

# Methods for Visualizing Biodiversity & Building Rewarding Collaborations

**Tamara Munzner**

Department of Computer Science  
University of British Columbia

***UBC Biodiversity Challenge Retreat, Hakai Institute  
11 June 2019***

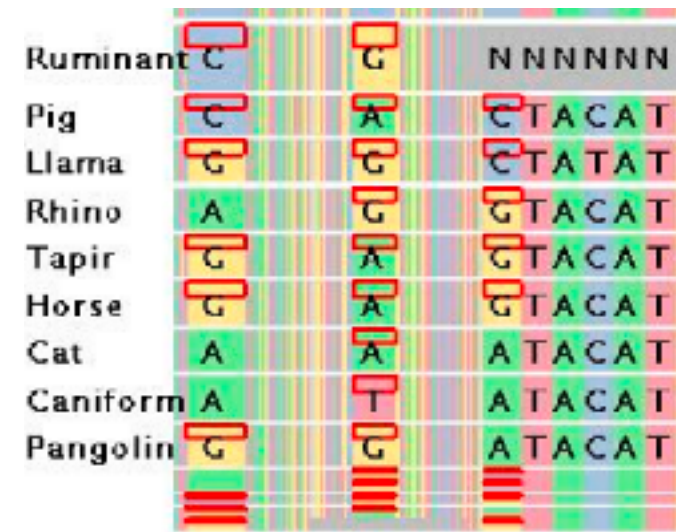
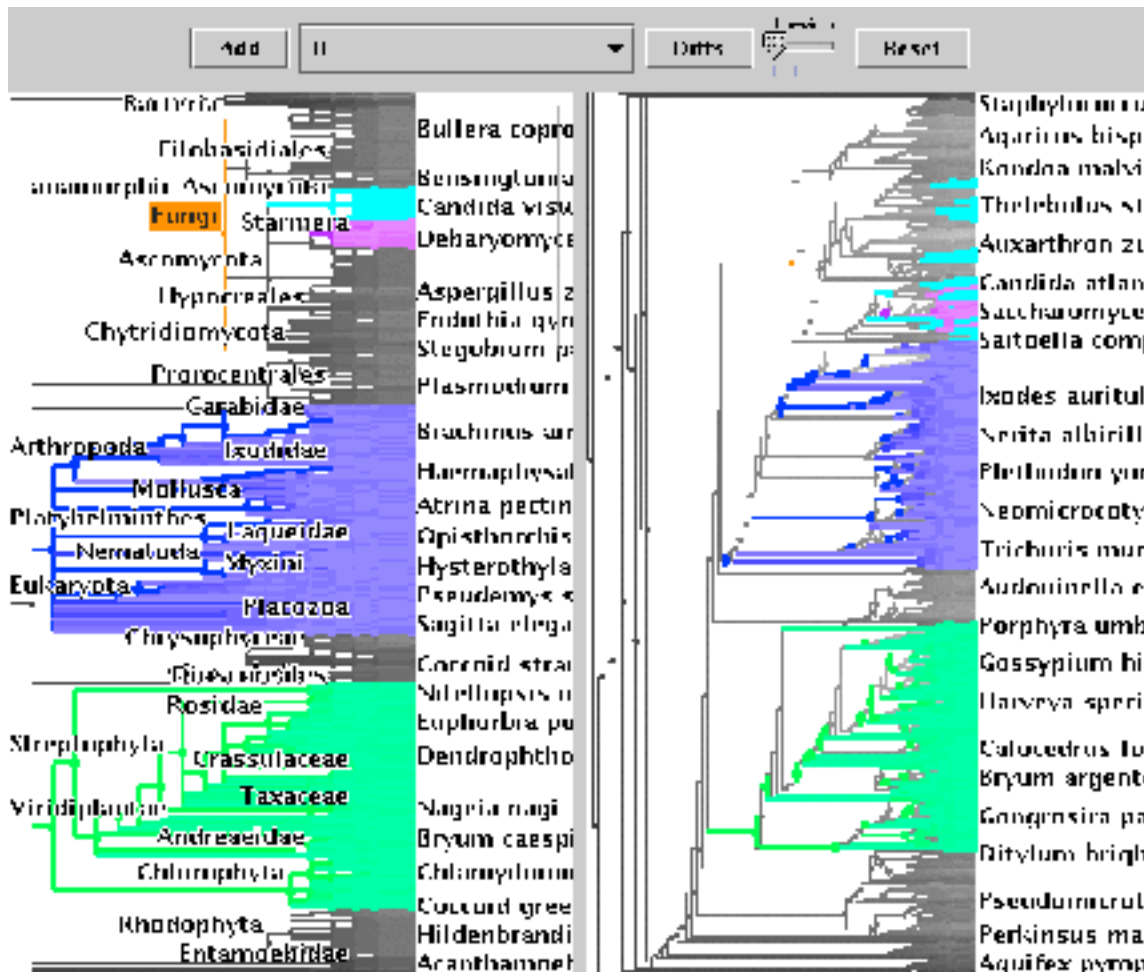
**[www.cs.ubc.ca/~tmm/talks.html#hakai19-methods](http://www.cs.ubc.ca/~tmm/talks.html#hakai19-methods)**



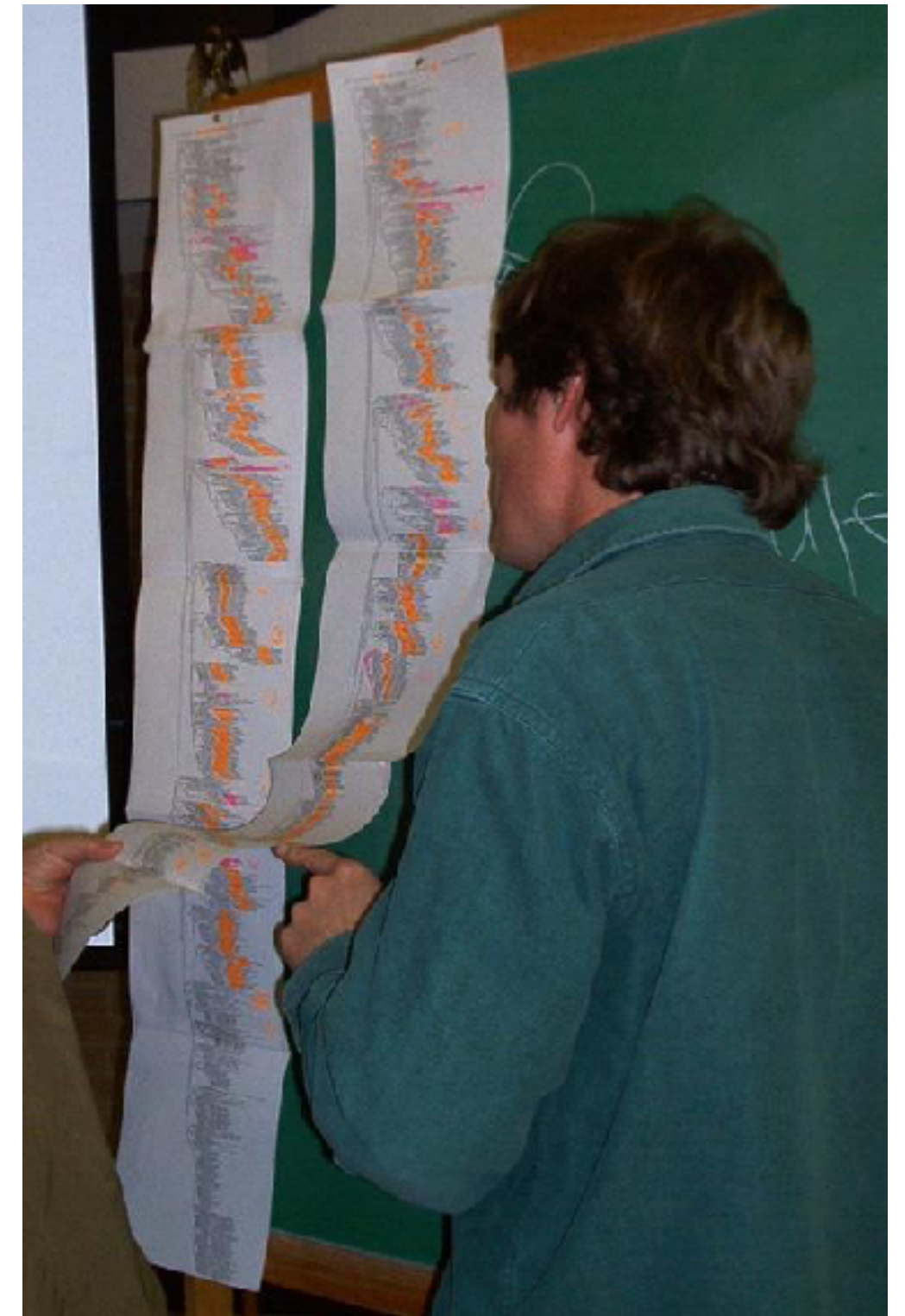
**[@tamaramunzner](https://twitter.com/tamaramunzner)**

# TreeJuxtaposer: Visual tree comparison

- driving problem from UT Austin Hillis Lab in 2001: phylogenetic trees
- algorithm focus on scale, later extended to gene sequences



SequenceJuxtaposer



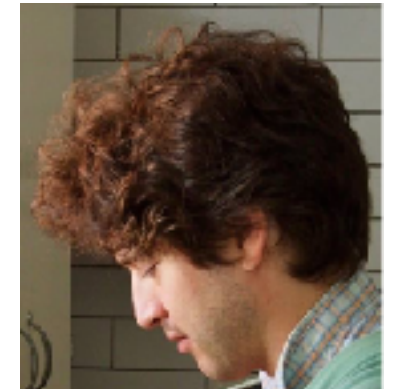
TreeJuxtaposer <https://youtu.be/GdaPj8a9QEO>

joint work with: Guimbretiere, Li, Zhang, and Zhou

# Cerebral: Integrating gene expression w/ interaction network

- automatic network layout by subcellular location, like hand-drawn diagrams
- multiple views with linked highlighting and navigation
- Cytoscape plugin, funded by Agilent

