A.A.s

Transcript

trans-anon

Protein

A.A. Chain
Domains
Regions
Active Sites
Bindings
Mod. Residue

Variant Data

B

Patient ID	Chr.	Coord.	Ref Base	Var Base	dbSNP129	dbSNP135	dbSNP137	COSMIC	A.A. Chng.	Gene	Ref. Gene
pid-anon	11	288816	G	T	.	.	.	*13028,	G60V	gene-anon	trans-anon
pid-anon	11	288816	G	T	.	.	.	*13012,	D61Y	gene-anon	trans-anon
pid-anon	11	288819	G	T	.	rs121918	.	*13014,	A72S	gene-anon	trans-anon
pid-anon	11	288819	C	T	.	.	.	*13035,	E76Q	gene-anon	trans-anon
pid-anon	11	288821	G	C	.	.	.	*13016,	E76Q	gene-anon	trans-anon
pid-anon	11	288821	A	G	.	rs121918	.	*13017,	E76G	gene-anon	trans-anon
pid-anon	11	288821	G	T	E76D	gene-anon	trans-anon
pid-anon	11	292688	T	A	.	rs121918	.	*13020,	S502T	gene-anon	trans-anon
pid-anon	11	292688	T	G	.	.	.	*13020,	S502A	gene-anon	trans-anon
pid-anon	11	292688	C	T	.	.	.	13023	S502L	gene-anon	trans-anon

C

Sort By Gene:

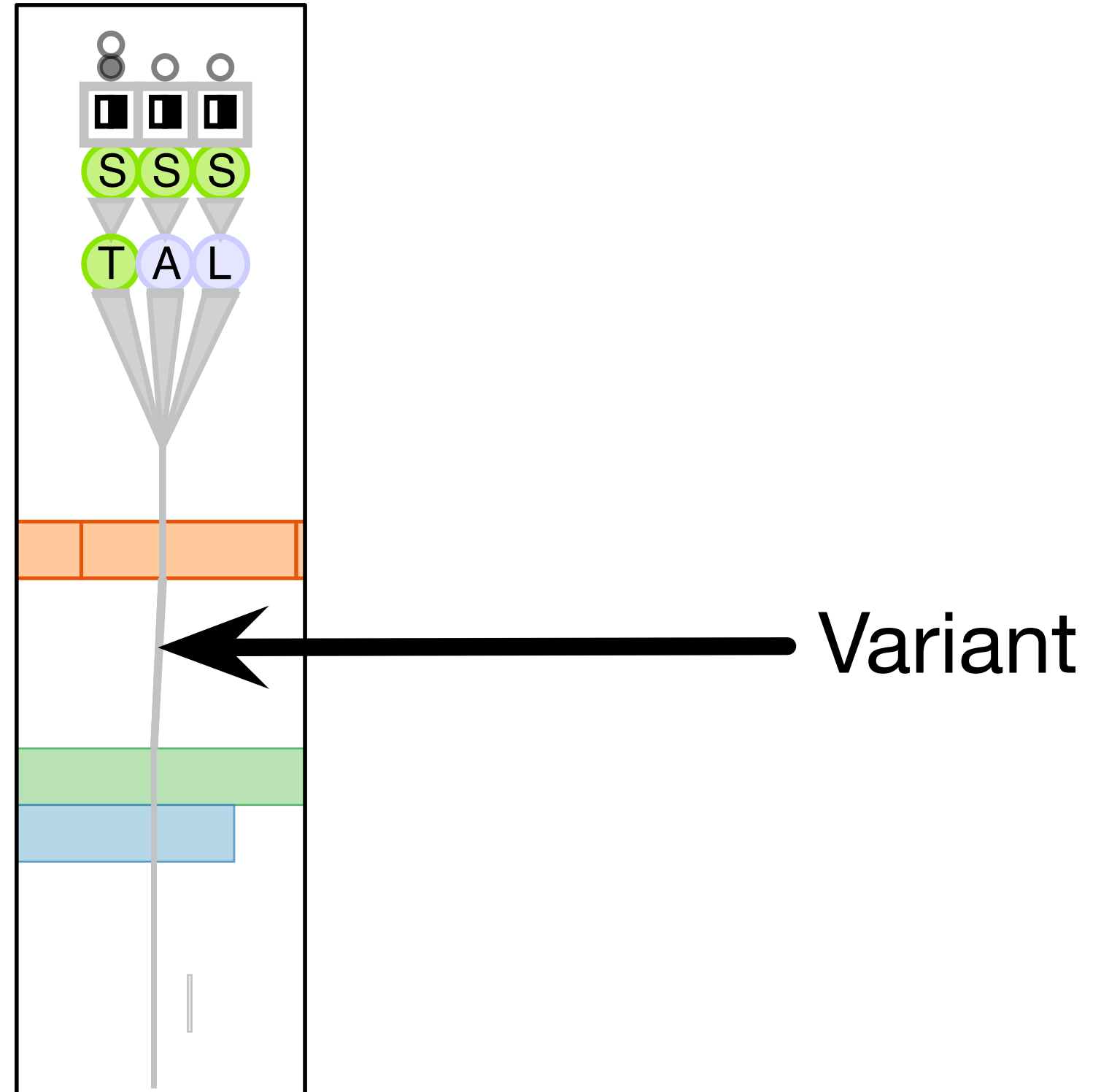
Alpha Cluster Score Variant Count

- DNMT3A (NM_022552)
- IDH2 (NM_002168)
- FLT3 (NM_004119)
- ANKRD36 (NM_001164315)
- ARID1B (NM_017519)
- STAG2 (NM_001042749)
- TNRC18 (NM_001080495)
- WT1 (NM_000378)
- ABCA13 (NM_152701)
- CEBPA (NM_004364)
- TET2 (NM_001127208)
- DNAH10 (NM_207437)
- GPSM1 (NM_015597)
- ASXL1 (NM_015338)
- DNAH1 (NM_015512)
- DNAH6 (NM_001370)
- FAT1 (NM_005245)
- MDN1 (NM_014611)
- PTPN11 (NM_002834)
- DNAH11 (NM_003777)
- DNAH3 (NM_017539)
- DNAH9 (NM_001372)

Peripheral supporting data

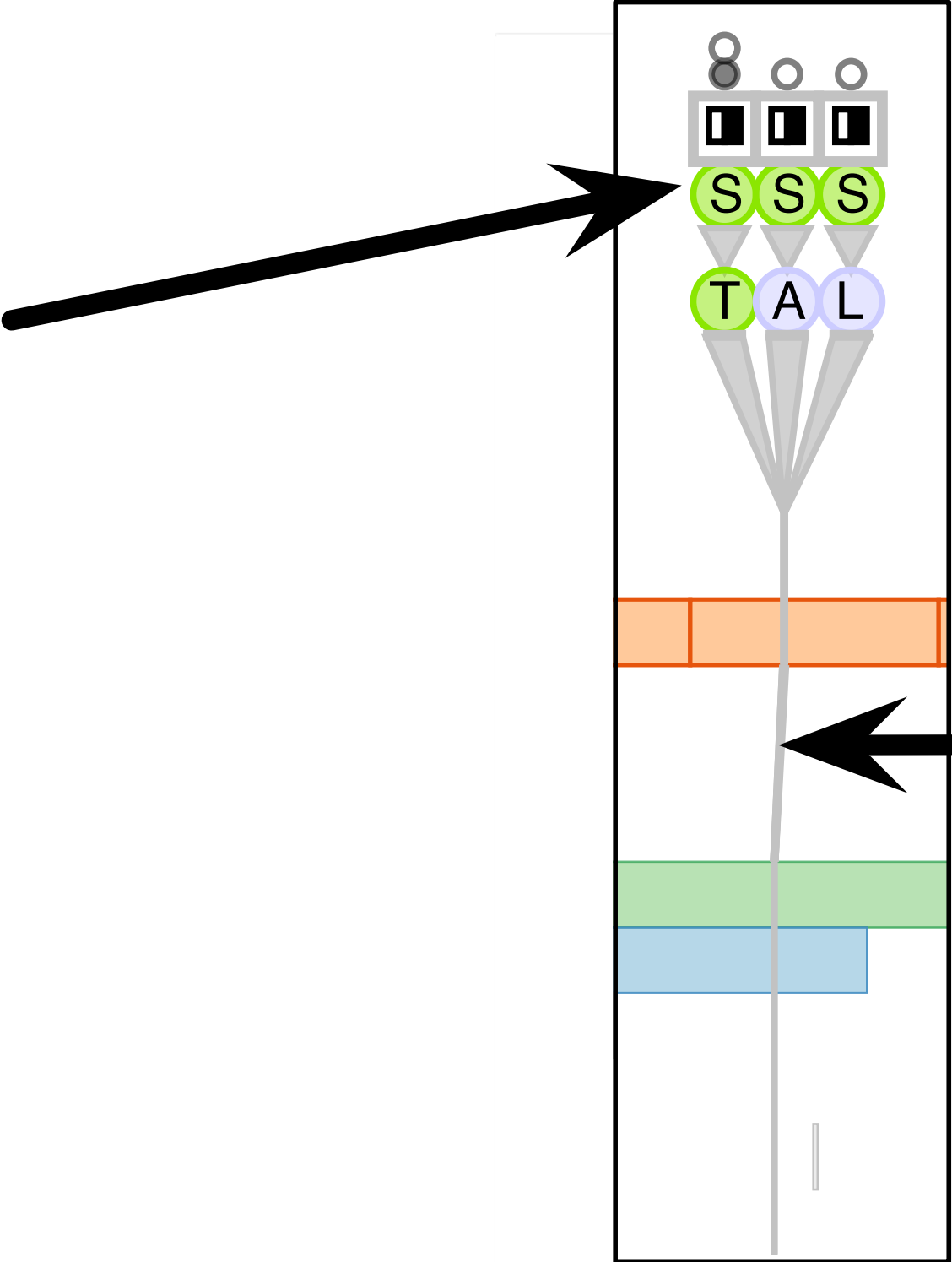
Design information-dense visual encoding

