Bioinformatics II
Winter Term 2016/17

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Chapter 6:
Visualization Design

Jun.-Prof. Dr.-Ing. Thomas Schultz

URL: http://cg.cs.uni-bonn.de
E-Mail: schultz@cs.uni-bonn.de
Office: Friedrich-Ebert-Allee 144, 53113 Bonn

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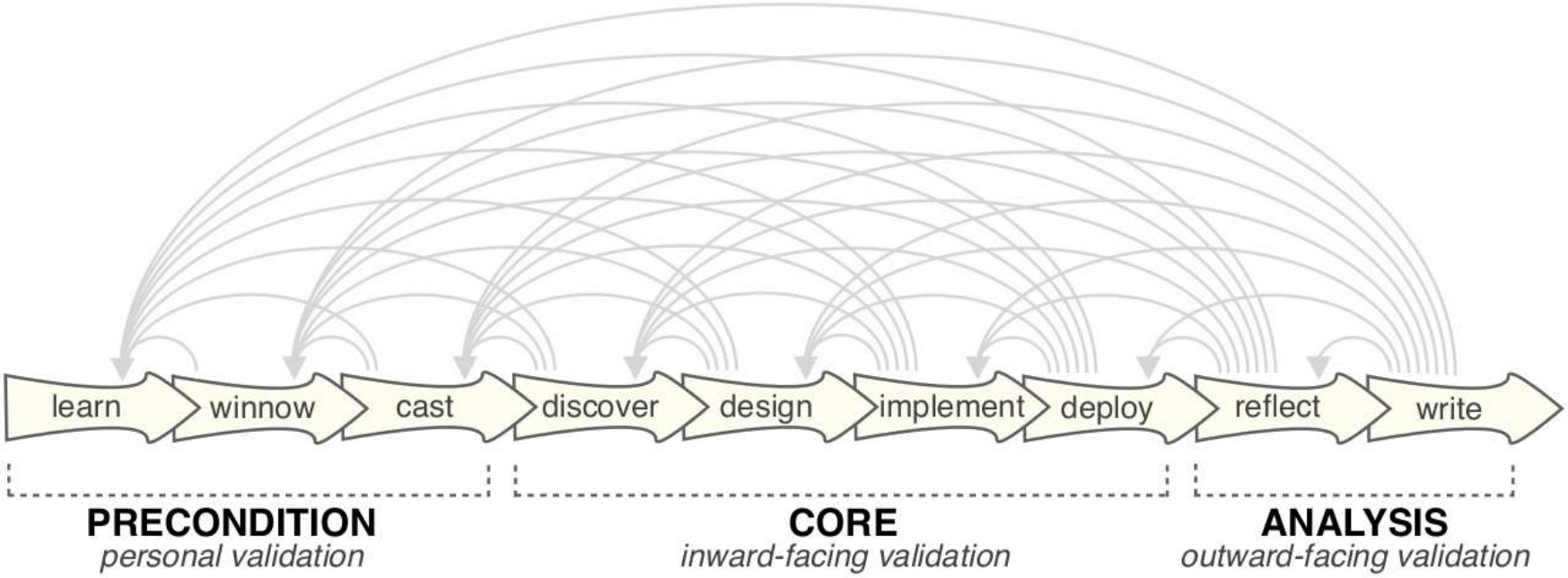
Motivation

- **Lecture so far:**
  - Human visual perception
  - Visualization of multidimensional data
  - Dimensionality Reduction
  - Visualization of graphs
- How to use this knowledge to **produce software that is useful for collaborators** (e.g., biologists):
  - Visualization Design Process
  - Classification of Marks and Channels
  - Visualization Pipelines
  - Example Systems

Section 6.1:
Visualization Design Process

Methodology for Visualization Design

- Nine-stage design methodology [Sedlmair et al. 2012]
  - Guidelines for developing visualization software prototypes for scientific collaborators

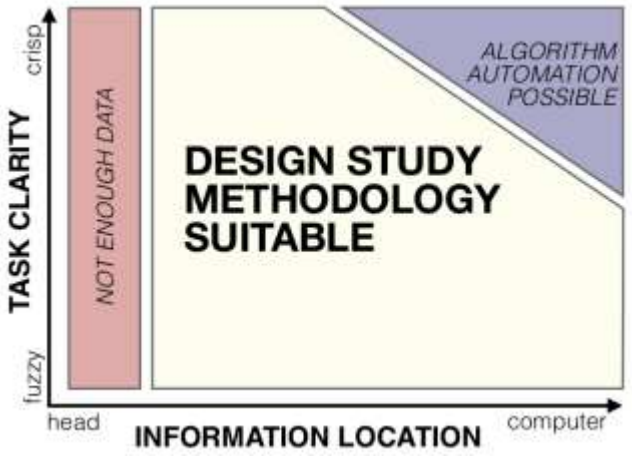


Learn

- **Perception:** Be aware of limitations of the human visual system
- **Techniques:** Have a broad perspective of available tools
  - Explains “superficial” treatment of alternative techniques within this lecture
  - Assignments provide opportunity to become familiar with widely applicable software packages
- **Methodology:** Know how to build collaborations and create systems
  - Today’s lecture!
- **Read up** on literature relevant to your project!

Winnow

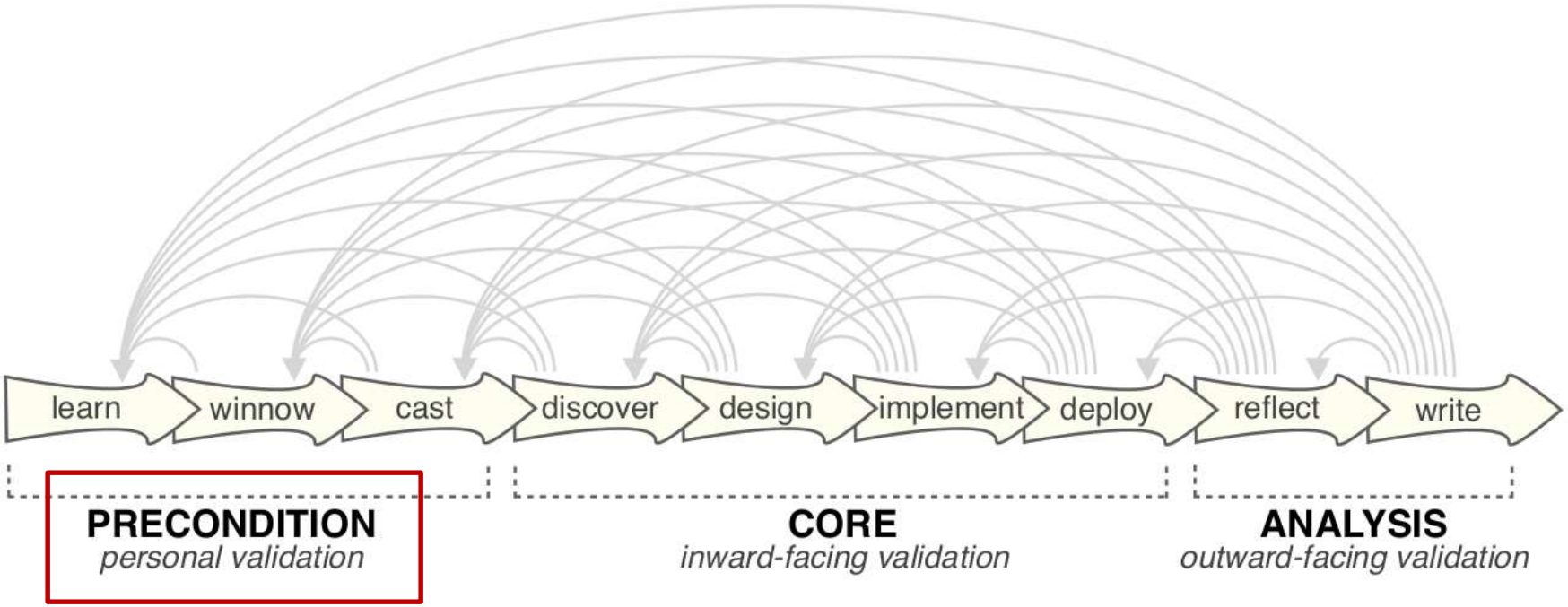
- Selection of collaborators / projects
  - "Talk with many, stay with few"
- **Practical Criteria:**
  - Does data exist, is it enough, can I have it?
  - Can I and can they devote enough time?
- **Intellectual Criteria:**
  - Is the problem interesting and relevant?
  - Do existing solutions suffice?
  - Is visualization suitable?
- **Interpersonal Criteria**



Cast

- Be aware of **important roles** in the project
  - **Front line analyst** (e.g., PhD student)
    - User of your tool
    - Performs day-to-day analysis of the data
    - Often generates the data
  - **Gatekeeper** (e.g., Professor)
    - Grants and denies access to data (and permission to publish about it)
    - Decides on how resources are spent
  - **Fellow tool builders**
    - Avoid relying on their characterization of the problem alone

Core Stage


learn
winnow
cast
discover
design
implement
deploy
reflect
write
PRECONDITION
personal validation
CORE
inward-facing validation
ANALYSIS
outward-facing validation

Discover

- Understand the domain user's **research questions, data analysis problems, and tasks**
- **Methods:**
  - *Talking:* Iterative (get feedback on your abstraction)
  - *Fly-on-the-wall:* Silently observing
  - *Contextual inquiries:* Interrupt and ask
  - *Reading* domain literature