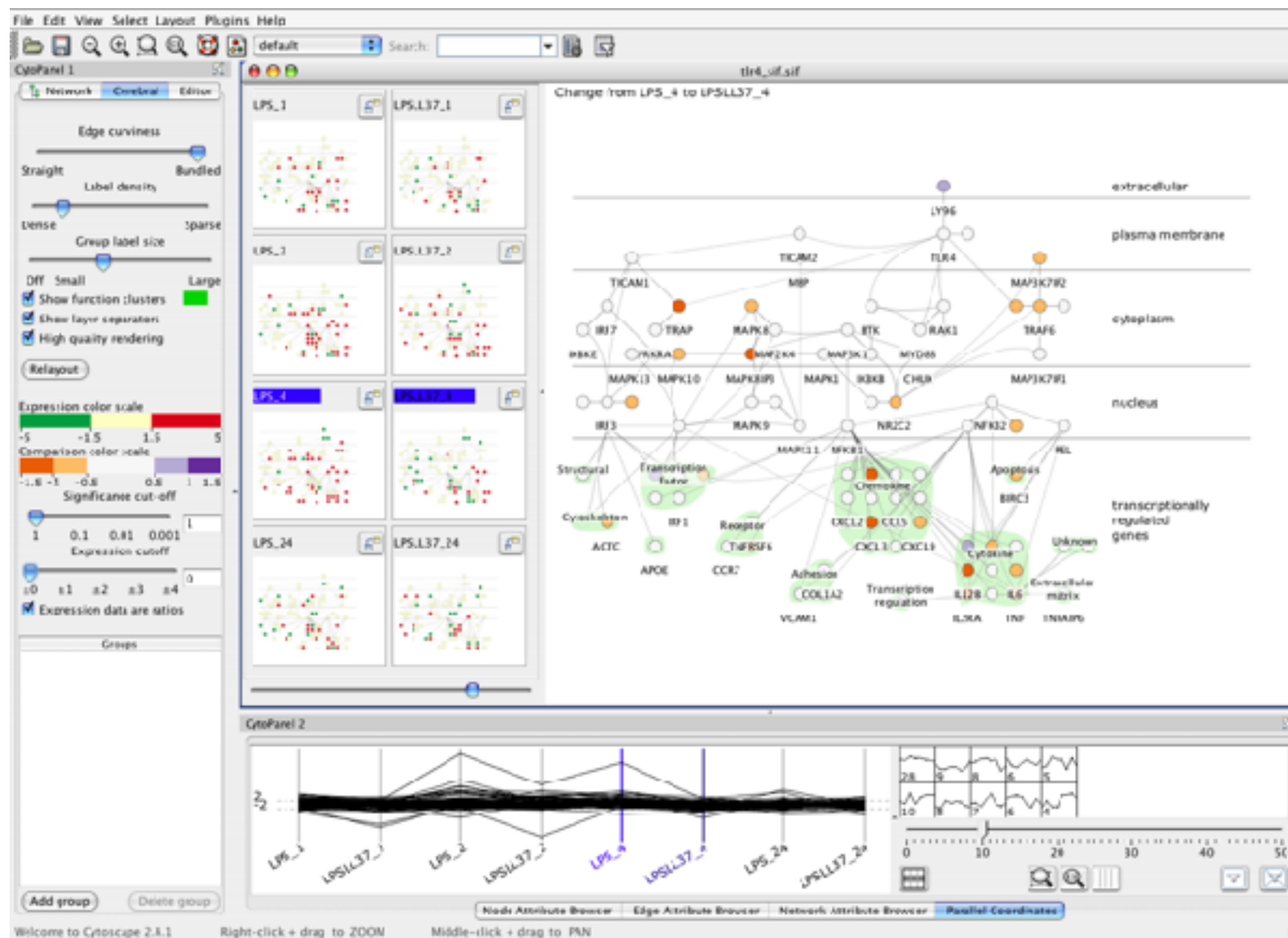
Aaron Barsky



Jenn Gardy  
(Microbio: Hancock)



Robert Kincaid  
(Agilent)



Cerebral <https://youtu.be/76HhG1FQnql>



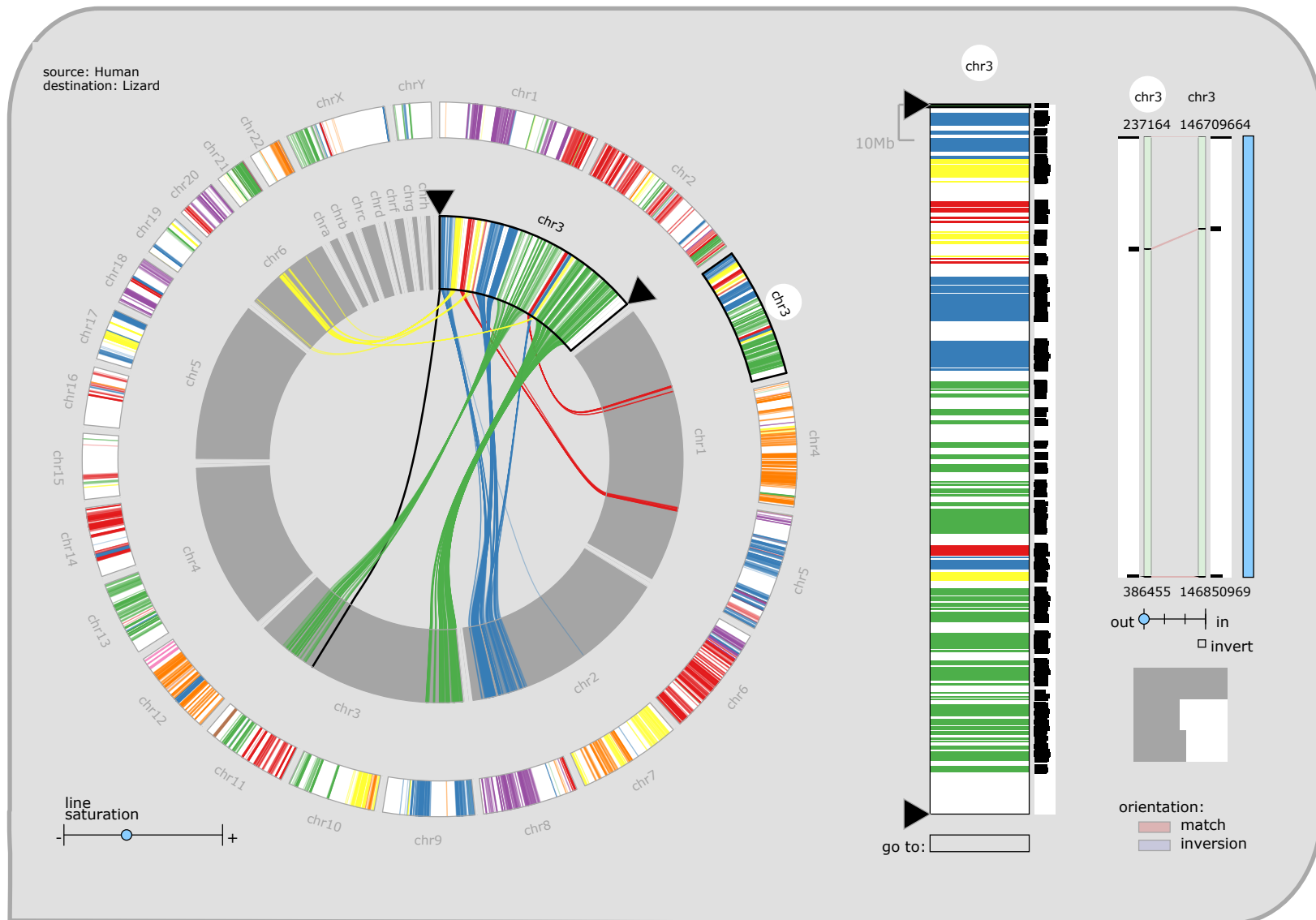
# MizBee: Comparing genomes between species

- driving problems: Broad Inst. biologists studying fungus (Ma) and stickleback/pufferfish (Grabherr)
- two use phases: first fully validate computational pipeline, then can analyze biological questions
- investigated whole-genome duplication events, refined syntenic block construction algorithm

Hanspeter Pfister  
(Harvard)



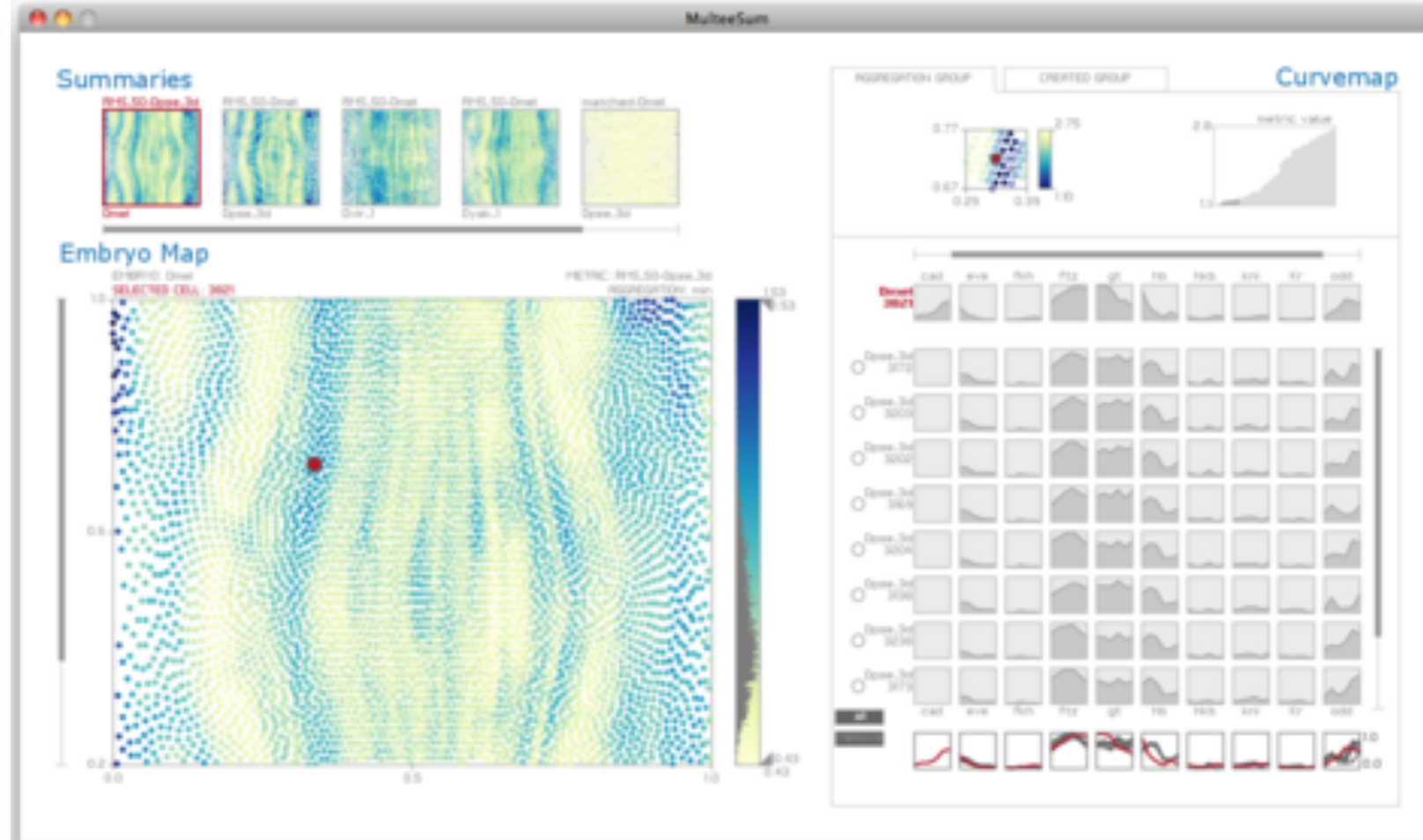
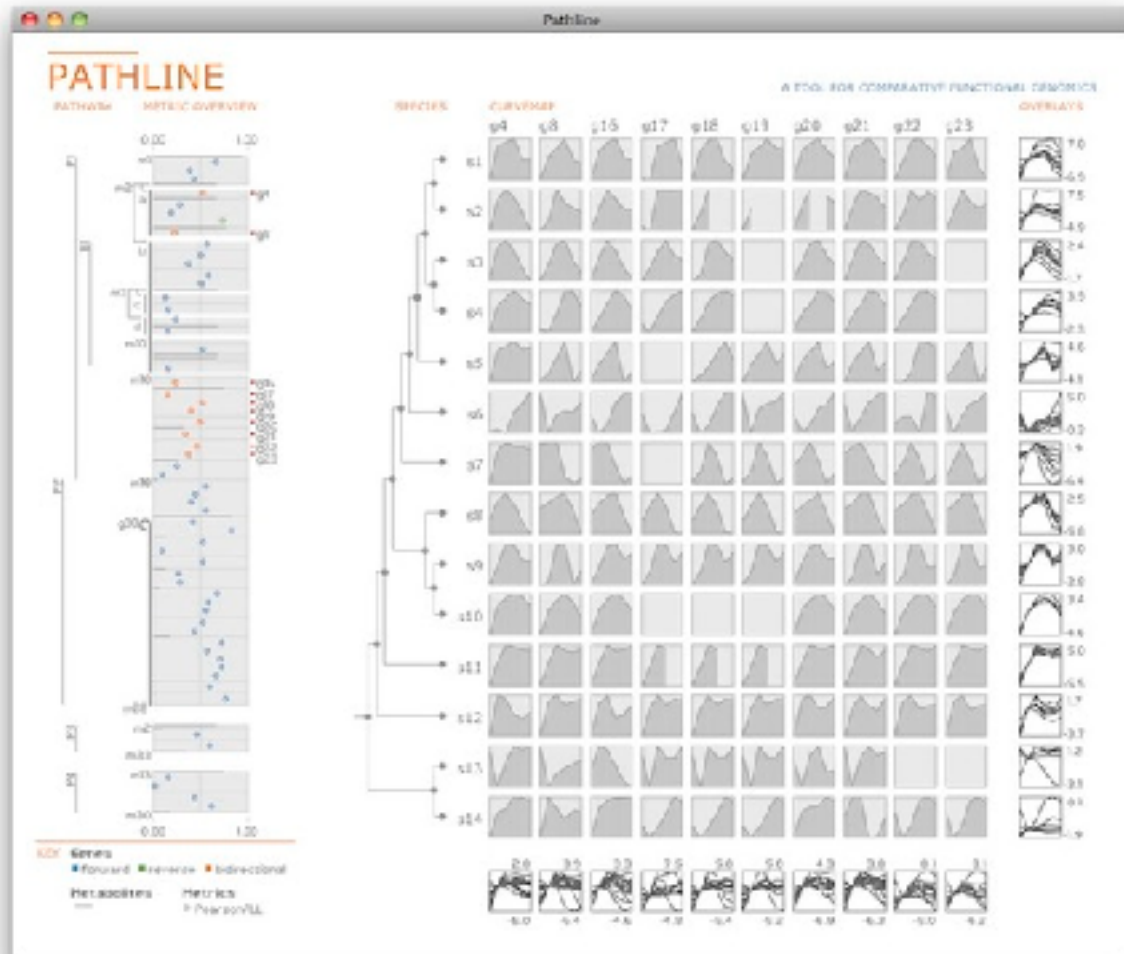
Miriah Meyer