- show all attributes necessary for variant analysis
 - match salience with importance for analysis task
- variant not just a thin line!
- emphasize with high salience
 - collocated variants fan out at top
 - grey variant vertical stroke intersects horizontal colored protein regions



Design information-dense visual encoding

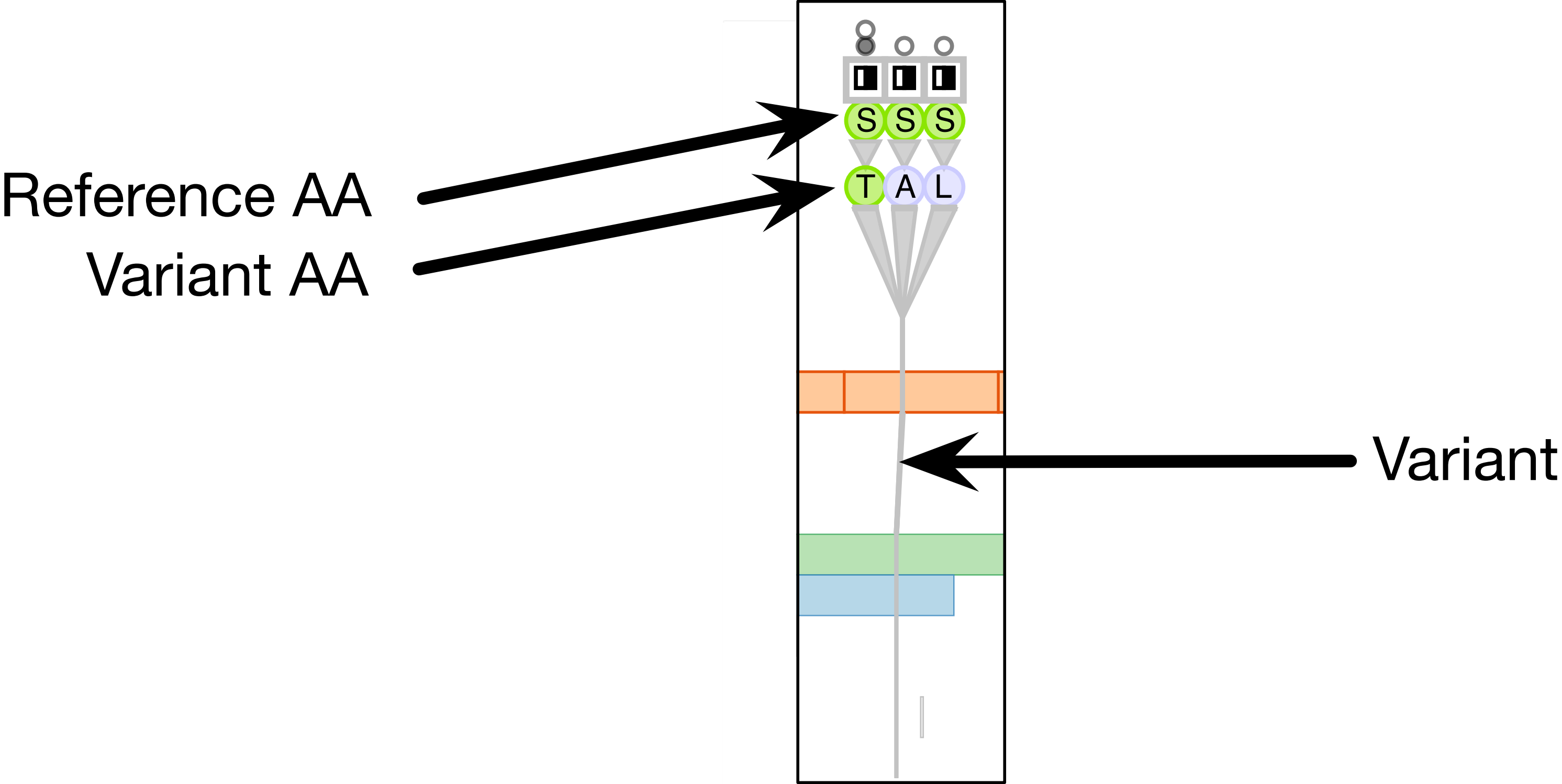
Reference AA



Variant



Design information-dense visual encoding



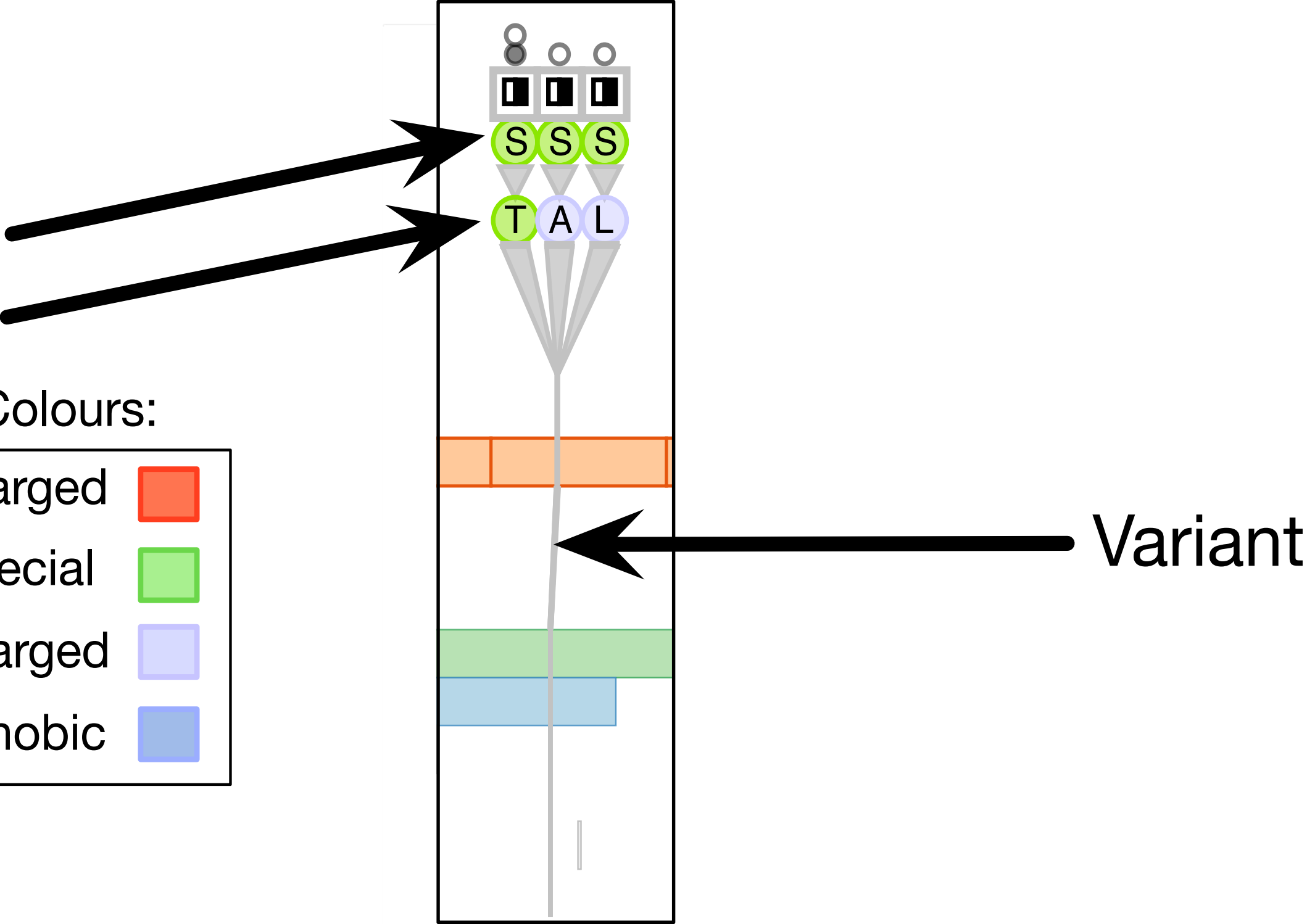
Design information-dense visual encoding