Data Abstraction

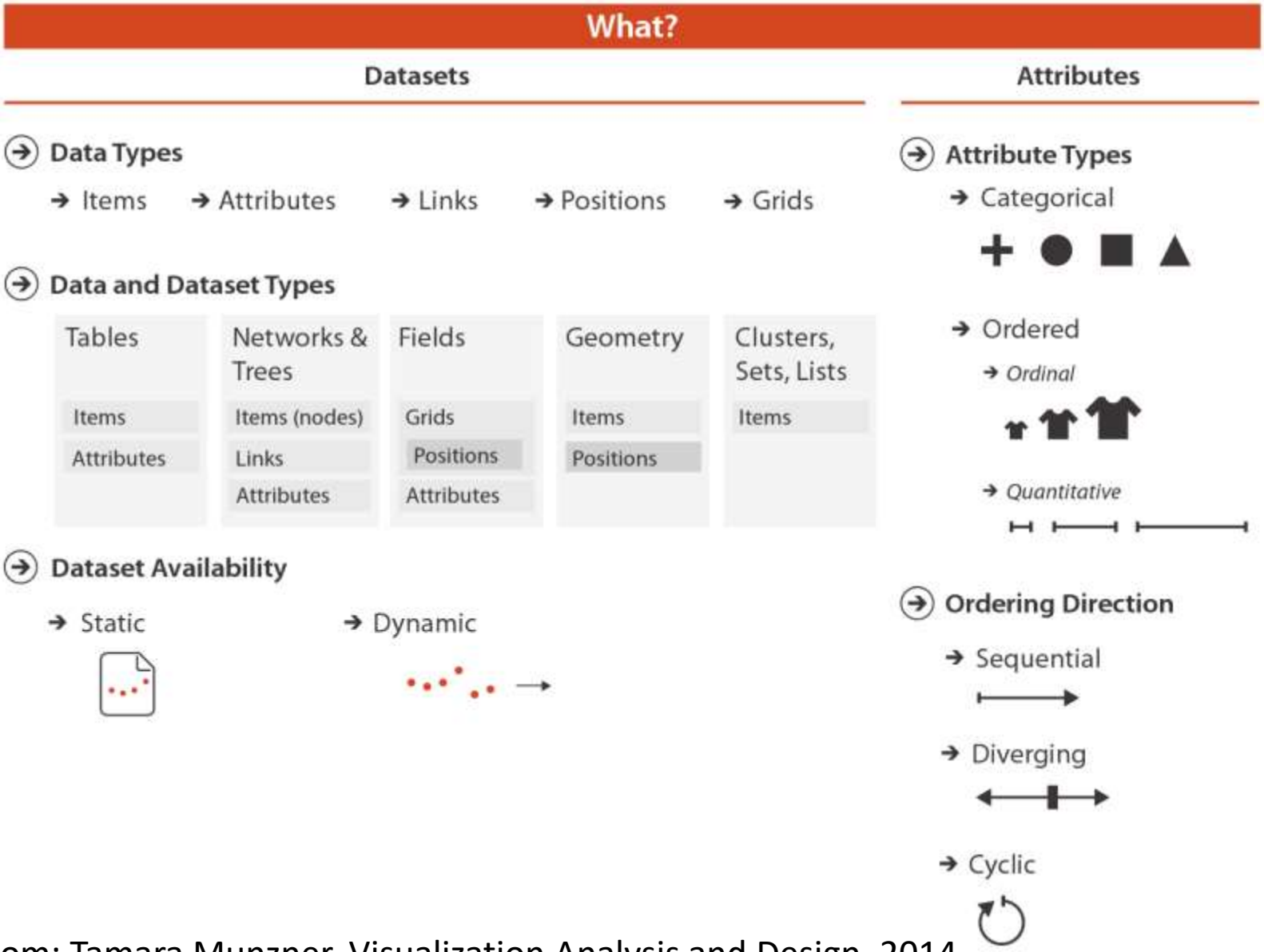


Figure from: Tamara Munzner, Visualization Analysis and Design, 2014

Data Abstraction: Dataset Types

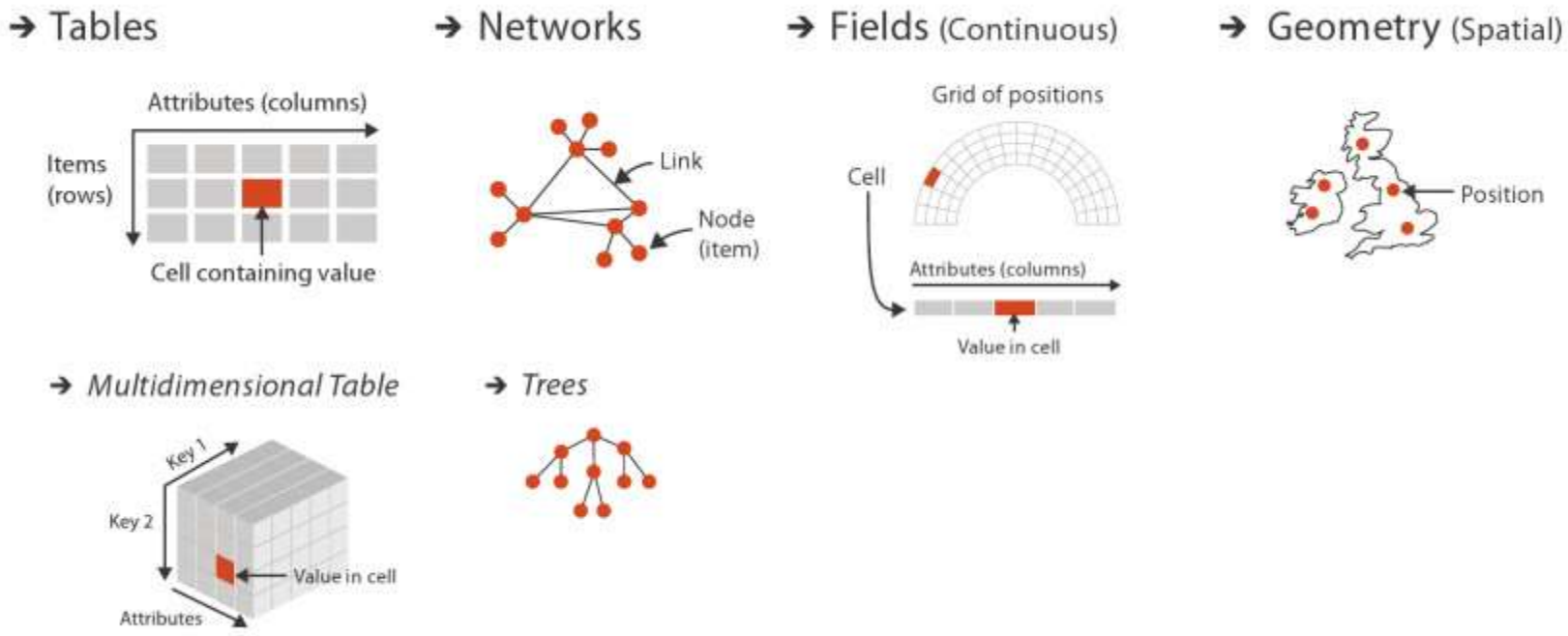


Figure from: Tamara Munzner, Visualization Analysis and Design, 2014

Task Abstraction

Images from Tamara Munzner, Visualization Analysis and Design, 2014

Design

- **Goal** of visualization is to create a solution
  - for a specific task
  - performed by a specific group of users
  - on specific data
- **Satisfy** users, do not attempt to **optimize**
  - contradictory objectives are the norm