# Comparative functional genomics

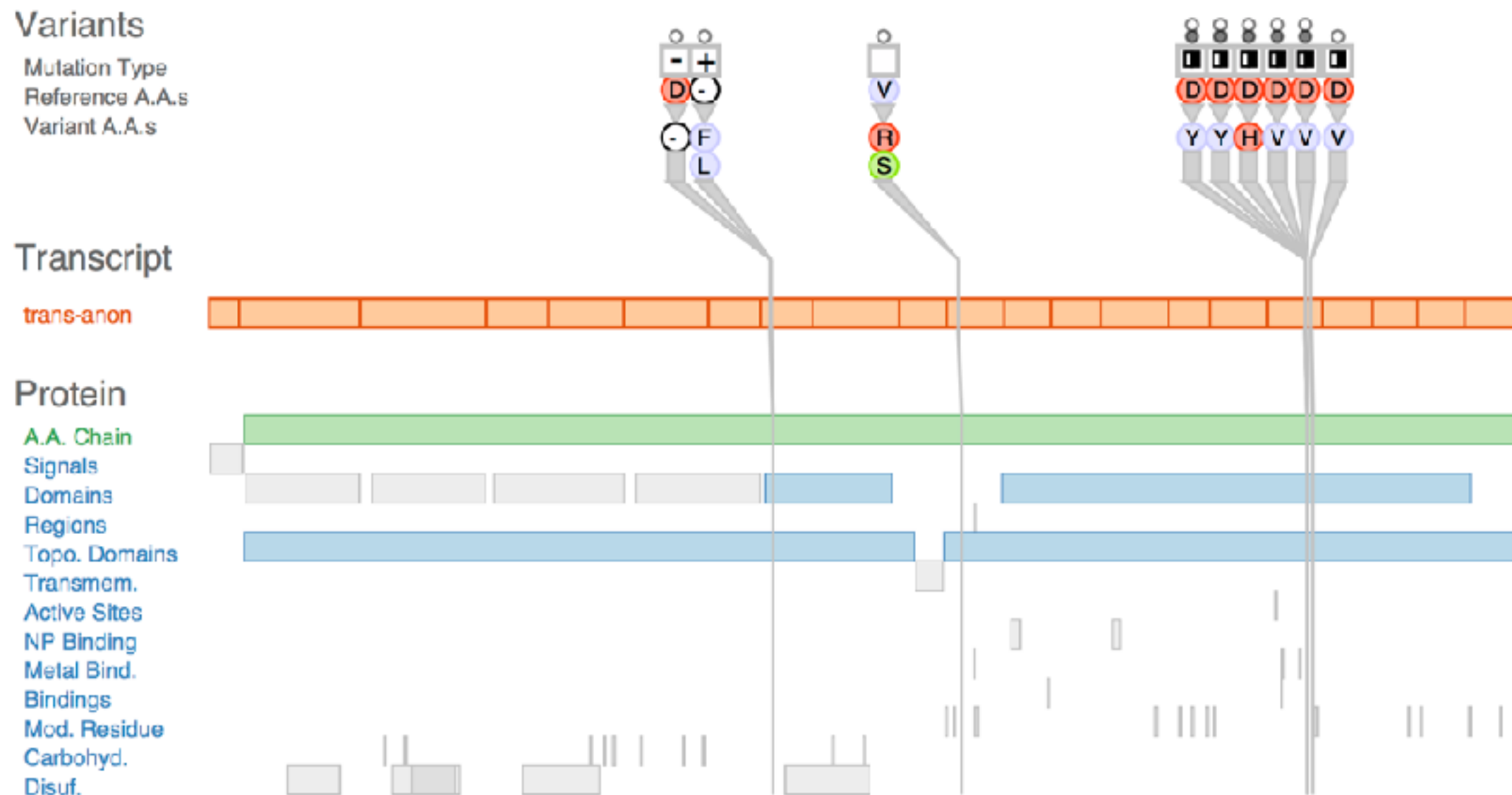
- Pathline: multiple pathways, multiple genes, multiple species - over time
  - Broad Institute, Regev Lab
  - curvemaps as alternative to heatmap
- MulteeSum: all that + spatial location (cells within fruitfly embryo)
  - Harvard Med School, dePace Lab
  - compare summaries across multiple computational workflows



joint work with: Meyer, Pfister, Wong, Styczynski, dePace

# Variant View: Visualizing sequence variants in genetic context

- concise overview supports reasoning about variant type & location
  - across several levels of biological context (vs extensive navigation w/ genome browsers)



Joel Ferstay



Cydney Nielsen  
(BC Cancer)





# Aggregated Dendrograms: Visual comparison between many phylogenetic trees

- concisely summarize trees interactively wrt bio meaningful criteria
  - one use case: compare gene trees to species trees



Zipeng Liu



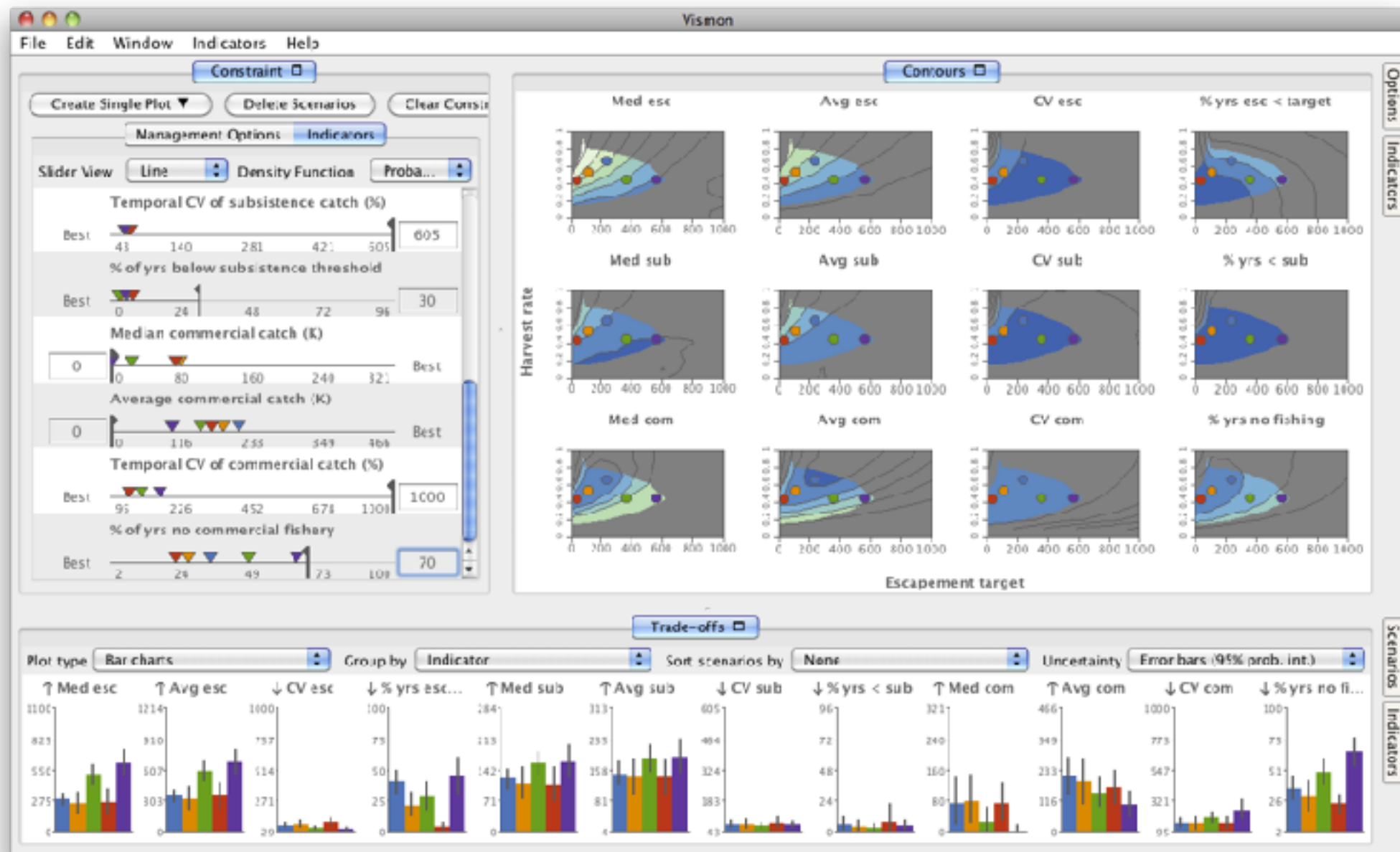
Shing Hei Zhan





# Vismon: Fisheries simulation

- supporting decision-makers not expert in simulation & stats
  - sensitivity analysis, global trade-offs analysis, staged uncertainty