Reference AA

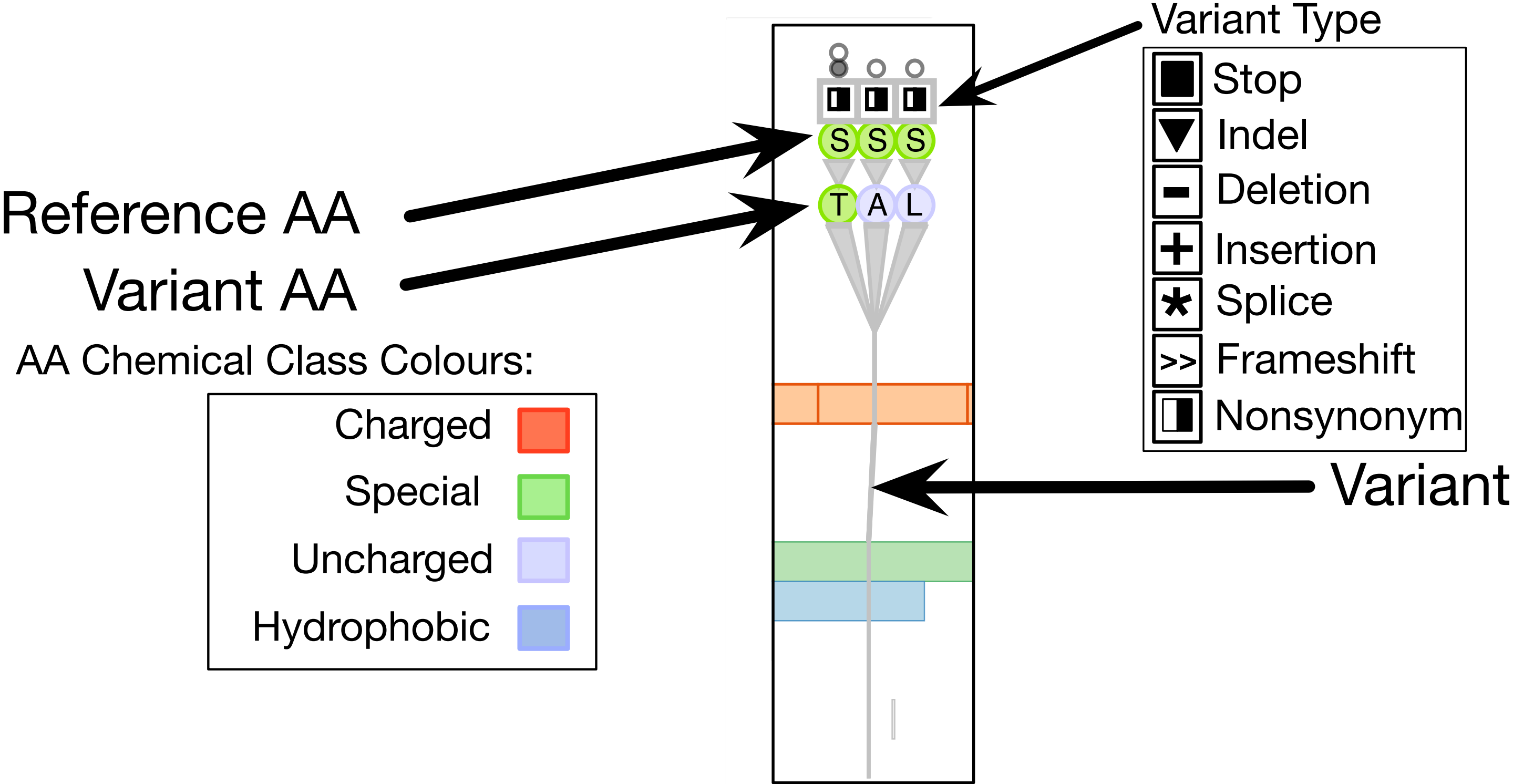
Variant AA

AA Chemical Class Colours:

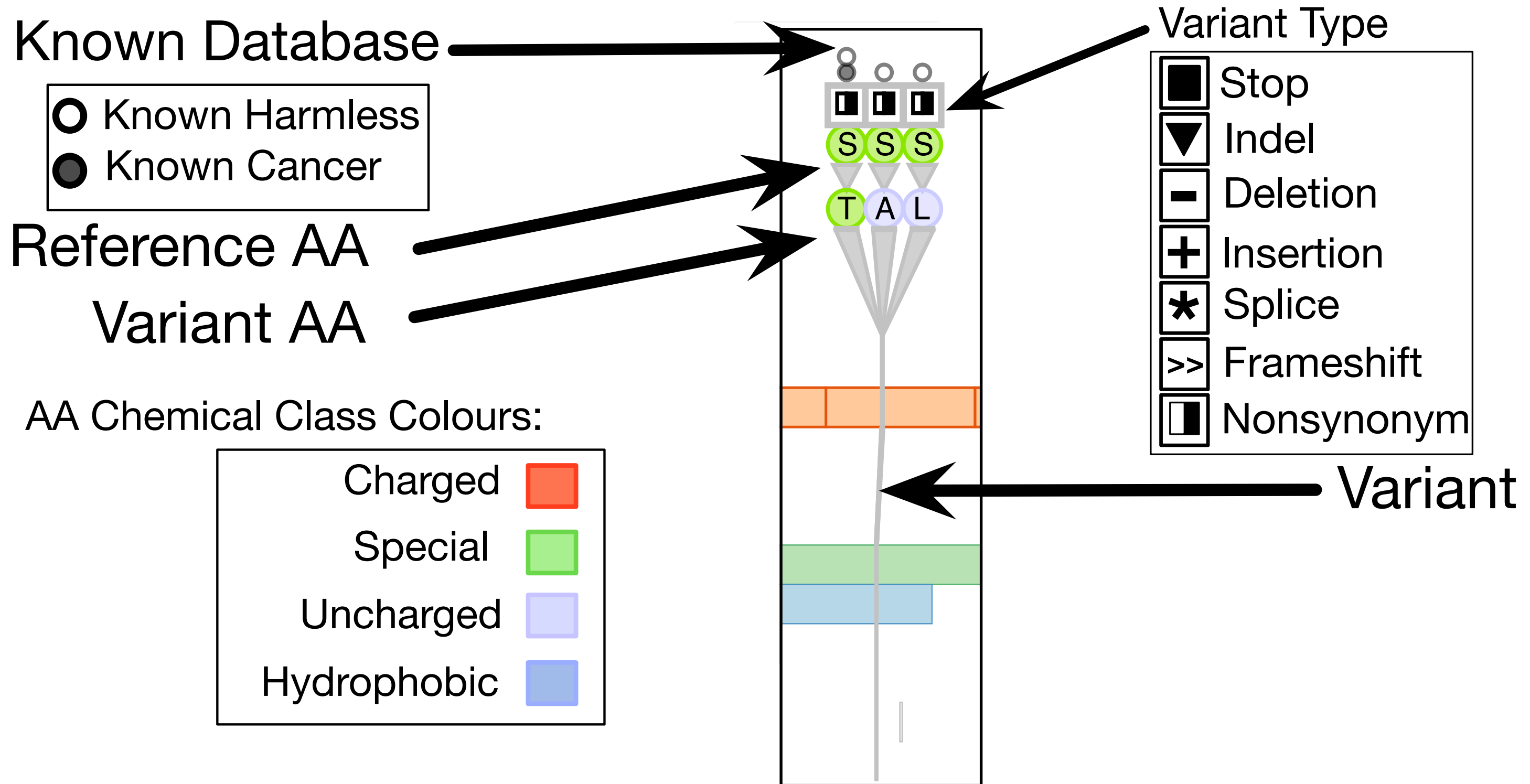
Charged	■
Special	■
Uncharged	■
Hydrophobic	■