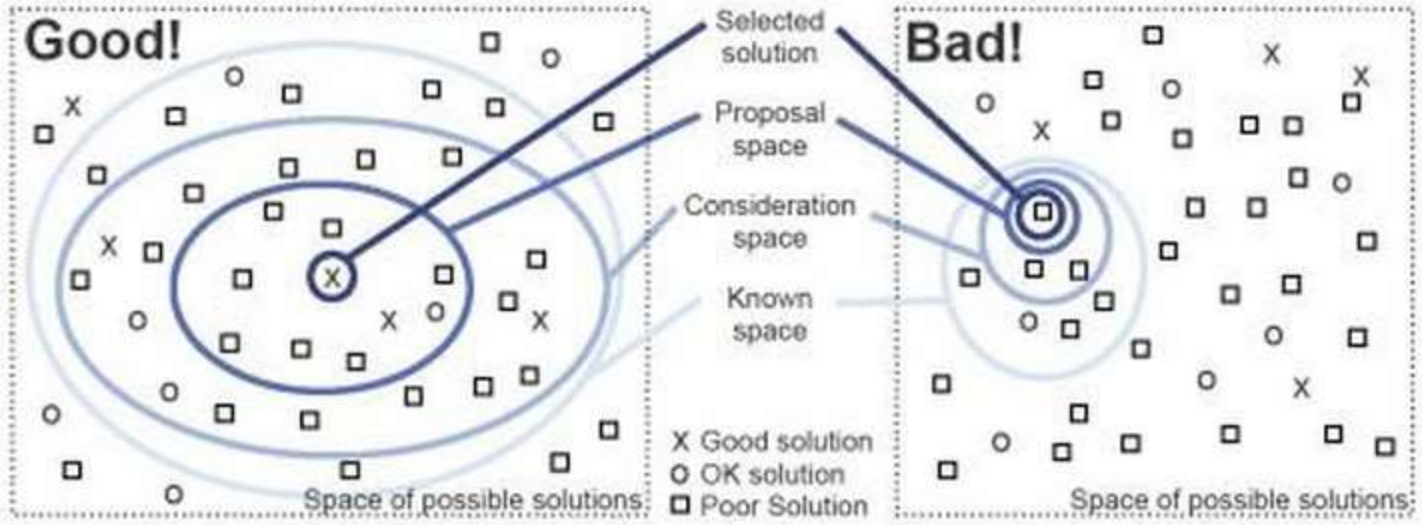
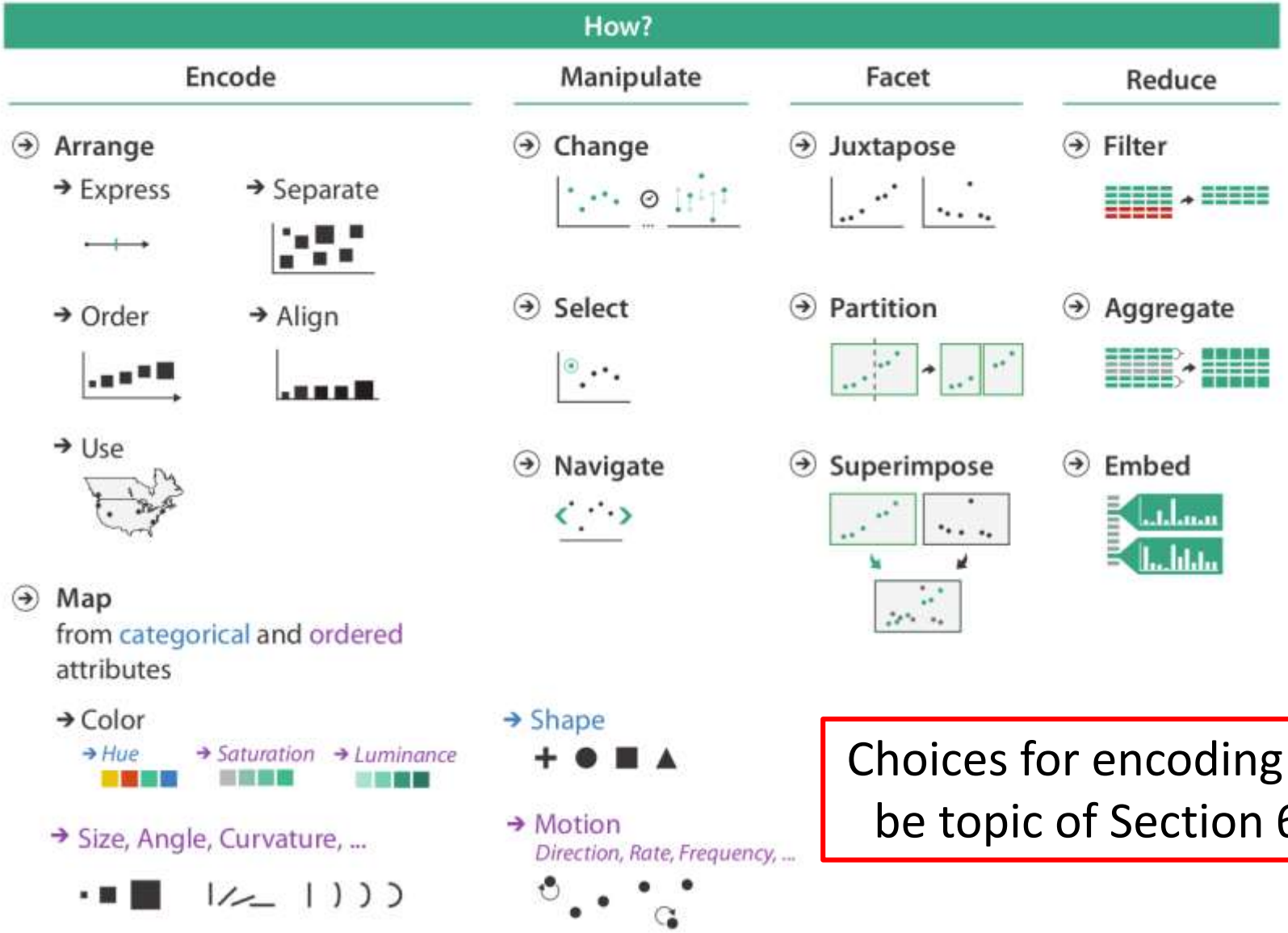


Figure from: Tamara Munzner, Visualization Analysis and Design, 2014

How to Construct a Vis Idiom



Choices for encoding will be topic of Section 6.2

Figure from: Tamara Munzner, Visualization Analysis and Design, 2014

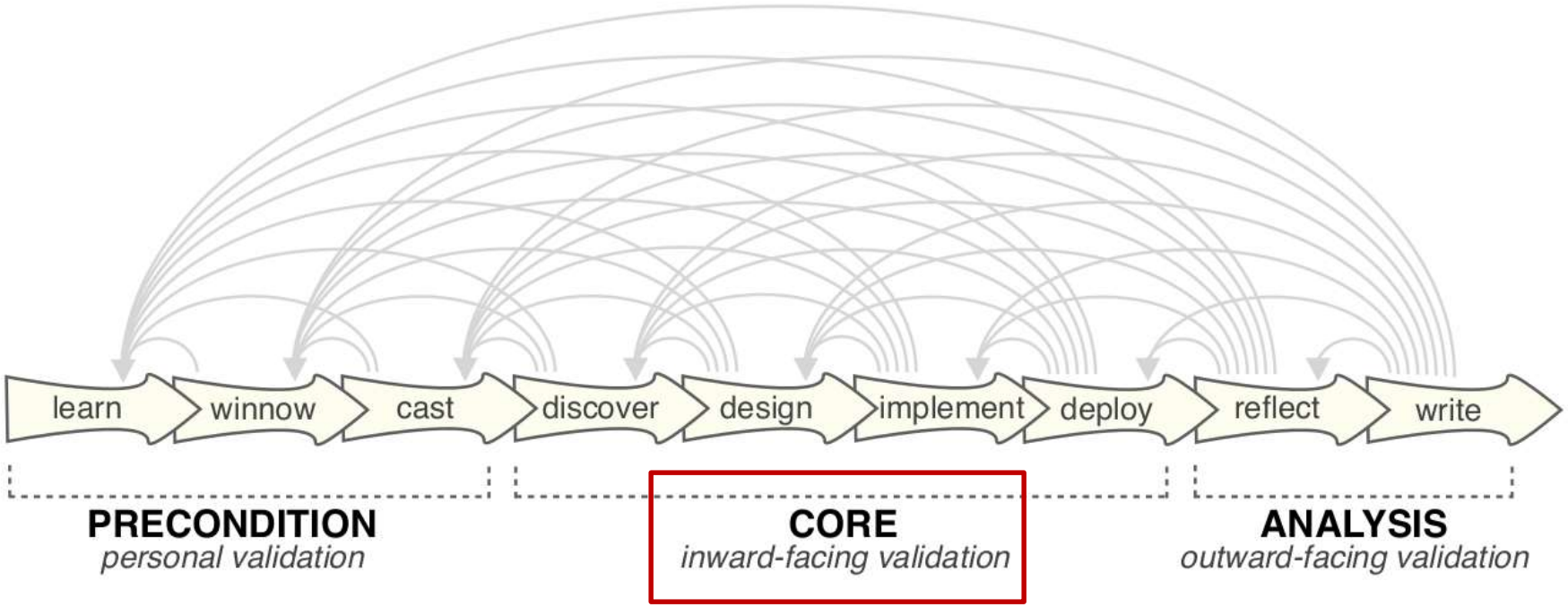
Implement

- **Prototypes** help confirm that you've correctly analyzed the users' needs
  - Avoid investing lots of time in creating a software that ends up not being used
  - Start with paper prototypes / "mock-ups"
  - Write "throw-away" code simply and rapidly
  - Make use of existing infrastructure
- Find middle ground on **usability**
  - With too little usability, tool will not be used
  - Usability should not push utility out of focus

Deploy

- Release your software “into the wild”
- **Validate** benefit from tool:
  - Faster or more accurate analysis
  - New insights (which might enable a higher degree of automation)
- **Case study:** Solve specific real problem with real users and real data
  - **Usage scenario:** Real data, analysis done by developer of tool
  - **Pair analytics:** Insight gained in tandem by computer / data and domain scientist