Maryam Booshehrian



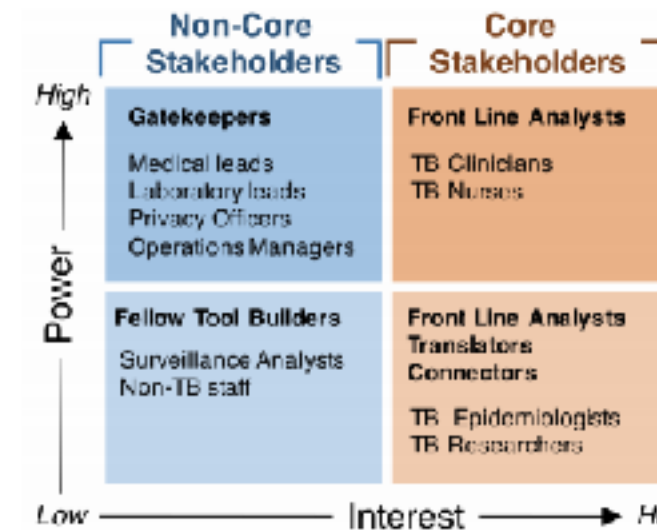
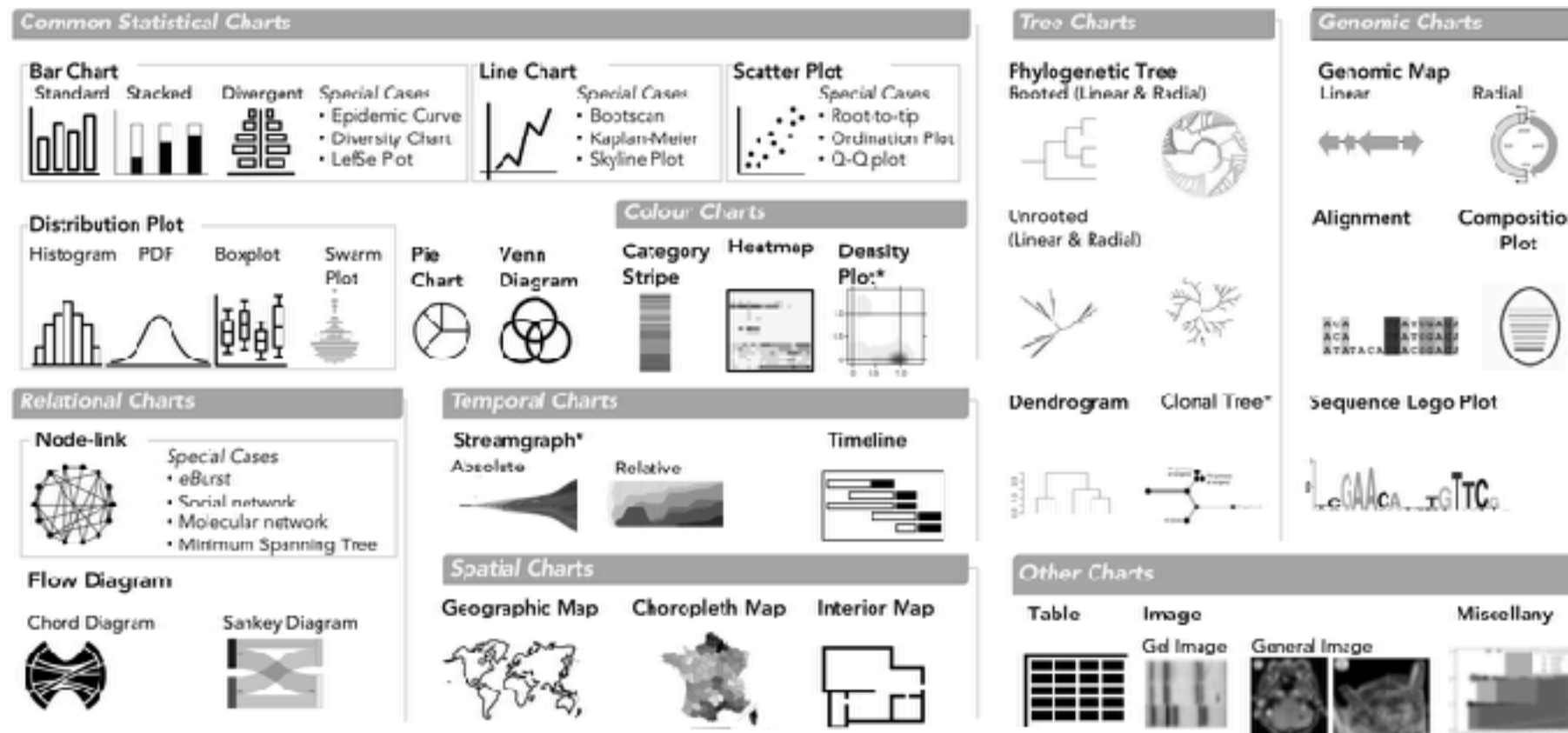
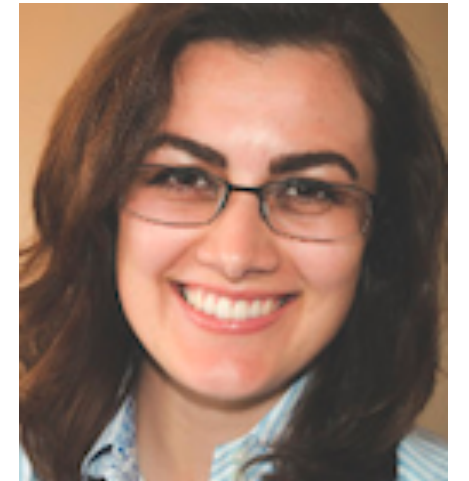
Torsten Moeller (SFU)



# Integrating visualization & biostats methods

- Human-centered design & qualitative coding
- Epidemiology/health expectations & constraints
- Mixed initiative: automation and manual analysis
- Mixed methods: when to use qual & when to use quant

Anamaria Crisan



## Regulatory & Organizational Constraints

Jenn Gardy  
BCCDC/SPPH



## Evidence-Based Design and Evaluation of a Whole Genome Sequencing Clinical Report for the Reference Microbiology Laboratory

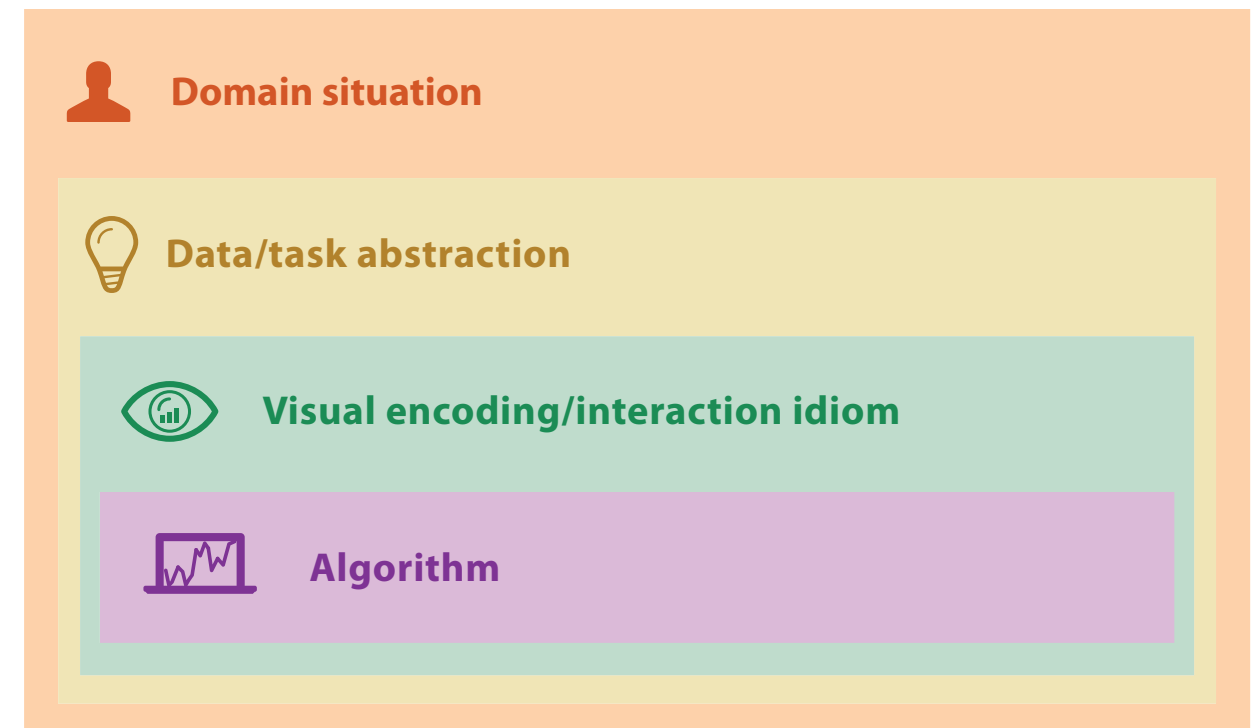
**GEViT: Genomic Epidemiology Visualization Typology**

<https://gevit.net>

# A Nested Model

*for Visualization Design and Validation*

<http://www.cs.ubc.ca/labs/imager/tr/2009/NestedModel>

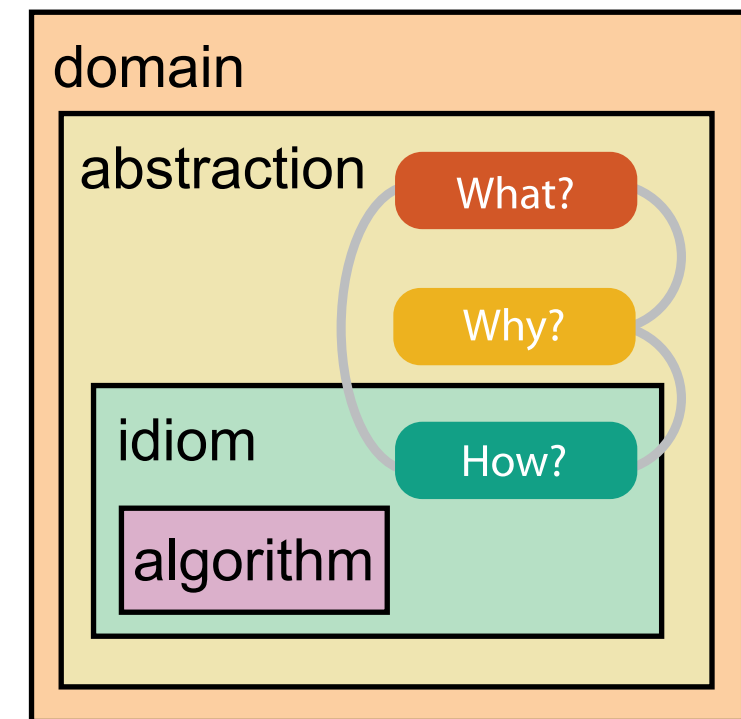




# Nested model: Four levels of visualization design


- *domain situation*
  - who are the target users?
- *abstraction*
  - translate from specifics of domain to vocabulary of visualization
    - **what** is shown? **data** abstraction
    - **why** is the user looking at it? **task** abstraction
- *idiom*
  - **how** is it shown?
    - **visual encoding** idiom: how to draw
    - **interaction** idiom: how to manipulate
- *algorithm*
  - efficient computation

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




[A Multi-Level Typology of Abstract Visualization Tasks  
Brehmer and Munzner. *IEEE TVCG* 19(12):2376-2385,  
2013 (Proc. InfoVis 2013).]