Design information-dense visual encoding



Design information-dense visual encoding



Design information-dense visual encoding

Known Database

- Known Harmless
- Known Cancer

Reference AA

Variant AA

AA Chemical Class Colours:

- Charged ■
- Special ■
- Uncharged ■
- Hydrophobic ■

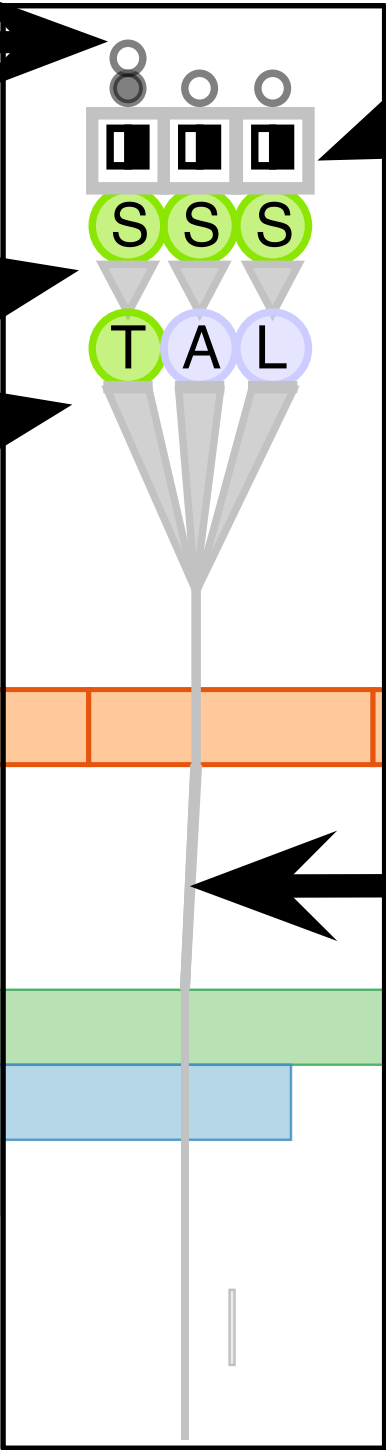
Variant Type

- Stop
- ▼ Indel
- ▬ Deletion
- ⊕ Insertion
- * Splice
- >> Frameshift
- ▬ Nonsynonym

Variant

Transcript/Region Colours:

- Transcript ■
- AA Chain ■
- All Other Regions ■
- Non-Intersected Regions ■

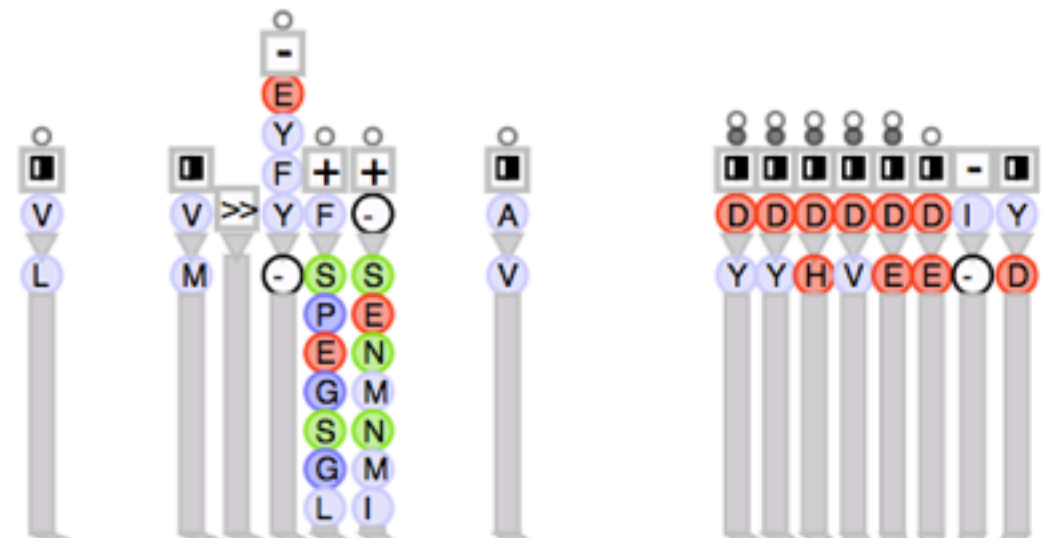


Results

Highly scored gene by sorting metric: known leukemia gene

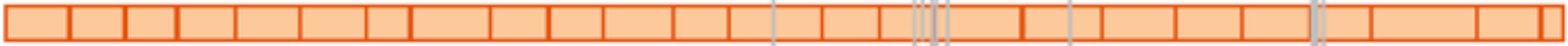
Variants

Mutation Type
Reference A.A.s
Variant A.A.s



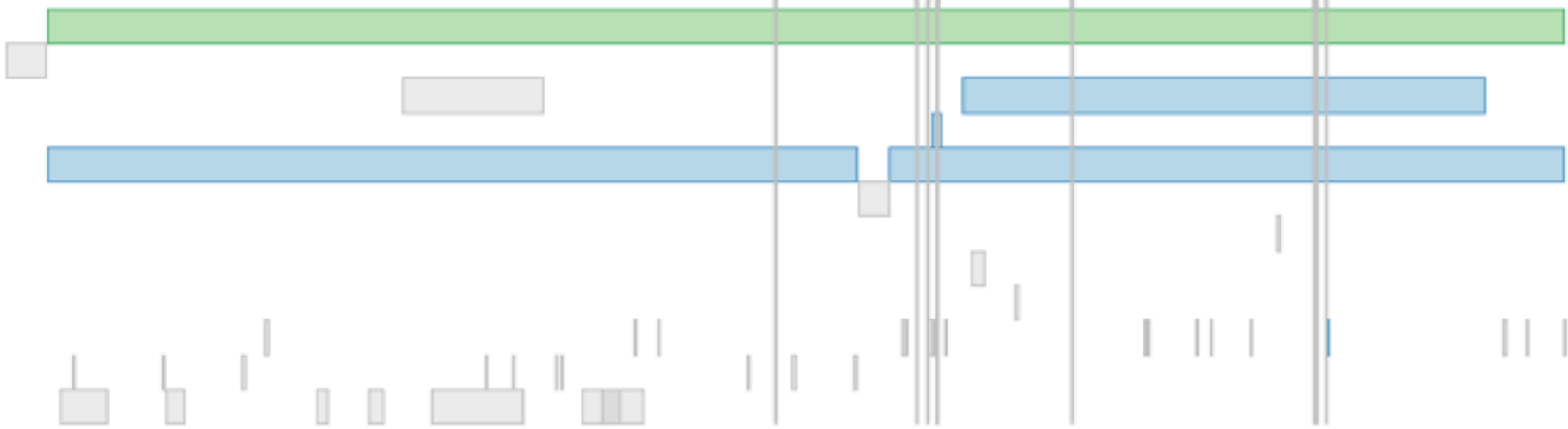
Transcript

trans-anon

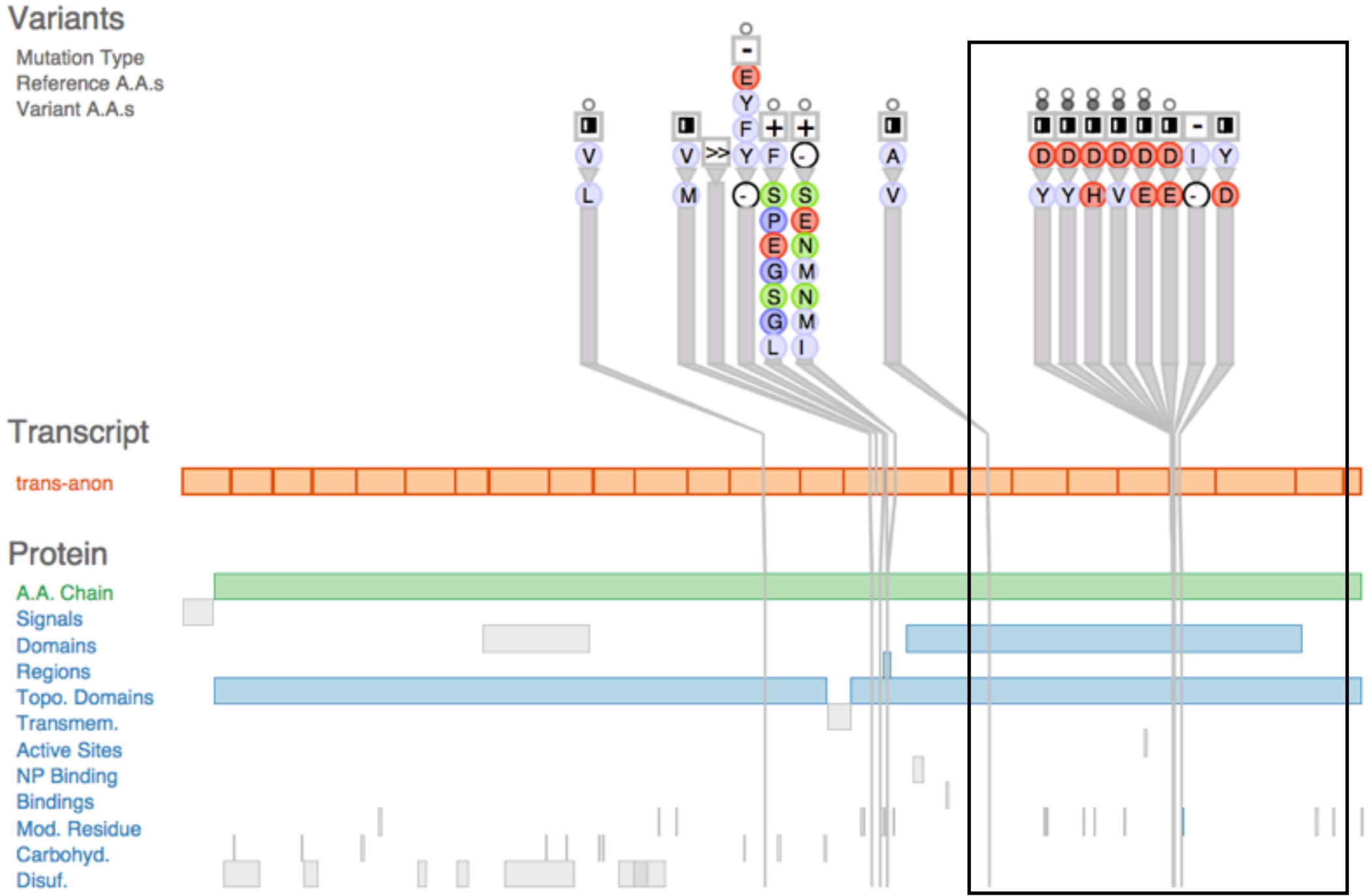


Protein

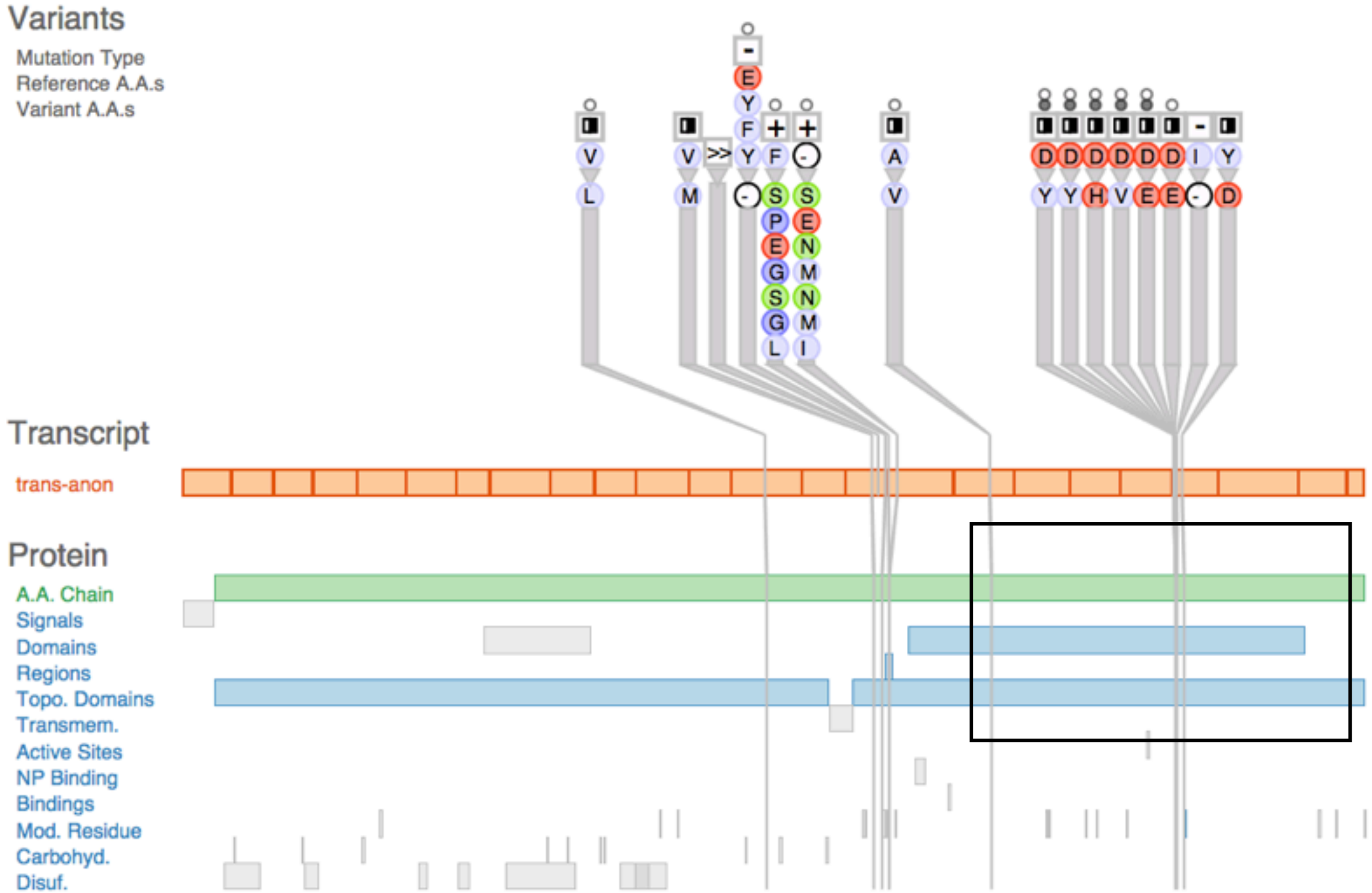
A.A. Chain
Signals
Domains
Regions
Topo. Domains
Transmem.
Active Sites
NP Binding
Bindings
Mod. Residue
Carbohyd.
Disuf.