Analysis Stage

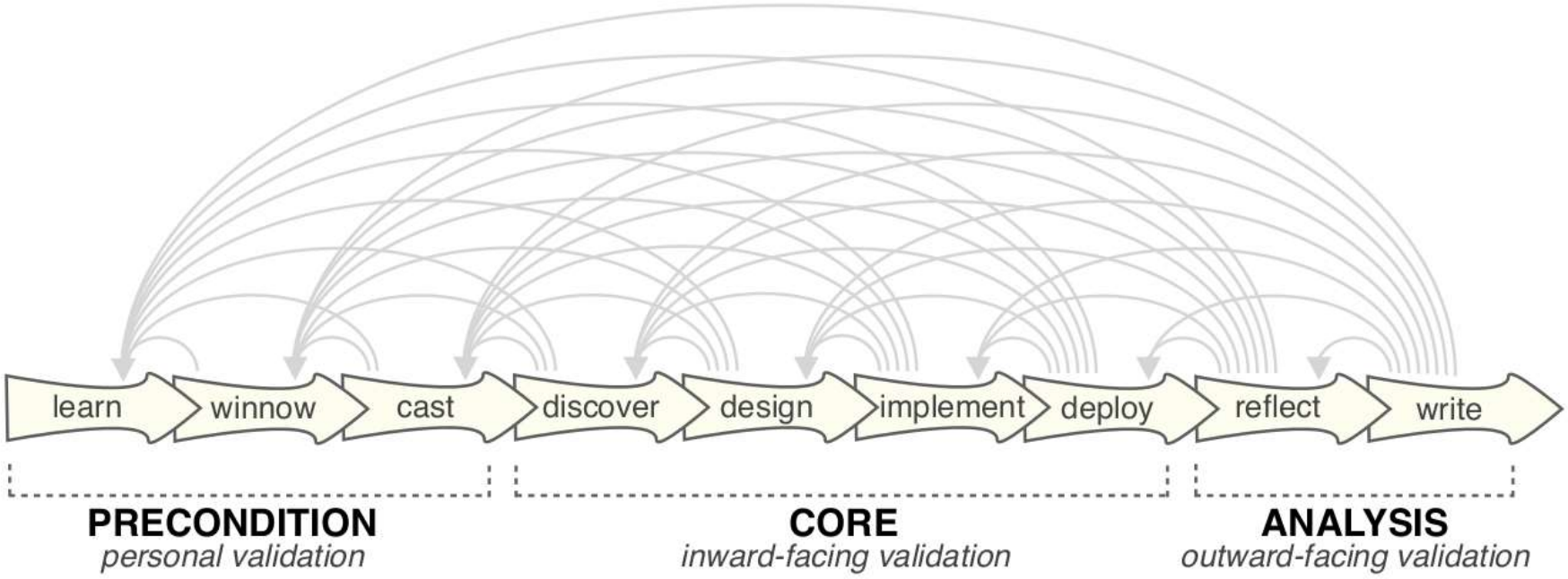


Reflect / Write

- **Reflect** on what you've learned from building the tool
  - How to do better next time?
  - Confirm, refine, reject, propose guidelines
- In an academic context, **report** on your tool in a thesis / scientific paper
  - Describe the tool and evaluation
  - Justify design choices
  - Discuss lessons learned

Summary: Nine-Stage Process

- Nine-stage design methodology provides useful guidance / structure for interdisciplinary collaborations
- Helps avoid missing important steps

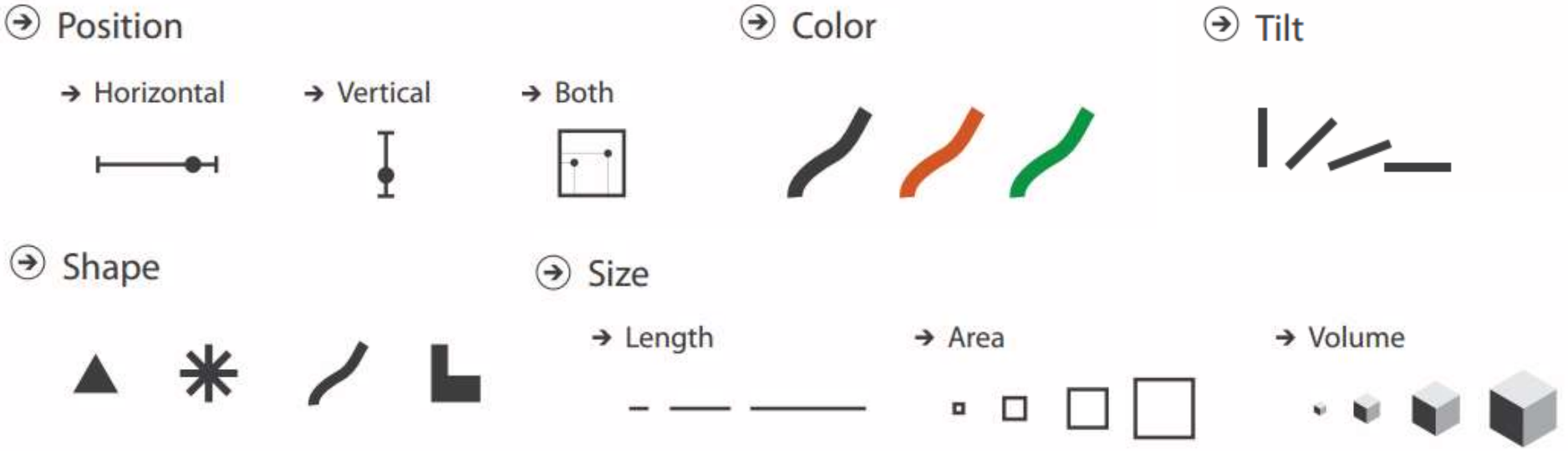


Section 6.2:
Marks and Channels

What are Marks and Channels?

- **Marks** are geometric primitives

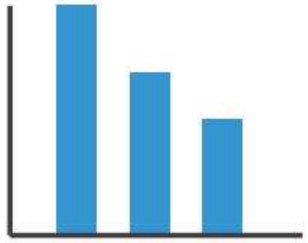
- **Channels** control visual appearance of marks



Images from Tamara Munzner, Visualization Analysis and Design, 2014

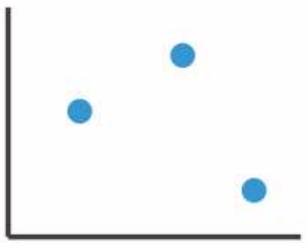
Combining Marks and Channels

- You can analyze common visualization idioms as combinations of marks and channels:



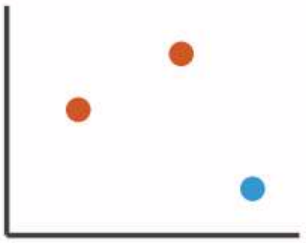
1:
vertical position

mark: line



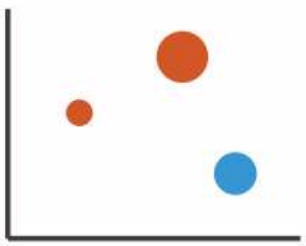
2:
vertical position
horizontal position

mark: point



3:
vertical position
horizontal position
color hue

mark: point

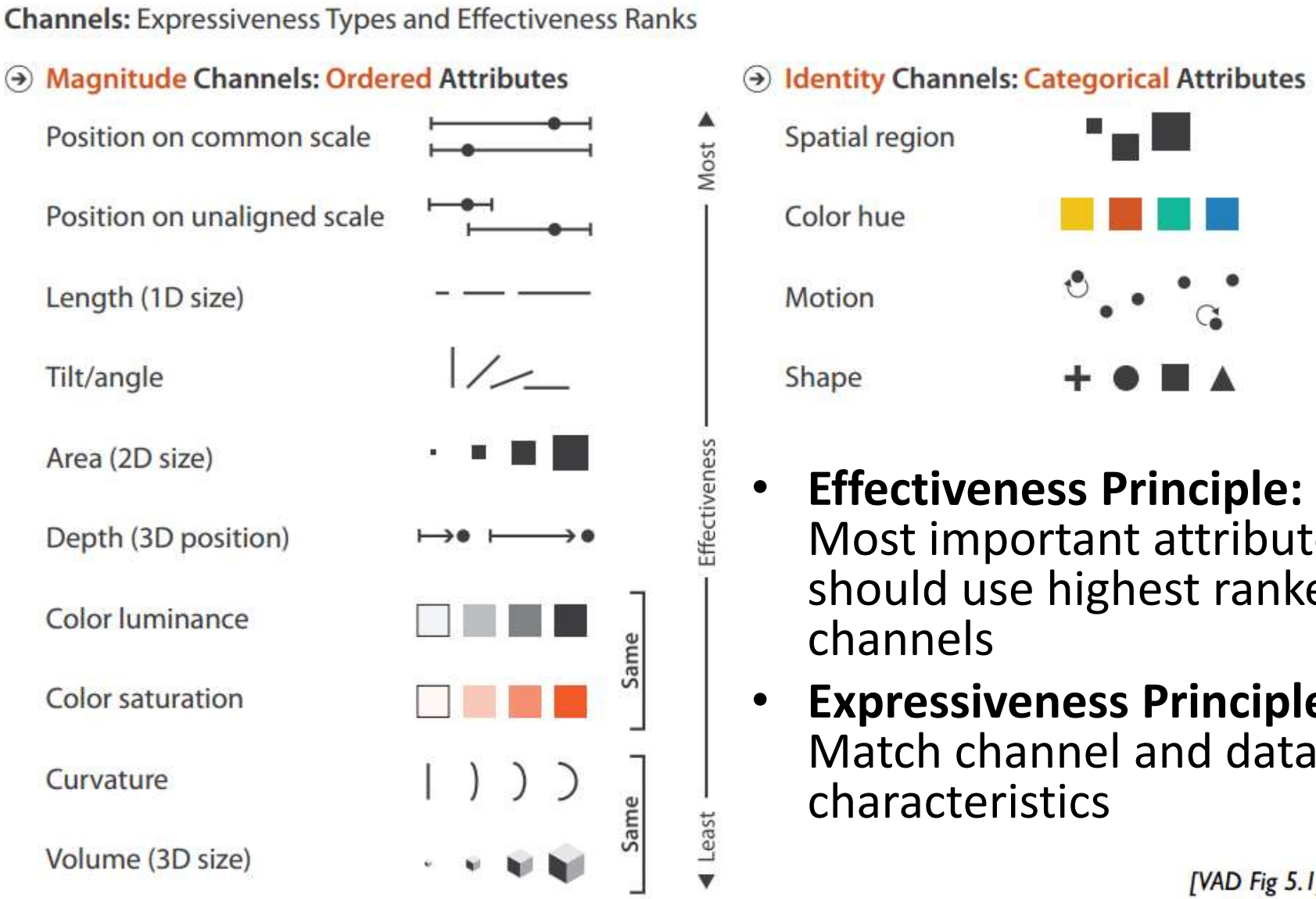


4:
vertical position
horizontal position
color hue
size (area)