# Different threats to validity at each level

 **Domain situation**  
You misunderstood their needs

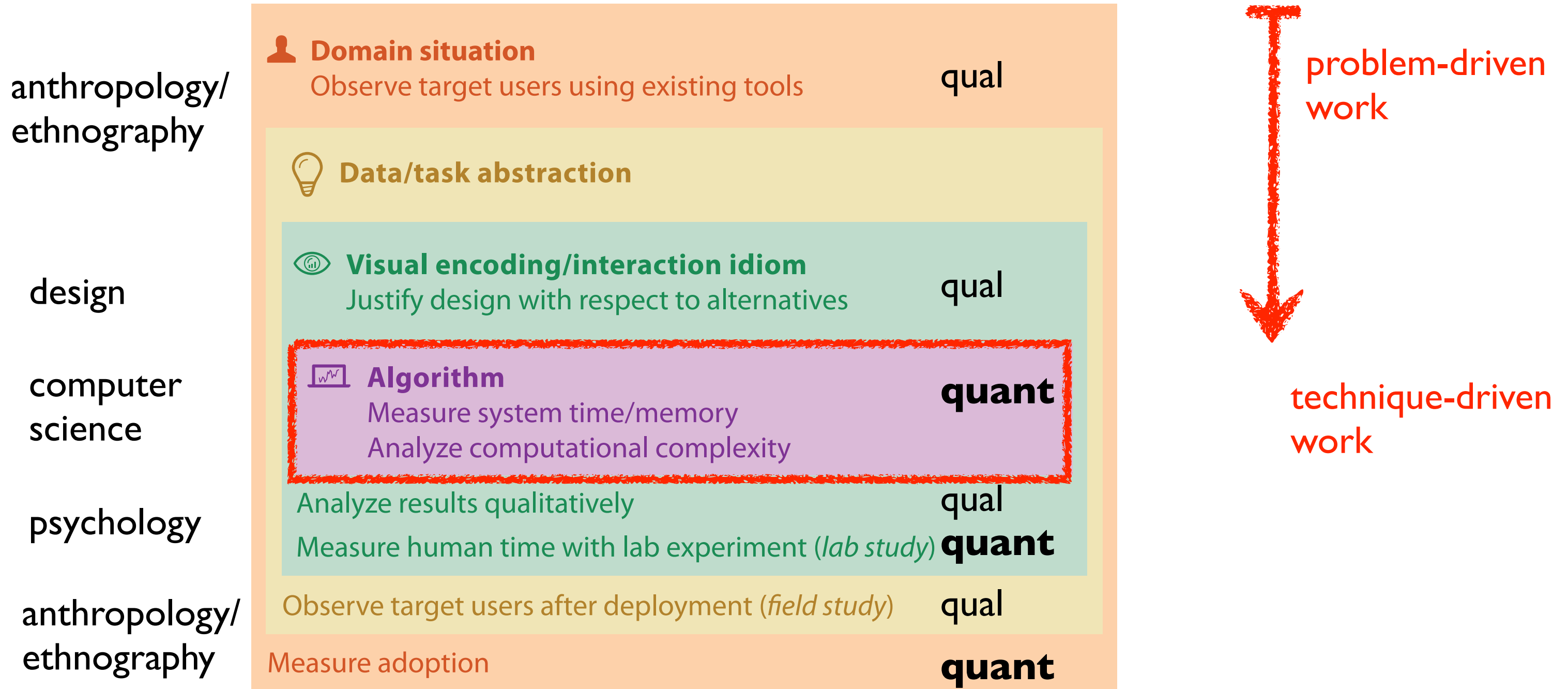
 **Data/task abstraction**  
You're showing them the wrong thing

 **Visual encoding/interaction idiom**  
The way you show it doesn't work

 **Algorithm**  
Your code is too slow

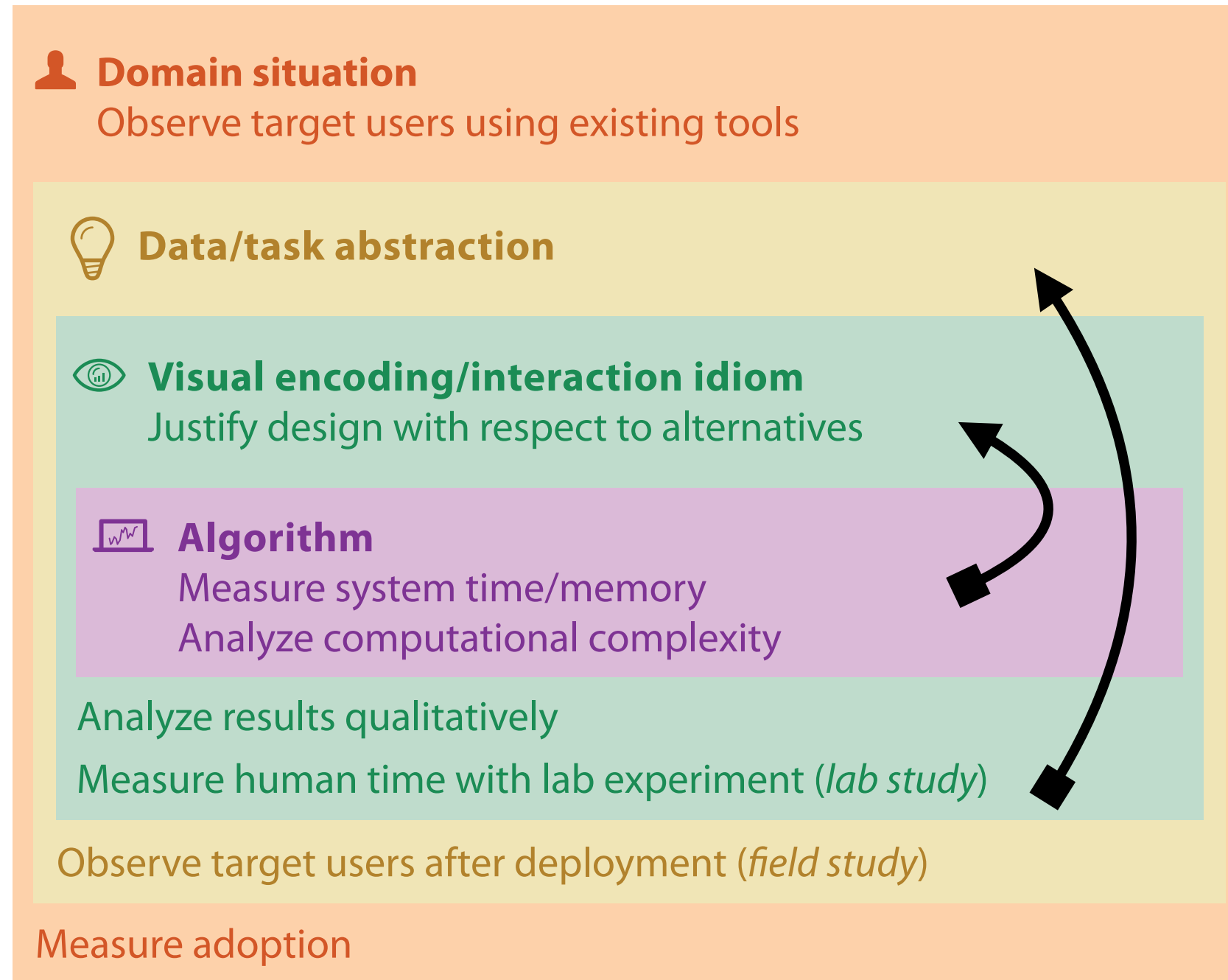
# Interdisciplinary: need methods from different fields at each level

- mix of qual and quant approaches (typically)