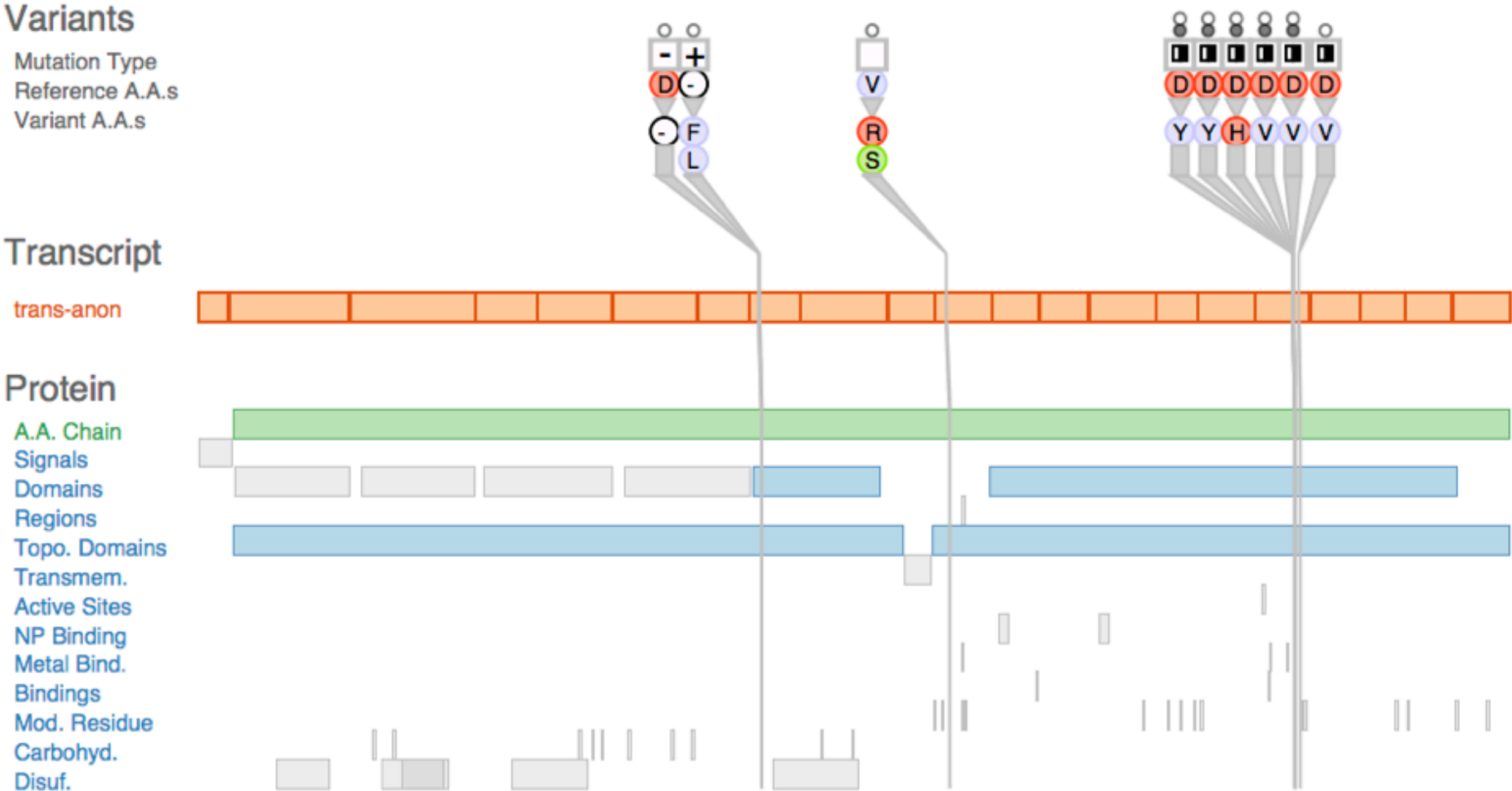
Visual inspection reveals collocation of variants



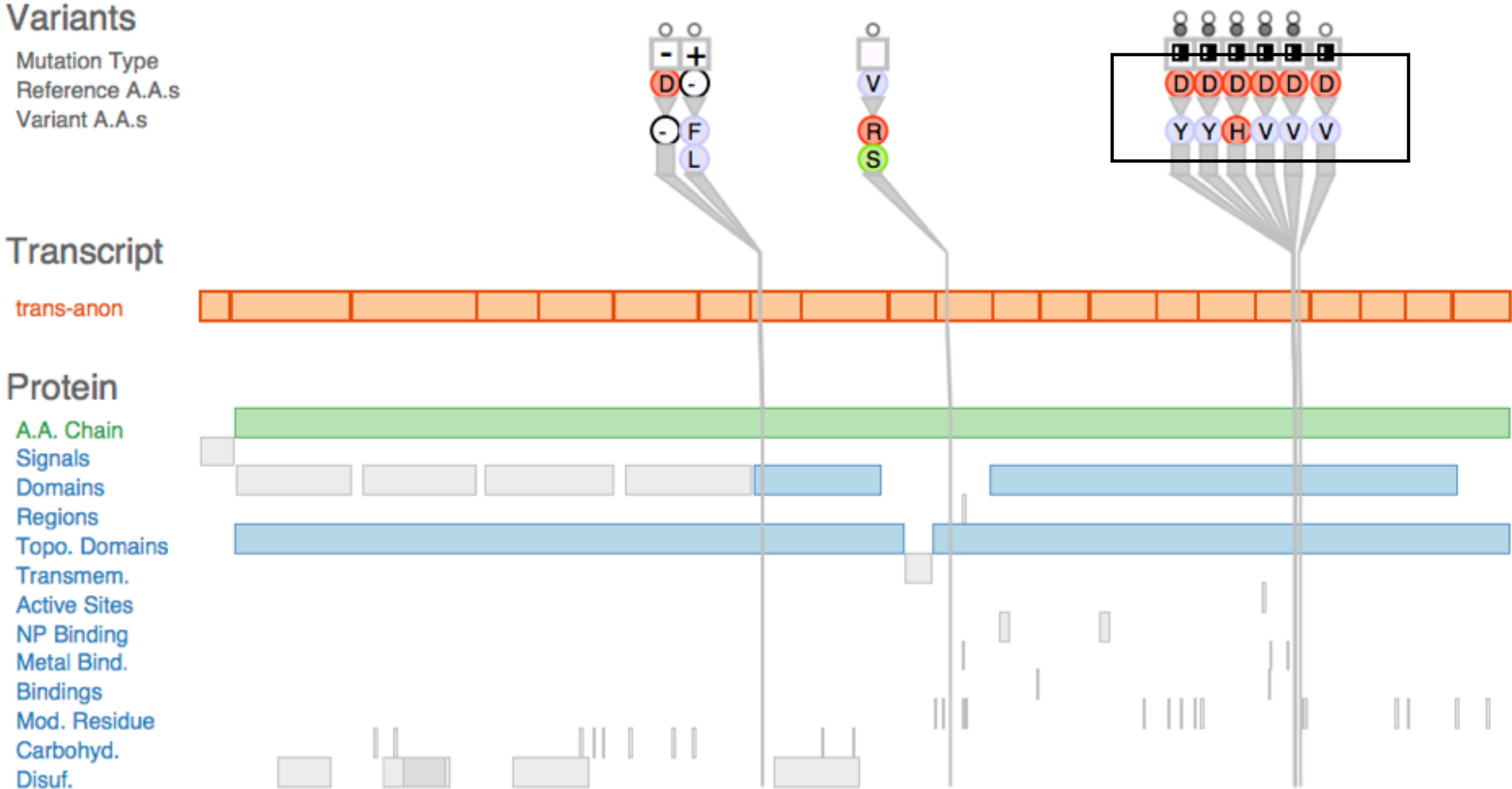
Several functional protein regions affected



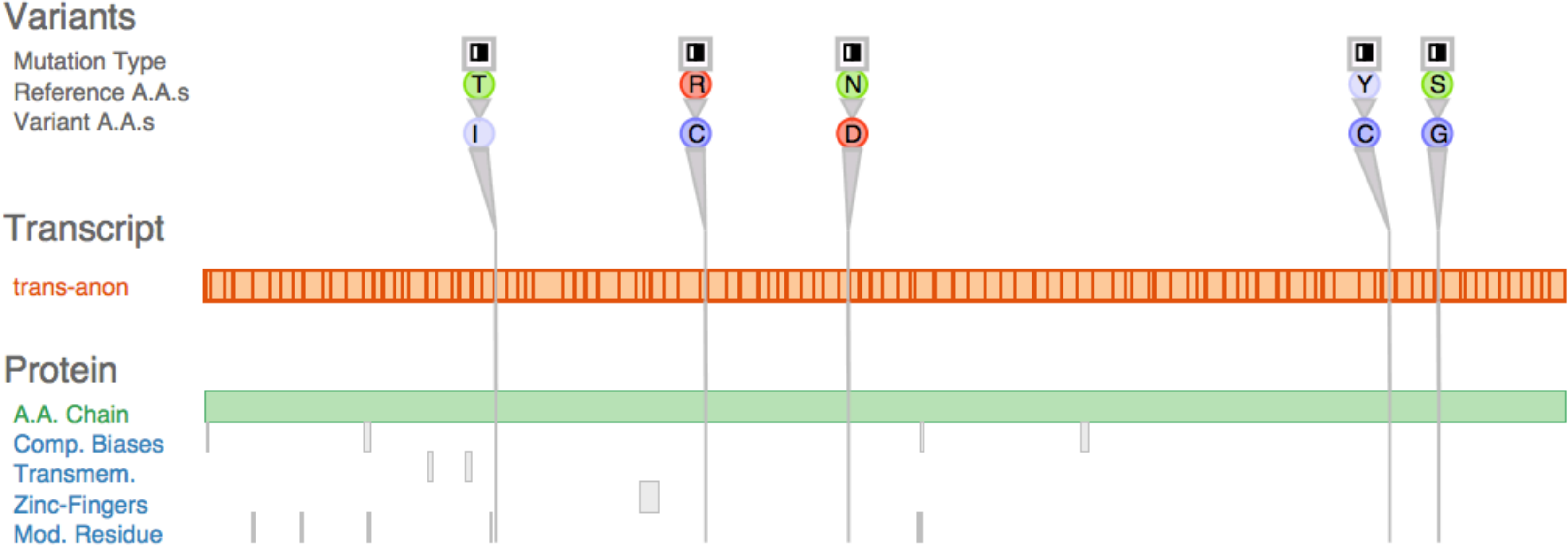
Highly scored by metric: not previously known, good candidate