mark: point

Images from Tamara Munzner, Visualization Analysis and Design, 2014

Effectiveness of Channels



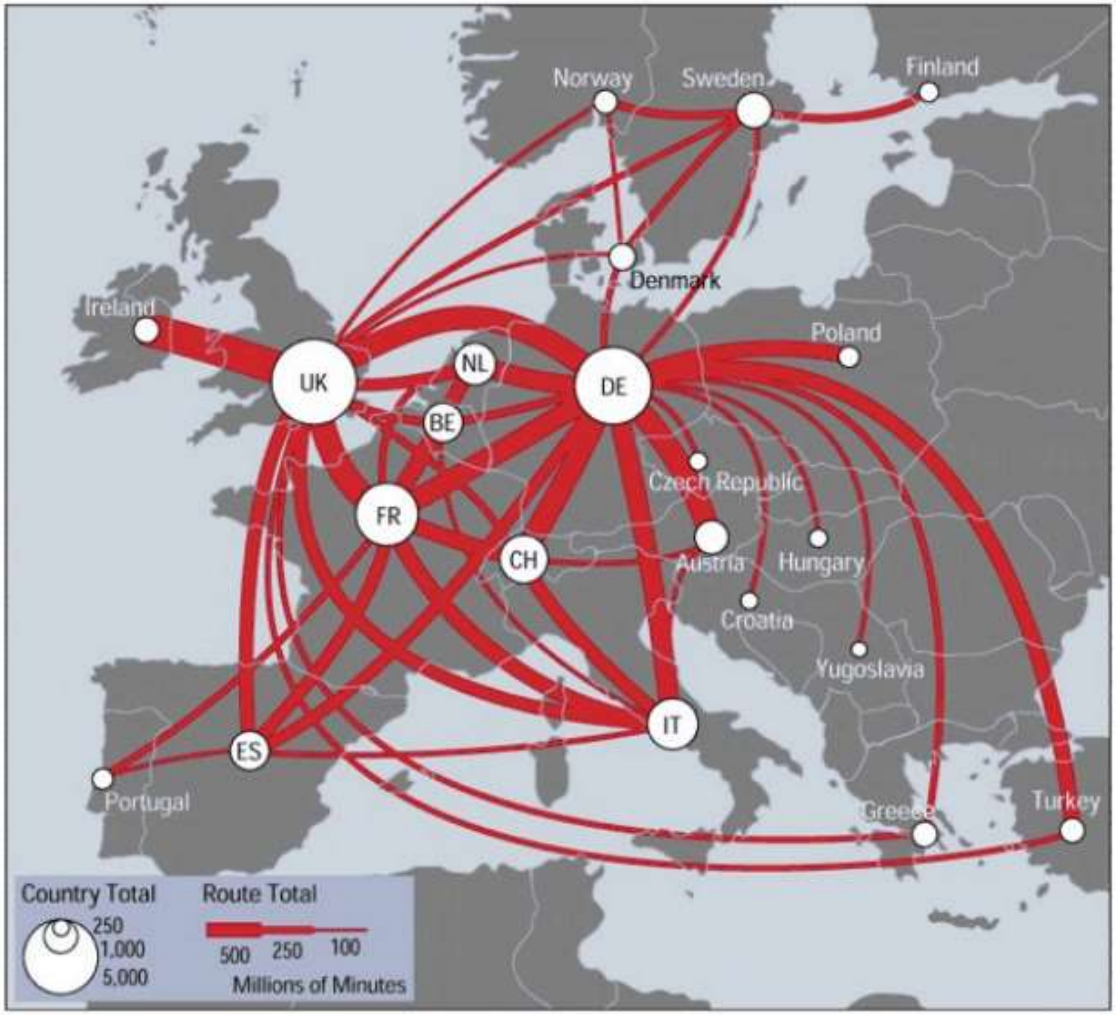
- **Effectiveness Principle:** Most important attributes should use highest ranked channels
- **Expressiveness Principle:** Match channel and data characteristics

[VAD Fig 5.1]

Images from Tamara Munzner, Visualization Analysis and Design, 2014

Expressiveness: How Many Levels?

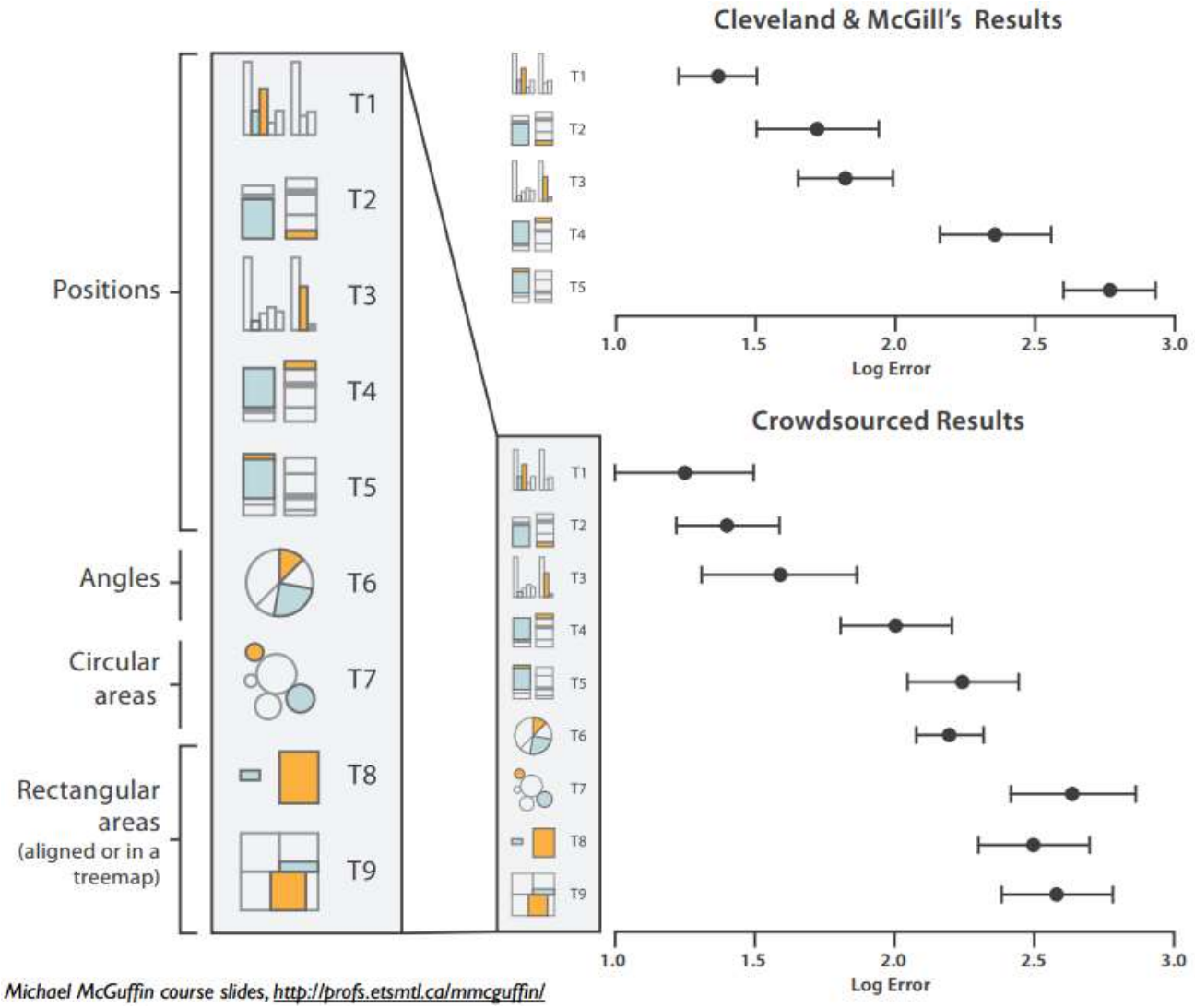
- Some channels only allow us to reliably distinguish between few levels
- Verify that this matches your number of attributes
- Bin if needed



[mappa.mundi.net/maps/maps_014/telegeography.html]

Effectiveness: How do we know?