# Mismatches: Common problem

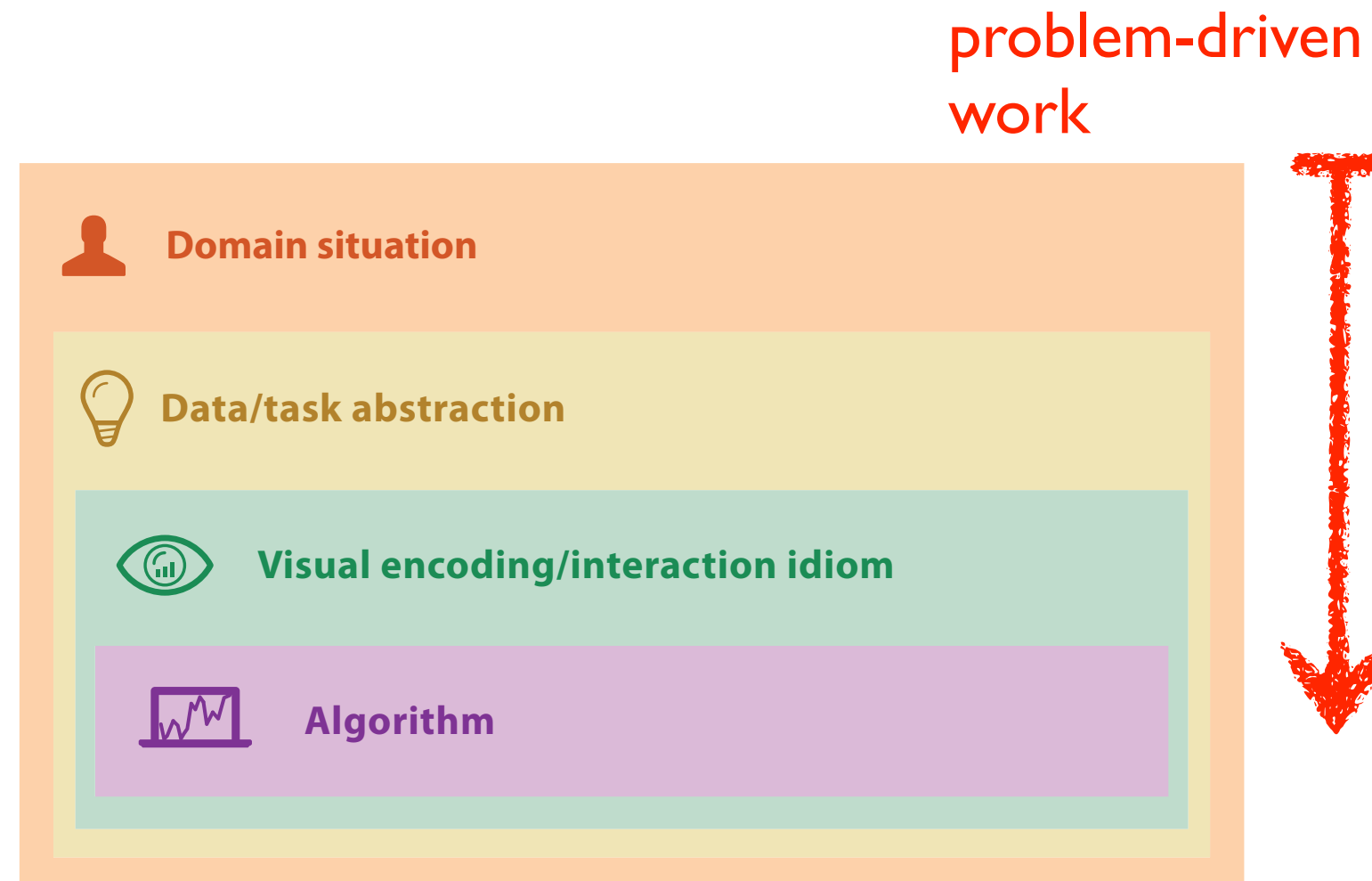


benchmarks can't confirm design

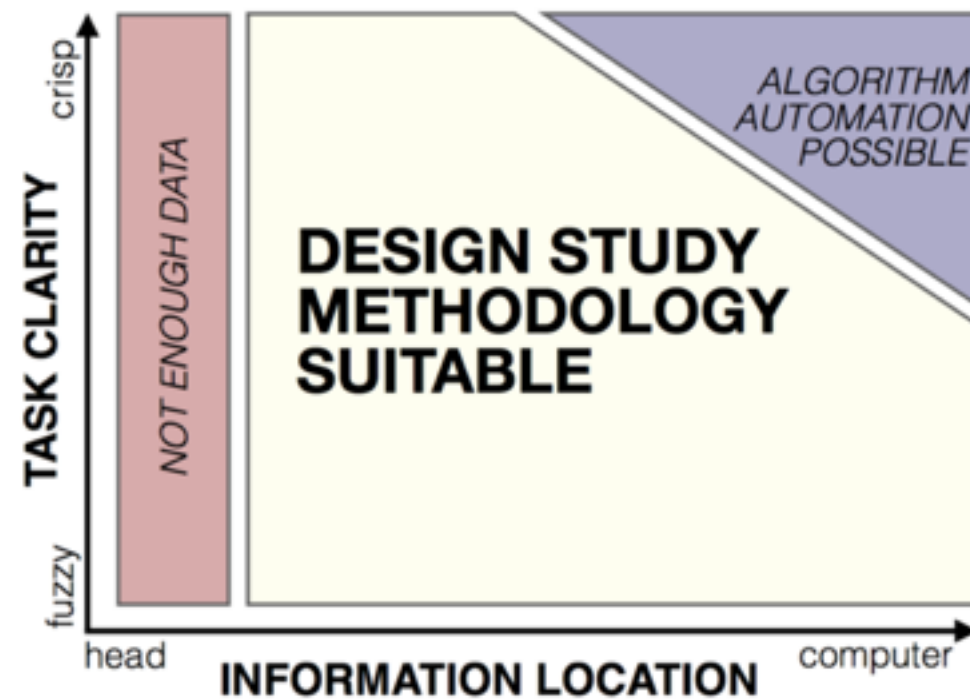
lab studies can't confirm task abstraction

# Problem-driven collaborations

- working with domain scientists
- translating from domain-specific language
  - how to pull this off?



# Building Rewarding Collaborations



Michael Sedlmair



Miriah Meyer



# Design Study Methodology

*Reflections from the Trenches and from the Stacks*

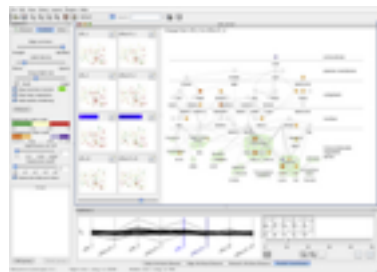
Tamara Munzner  
@tamaramunzner



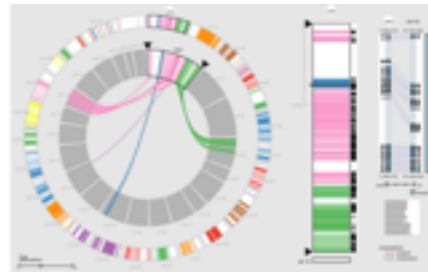
<http://www.cs.ubc.ca/labs/imager/tr/2012/dsm/>



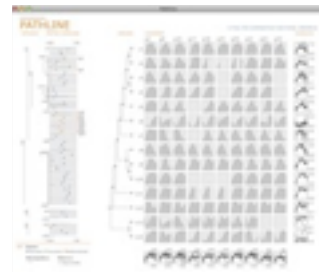
# Lessons learned from the trenches: 21 between us



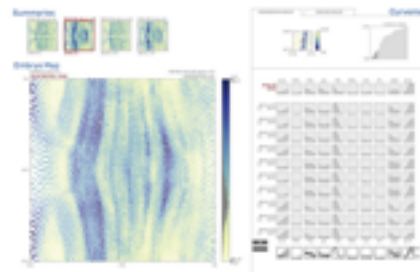
*Cerebral*  
genomics



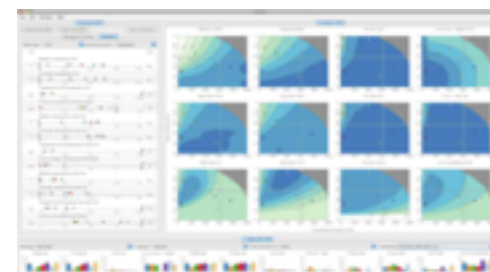
*MizBee*  
genomics



*Pathline*  
genomics



*MulteeSum*  
genomics



*Vismon*  
fisheries management



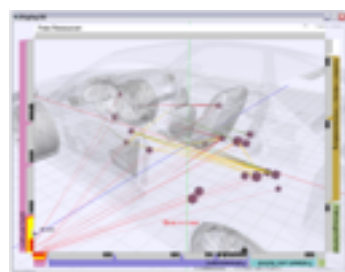
*QuestVis*  
sustainability



*WiKeVis*  
in-car networks



*MostVis*  
in-car networks



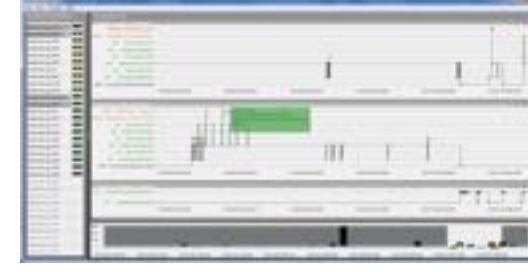
*Car-X-Ray*  
in-car networks



*ProgSpy2010*  
in-car networks



*RelEx*  
in-car networks



*Cardiogram*  
in-car networks



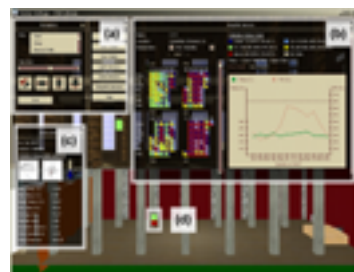
*AutobahnVis*  
in-car networks



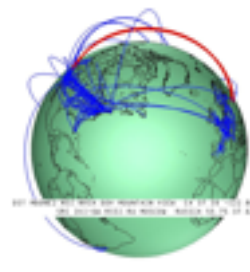
*VisTra*  
in-car networks



*Constellation*  
linguistics



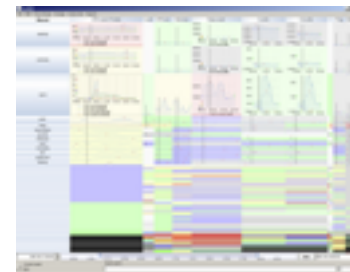
*LibVis*  
cultural heritage



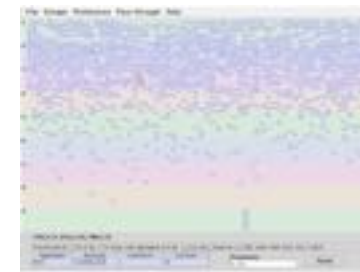
*Caidants*  
multicast



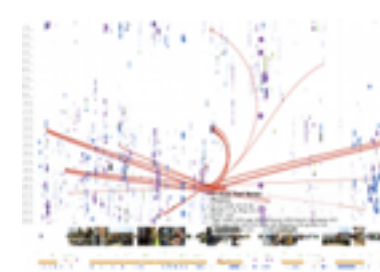
*SessionViewer*  
web log analysis



*LiveRAC*  
server hosting



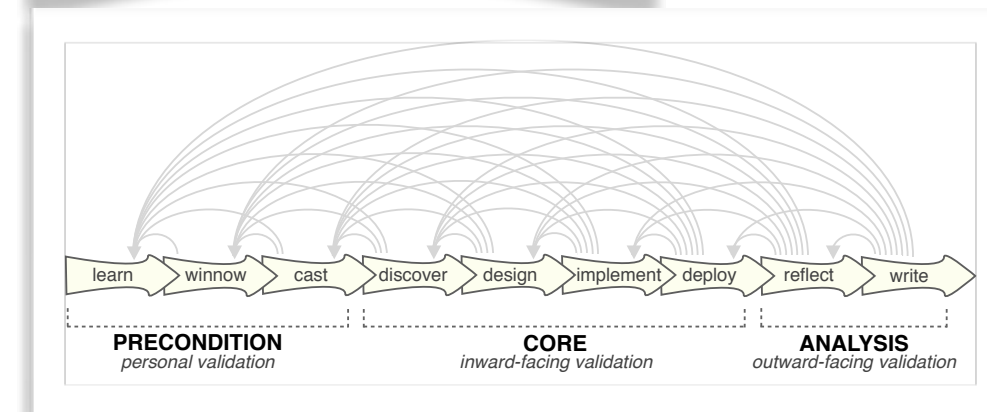
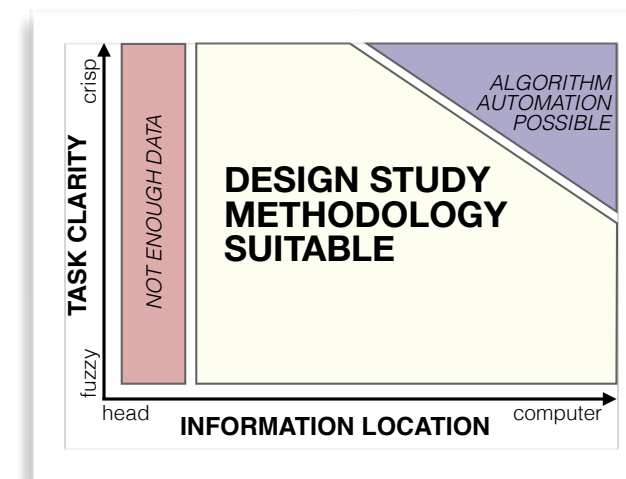
*PowerSetViewer*  
data mining



*LastHistory*  
music listening

# Methodology for problem-driven work

- definitions
- 9-stage framework
- 32 pitfalls & how to avoid them
- comparison to related methodologies



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



# Design study methodology: 32 pitfalls

- and how to avoid them

PF-1	premature advance: jumping forward over stages	general
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I'm a domain expert!  
Wanna collaborate?