Protein chemical class change evident



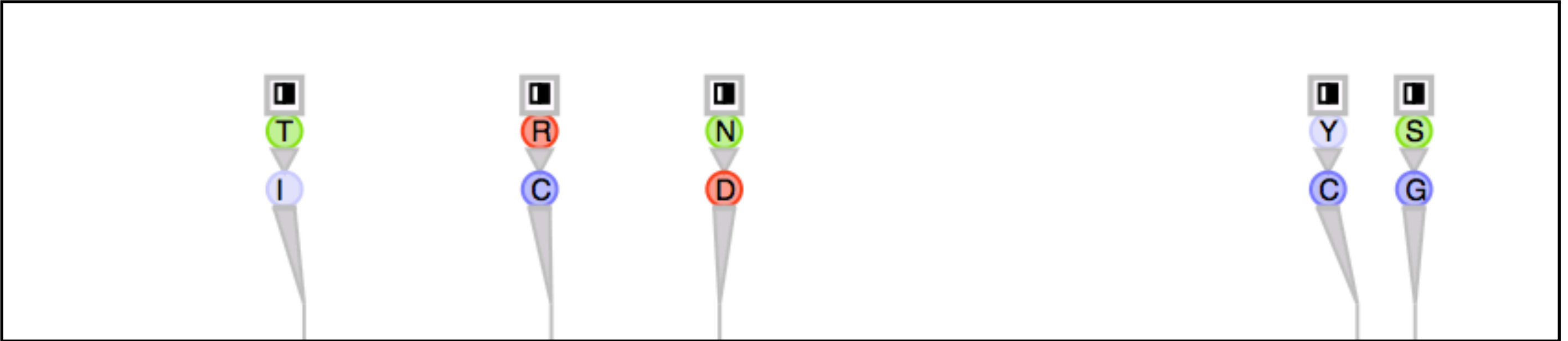
In contrast, low scoring gene



No collocation of variants

Variants

Mutation Type
Reference A.A.s
Variant A.A.s



Transcript

trans-acton

Protein

A.A. Chain
Comp. Biases
Transmem.
Zinc-Fingers
Mod. Residue

Mostly unaffected protein regions

Variants

Mutation Type
Reference A.A.s
Variant A.A.s

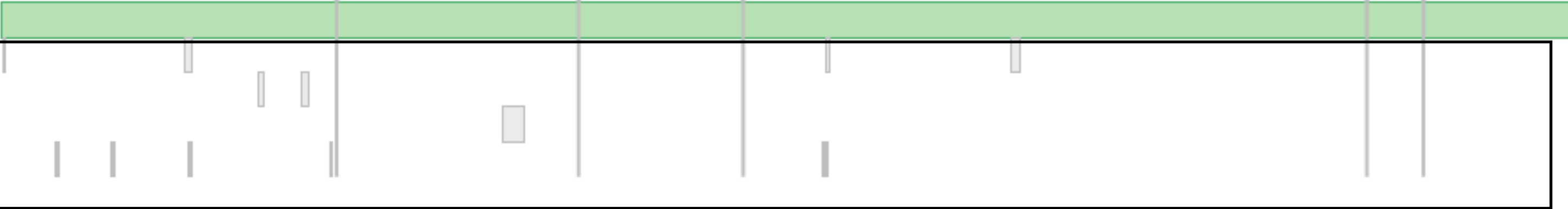


Transcript



Protein

A.A. Chain
Comp. Biases
Transmem.
Zinc-Fingers
Mod. Residue



Methods

Phase I: Winnow and Cast

5 months



- embedded within GSC for all stages
- winnow stage
 - considered and ruled out many potential collaborators
- cast stage
 - gatekeeper (PI)
 - two front-line analysts (postdocs)



more at:

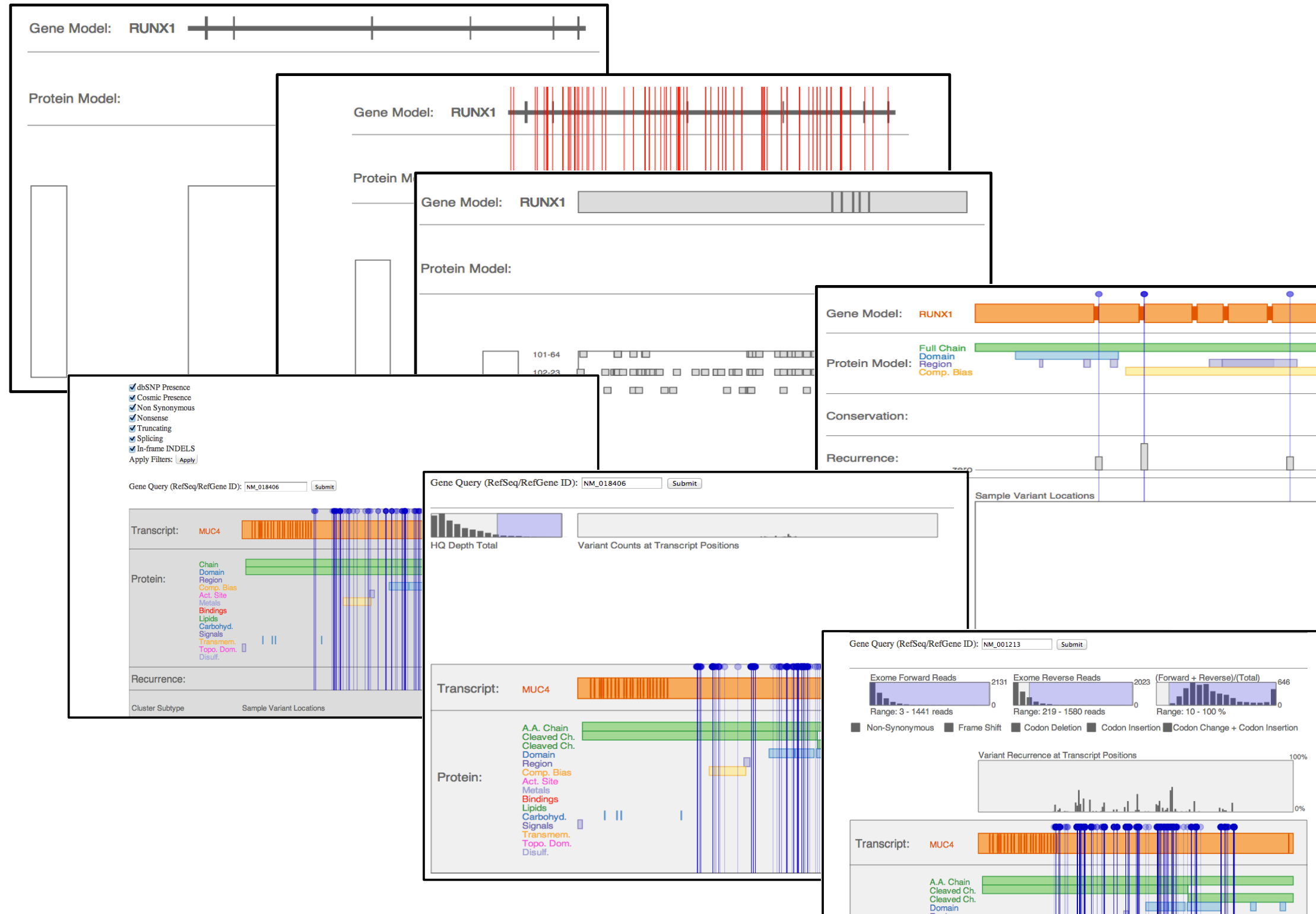
Design Study Methodology: Reflections from the Trenches and from the Stacks.
Sedlmair, Meyer, Munzner. *IEEE TVCG* 18(12): 2431-2440, 2012 (Proc. InfoVis 2012).