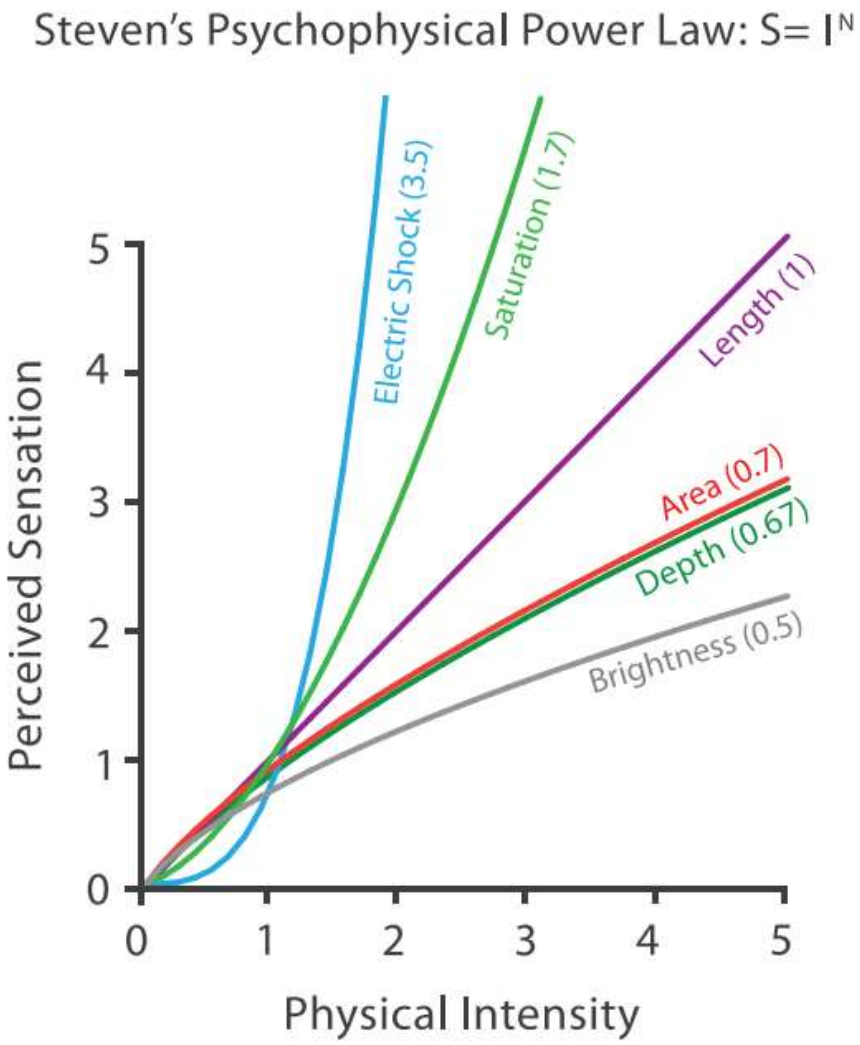
- Compare accuracy (or speed) on clearly defined tasks with different encodings



Michael McGuffin course slides, http://profs.etsmtl.ca/mmcguffin/

Effectiveness: Why?

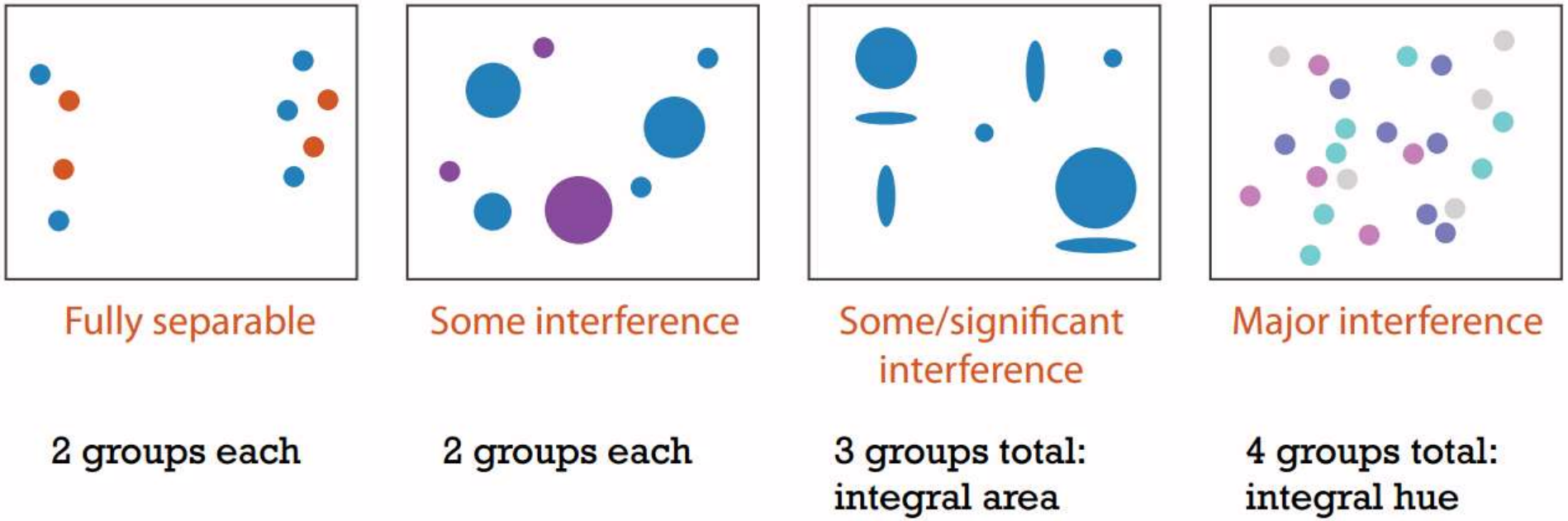
- Differences in accuracy explained by Steven‘s Psychophysical Power



Images from Tamara Munzner, Visualization Analysis and Design, 2014

Combinations of Channels

- Keep in mind separability vs. integrability:



Images from Tamara Munzner, Visualization Analysis and Design, 2014

Summary: Marks and Channels

- **Marks** are the geometrical primitives used for visualization
- **Channels** control their appearance
- Channels should be matched to data in order to be **expressive**
- Some channels are more **effective** than others – use those for the most important attributes!

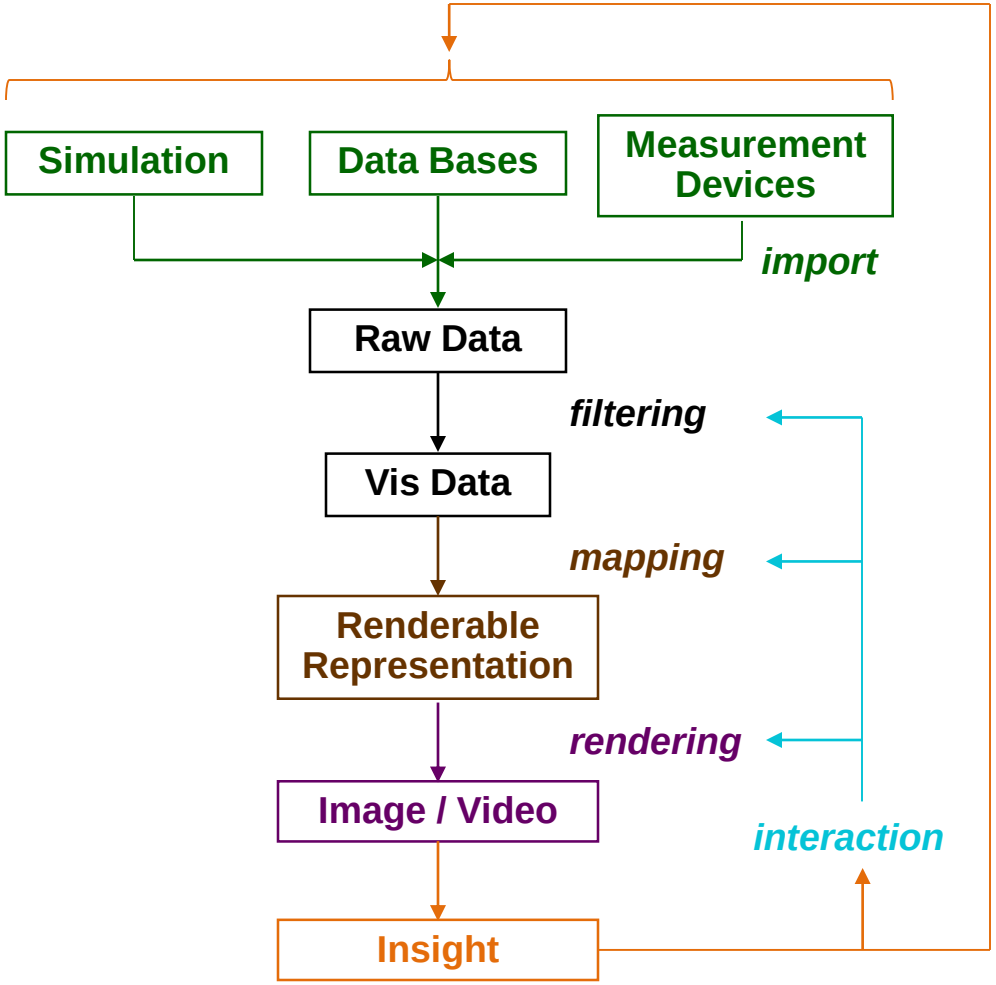
Section 6.3:
Visualization Pipelines

Visualization Pipelines: Motivation

- **Visualization Pipelines**
  - provide a scheme of how **data** is read in, filtered, mapped, and rendered during visualization
  - are a useful **abstraction** and common reference for many individually tailored solutions commonly found in visualization
  - guide organization of **class libraries**