Of course!!!



# considerations



Have **data**?  
Have **time**?  
Have **need**?  
...



# roles



Are you a  
target  
**user???**

... or maybe a  
**fellow tool  
builder?**





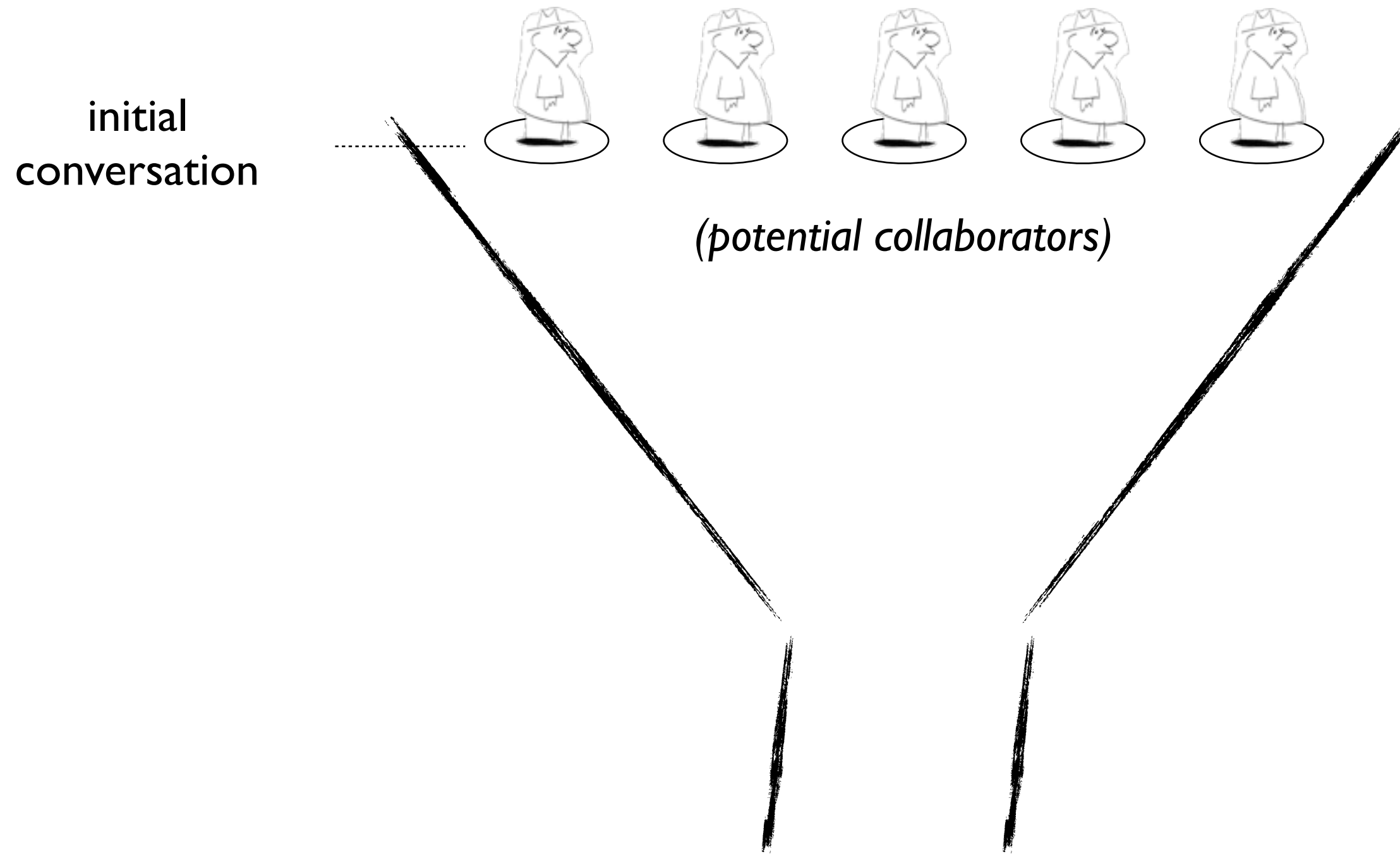
# METAPHOR

## Winnowing

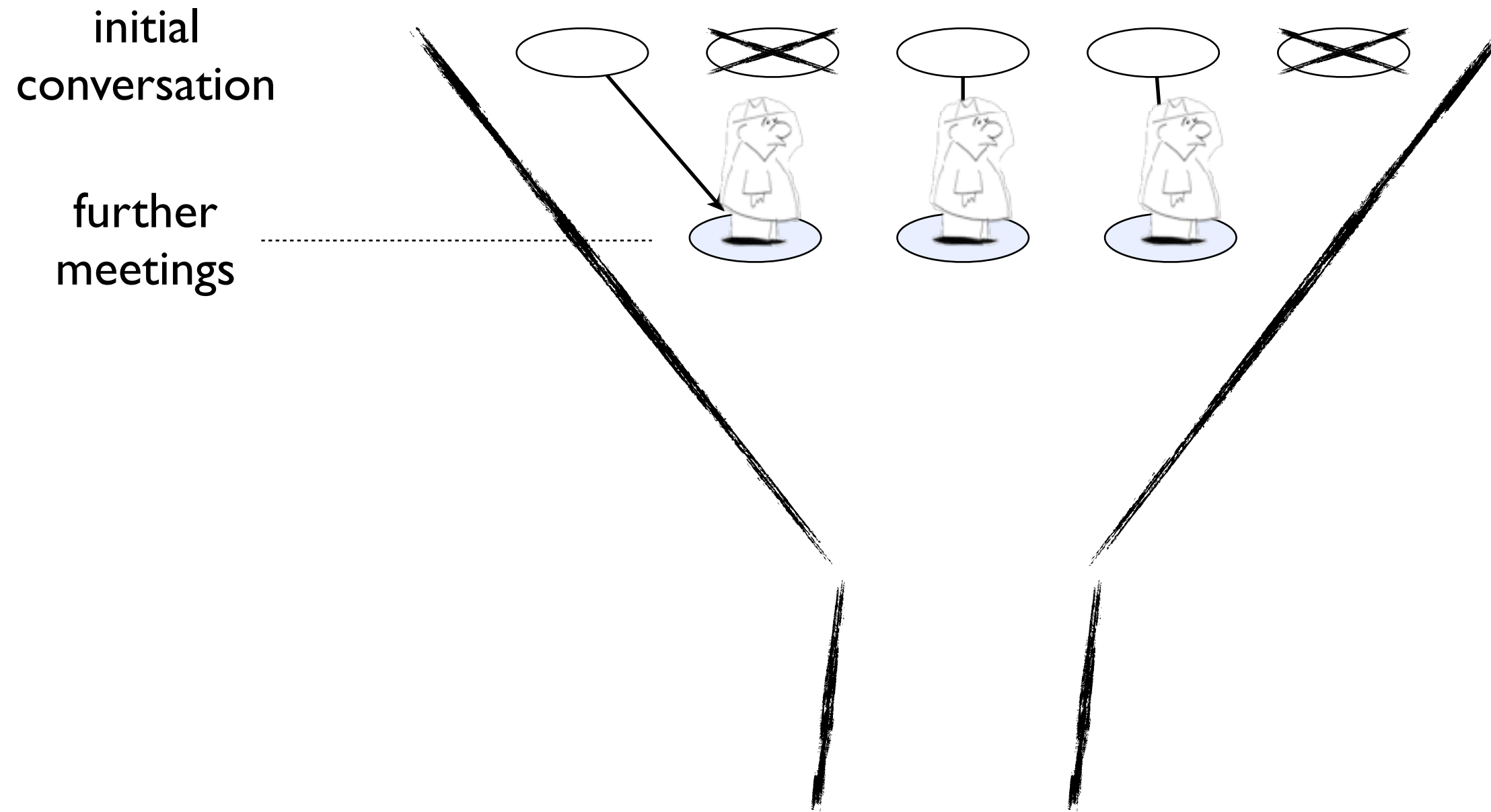




# Collaborator winnowing

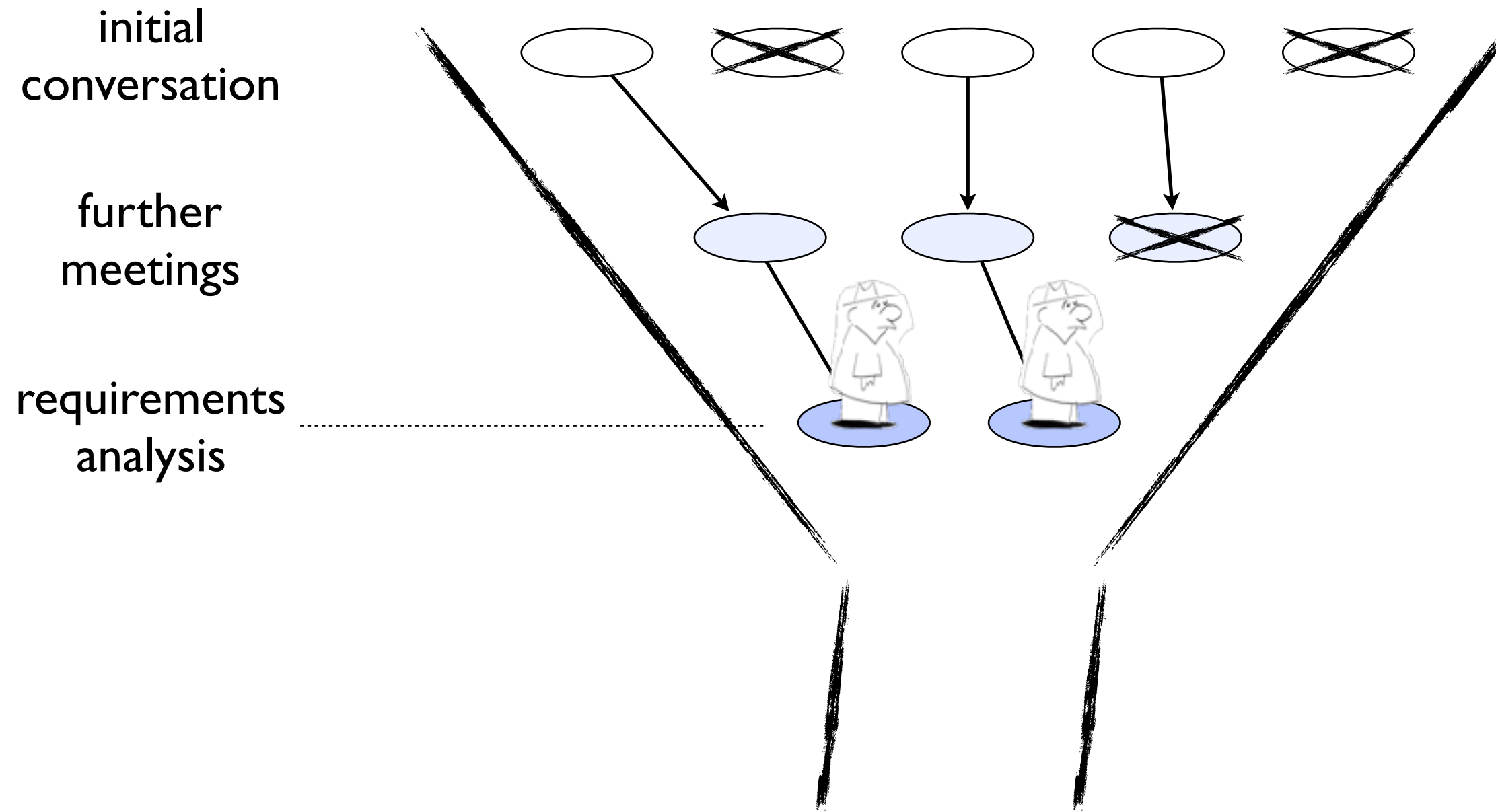


# Collaborator winnowing

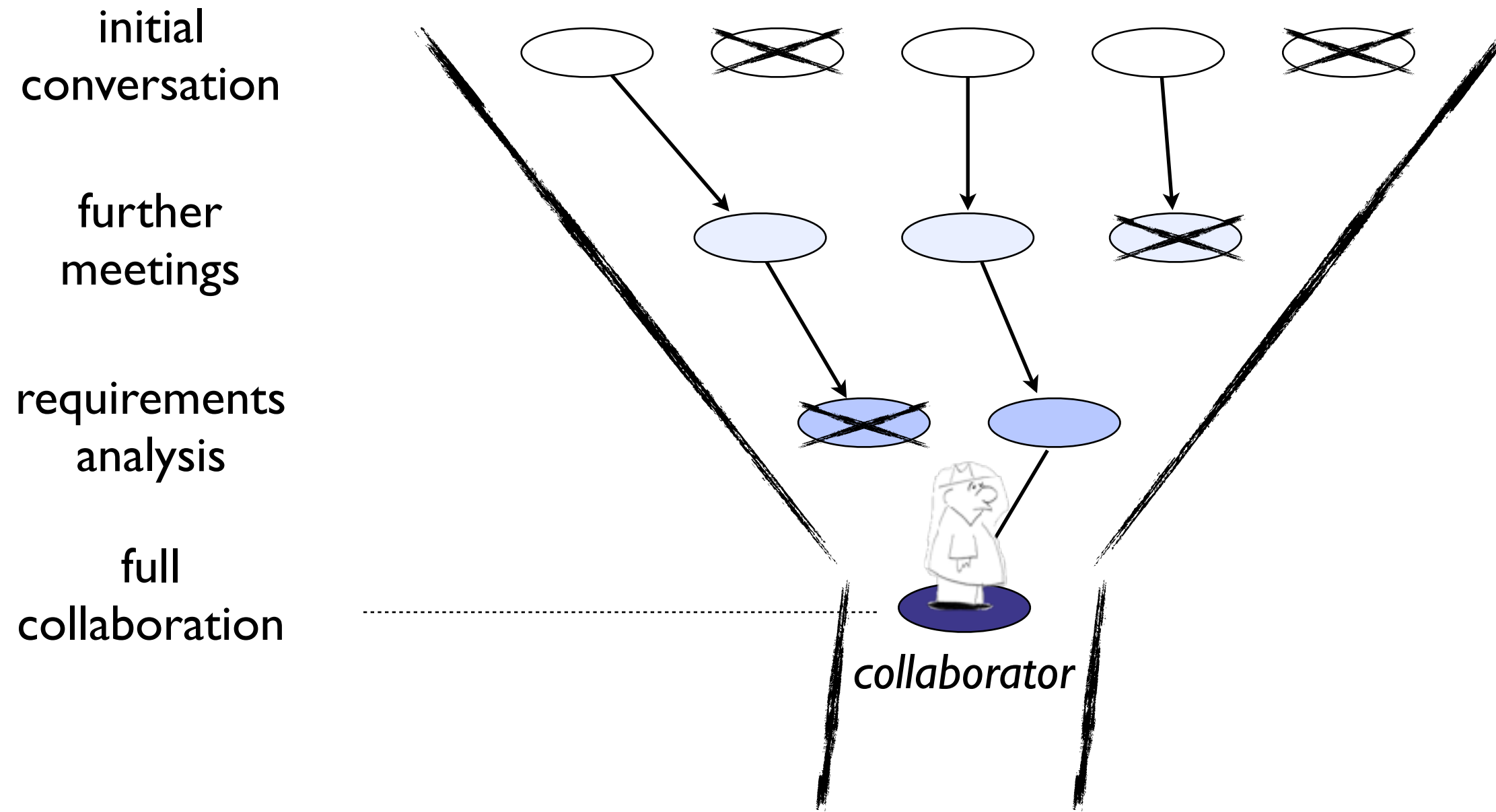




# Collaborator winnowing



# Collaborator winnowing



# Collaborator winnowing



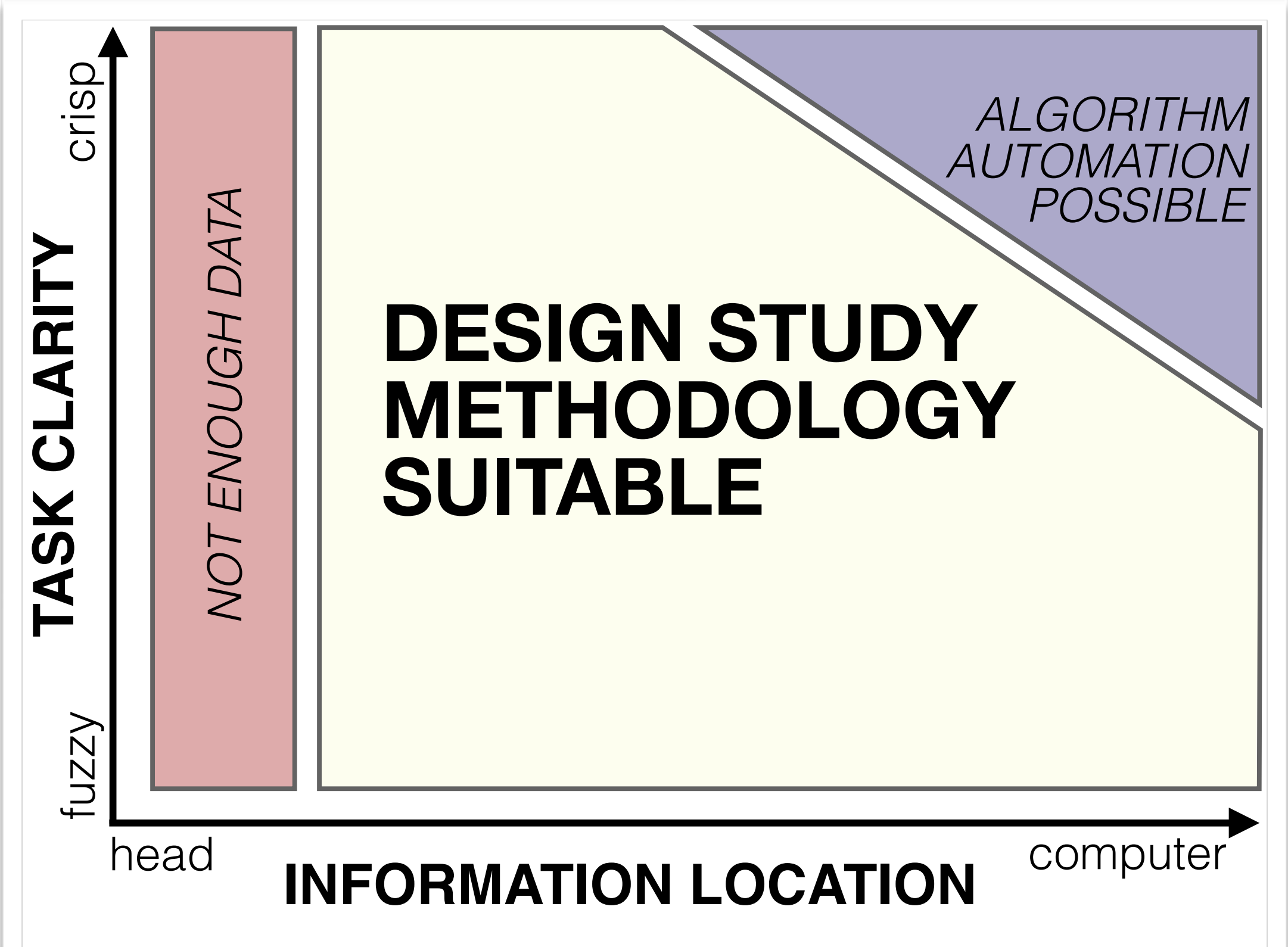
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# Design study methodology: definitions



# More Information

- this talk  
<https://www.cs.ubc.ca/~tmm/talks.html#hakai19-methods>
- papers, videos, software, talks, courses  
<http://www.cs.ubc.ca/group/infovis>  
<http://www.cs.ubc.ca/~tmm>

@tamaramunzner

## MEMBERS



Tamara Munzner



Anamaris Crizan



Zipeng Liu



Michael Oppermann



Steve Kasica



Shannah Fisher

## RECENT NEWS

2/2019 [news]:

Aggregated dendrograms for visual comparison between many phylogenetic trees

by Zipeng Liu, Shing-Hoi Zhan, and Tamara Munzner was accepted at *IEEE Transactions on Visualization and Computer Graphics*

[pre-print PDF]



10/2018 [UBC InfoVis @ IEEE VIS 2018]:

UBC InfoVis @ IEEE VIS 2018