Phase 2: Core Design

5 months



- main task abstraction
 - discover gene
- semi-structured interviews
 - every week for 1 hr
- iterative refinement
 - 8 data sketches deployed

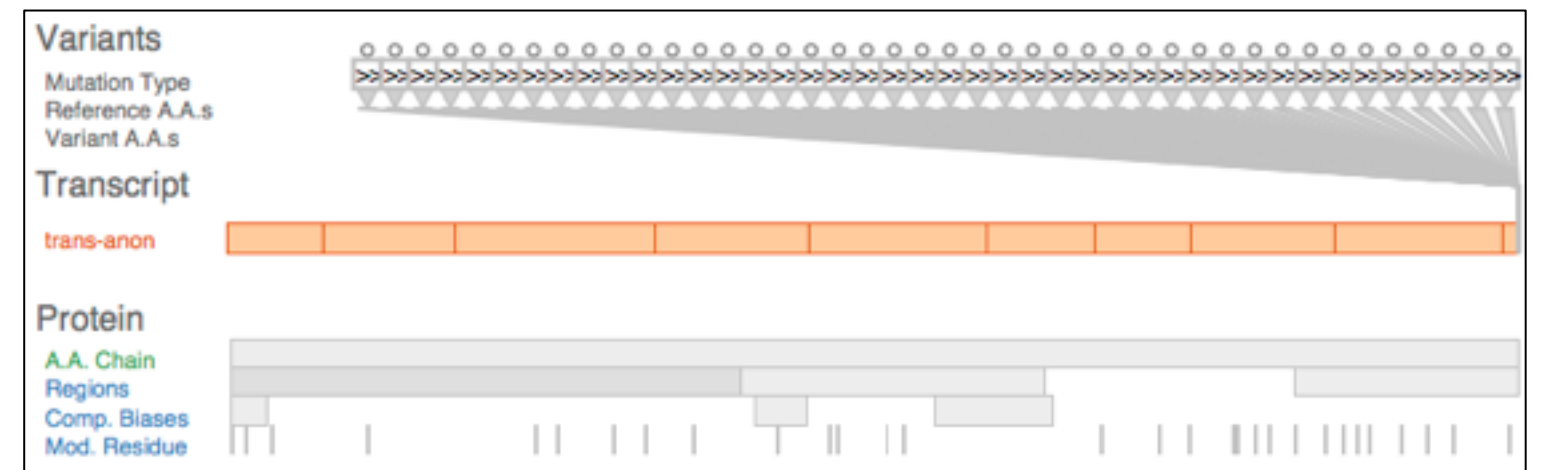


Phase 3: Two More Tasks

1 month



- two new analysts
 - connected by enthusiastic gatekeeper
- new task abstractions
 - compare patients
 - debug pipeline
- transferrable with minimal changes



Phase 4: Reflect and write

3 months



- abstraction innovation

- data abstraction: highly filtered *transcript coordinates* (vs genome coordinates)

- guidelines

- specialize first, generalize later

- good for domains with complex data

- high-level considerations

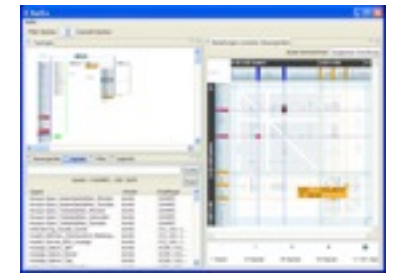
- identifying scales of interest

- what to visually encode directly vs what to support through interaction

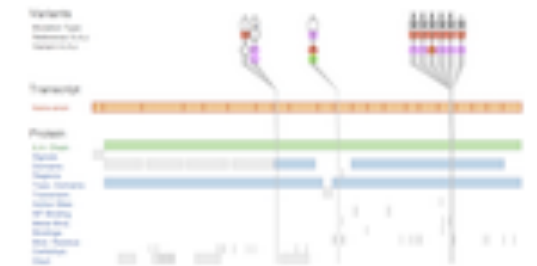
- when (and how) to eliminate navigation

Themes, Revisited

- what and why to show: task and data abstraction
 - task and data commonalities cross-cut domains
- how to show: visual encoding and interaction idioms
 - RelEx: reduce memory load with interaction
 - Variant View: reduce interaction load with better visual encoding
- transferability from design studies
 - DSM: reflection to confirm/refute/refine/propose guidelines

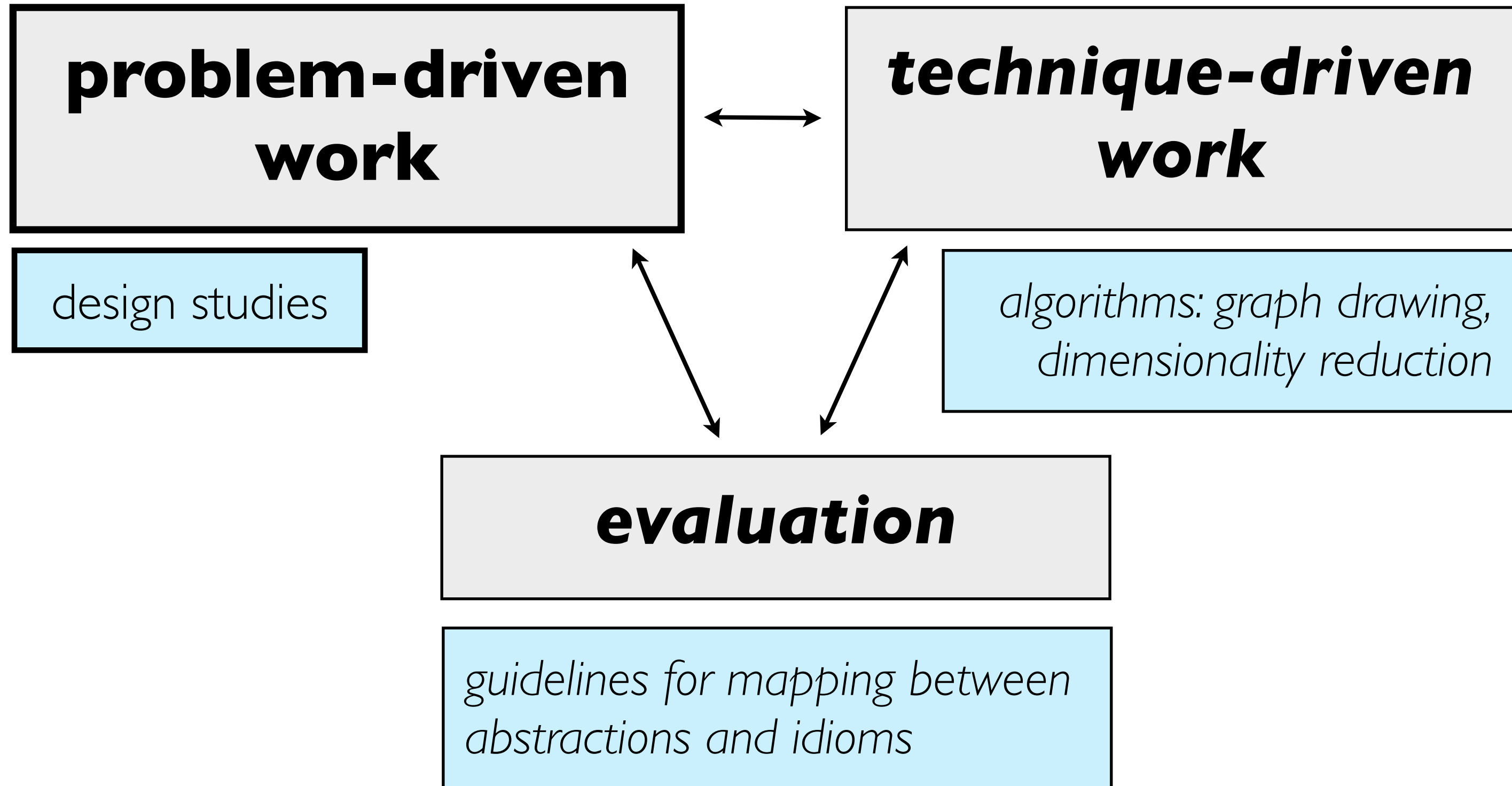


RelEx
in-car networks



VariantView
genomics

A Different Trio: Research Interests



Further Information

- further info

- <http://www.cs.ubc.ca/~tmm/talks.html#chicago14> (this talk, and many others)
- <http://www.cs.ubc.ca/group/infovis> (papers, software, videos)
- <http://www.cs.ubc.ca/~tmm/courses/infovis> (course: readings, lectures)
- <http://www.cs.ubc.ca/~tmm/courses/infovis/book> (book: to appear)

- open source software downloads

- <http://www.cs.ubc.ca/labs/imager/tr/2013/VariantView/VariantViewSoftware/>

- acknowledgements

- funding: NSERC, NSF
- joint work: all co-authors
 - Andreas Butz, Annika Frank, Joel Ferstay, Miriah Meyer, Cydney Nielsen, Michael Sedlmair
- feedback on this talk
 - Matthew Brehmer, Stephen Ingram