Visualization Pipeline

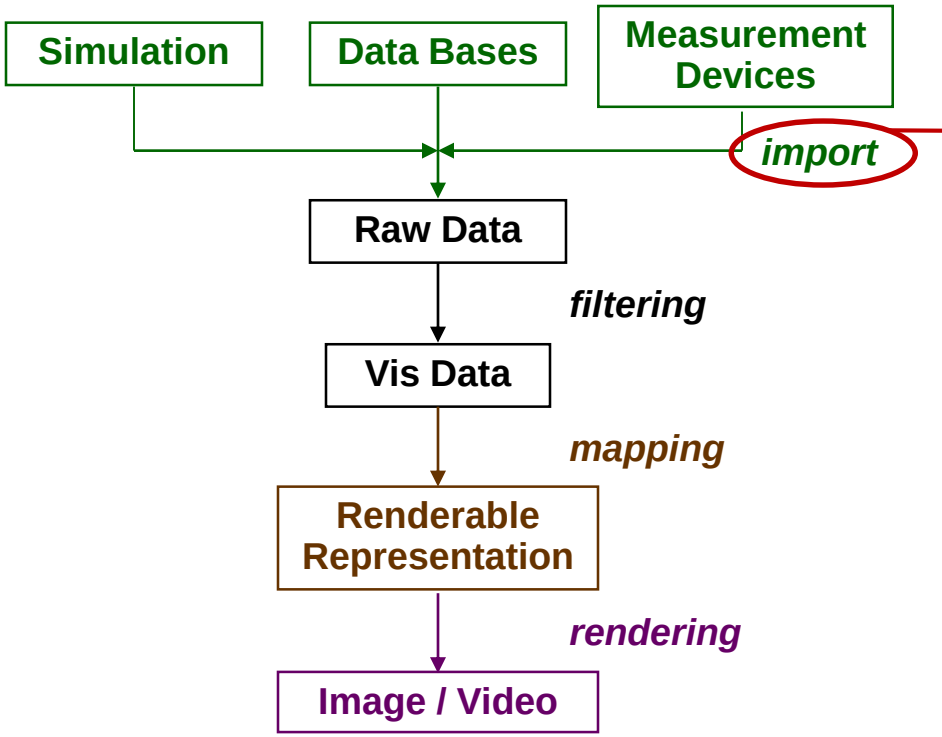
- Most visualizations follow a common scheme:



Examples of interaction:
- Filter out parts of the data
- Change level of detail
- Reorder PCP axes
- Switch between visualization techniques

A **crucial benefit** of computer-based visualization

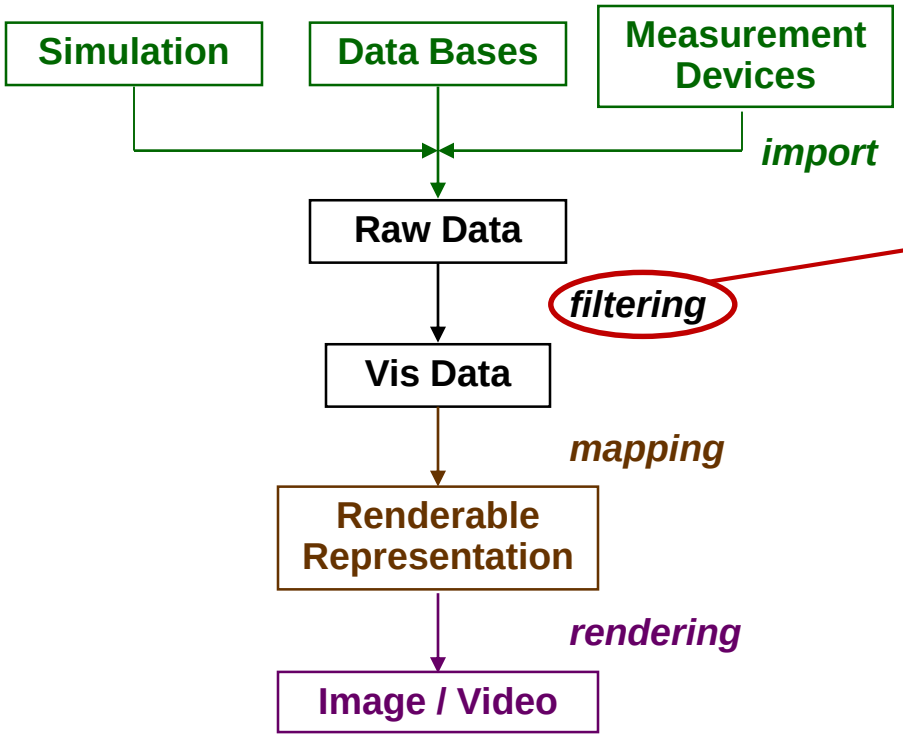
Import



Import:
data → data

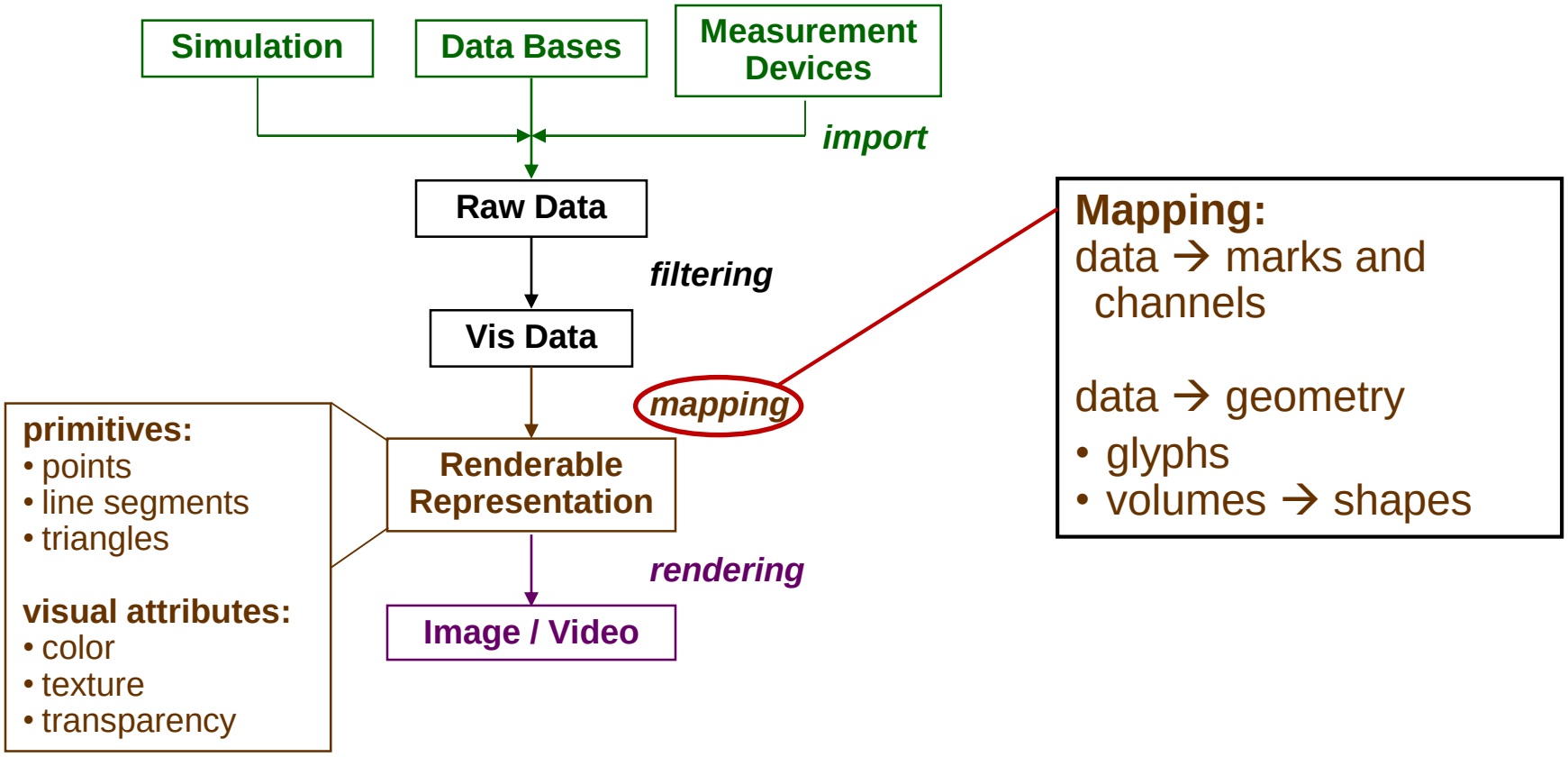
- data format conversion
- resampling
- interpolation
- imputation