At the dELIV Workshop, Anamaris Crizan and Madison Elliott will present the paper "How to evaluate an evaluation study? Comparing and contrasting practices in vis with those of other disciplines".

Michael Oppermann will give a talk entitled "Uncovering Spatiotemporal Dynamics from Non-Trajectory Data" at the Urban Data Visualization Workshop.

Tamara Munzner will participate in a panel at the VisGuides Workshop. We're co-hosting the (North) West Coast Party, on Thursday night.

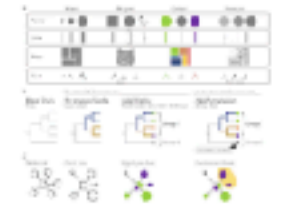


9/2018 [news]:

A systematic method for surveying data visualizations and a resulting genomic epidemiology visualization typology: GCVIT

by Anamaris Crizan, Jennifer L. Gardy, and Tamara Munzner was published in *Oxford Bioinformatics*

[paper]



8/2018 [news]:

Adjutant: an R-based tool to support topic discovery for systematic and literature reviews

by Anamaris Crizan, Tamara Munzner, and Jennifer L. Gardy was published in *Oxford Bioinformatics*

[paper]



8/2018 [news]:

Visiting Professor Takayuki Itoh

Takayuki Itoh from Okanawa University, Japan, was visiting our group between Jul - Aug 2018. Thanks for your visit, it was great having you here!



05/2018 [news]:

GoRS/Vis: Improving the Predicting of Self-interruption during Reading using Gaze Data

by Jan Pilzer, Sharmeen Mahmood, Vanessa Putnam, and Tamara Munzner was accepted to ETVIS 2018.

[pre-print PDF]