Filtering

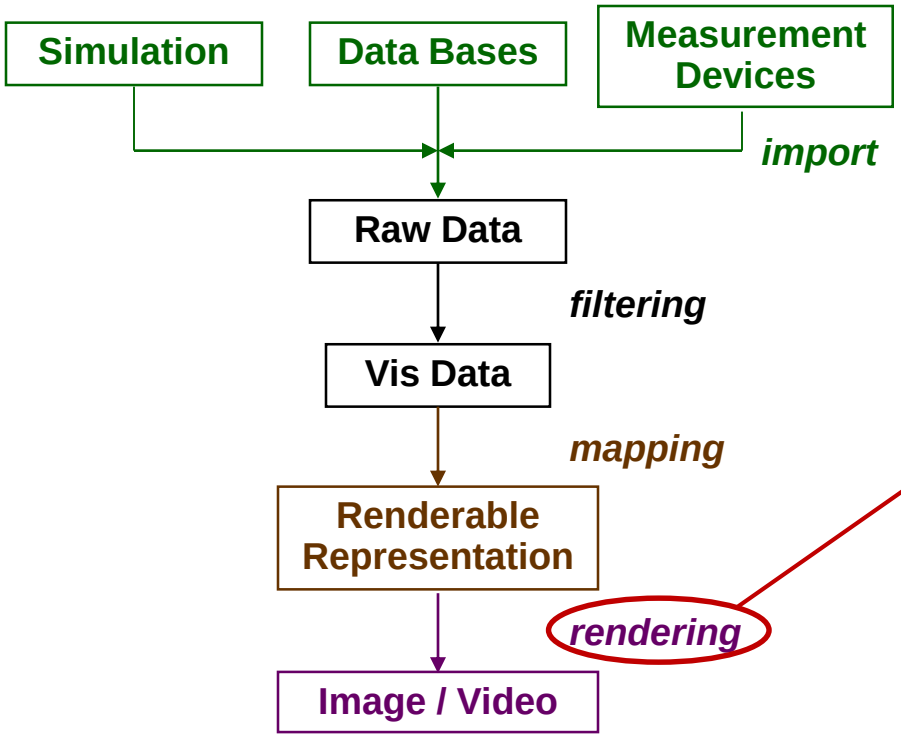


Filtering:
data → data
- aggregation
- denoising
- outlier removal

Mapping

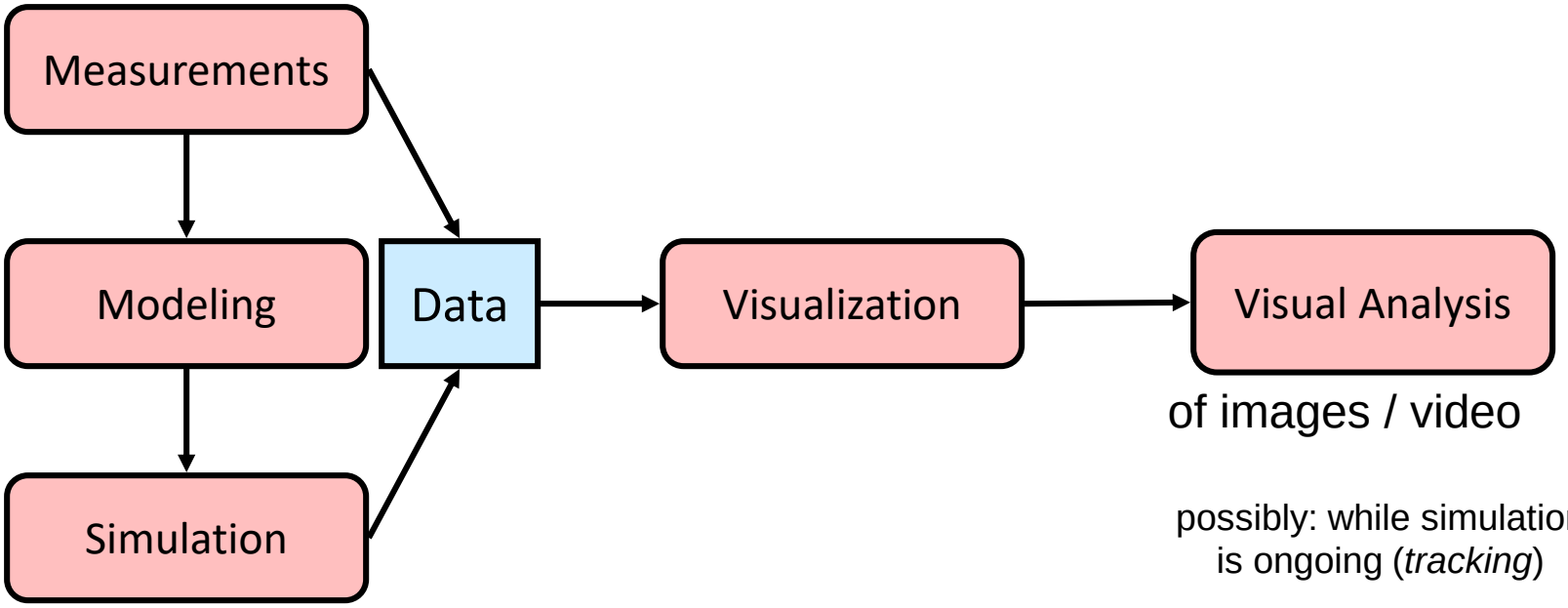

Simulation
Data Bases
Measurement Devices
import
Raw Data
filtering
Vis Data
mapping
Renderable Representation
rendering
Image / Video
primitives:
• points
• line segments
• triangles
visual attributes:
• color
• texture
• transparency
Mapping:
data → marks and channels
data → geometry
• glyphs
• volumes → shapes

Rendering

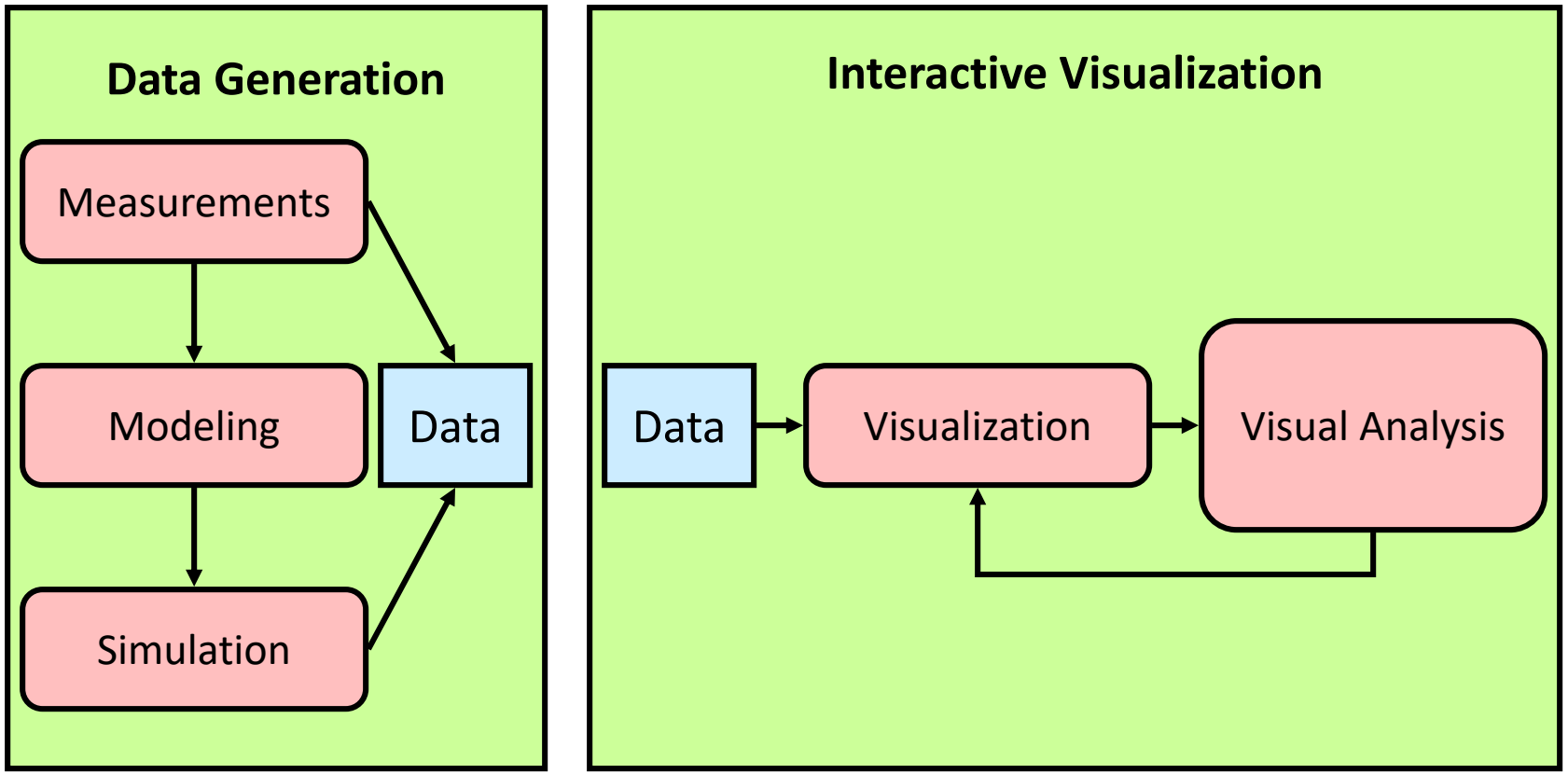


Rendering:
- Rasterization
- 3D Volume Rendering
- "realistic" rendering, e.g., shadows, lighting, shading
- "illustrative" rendering

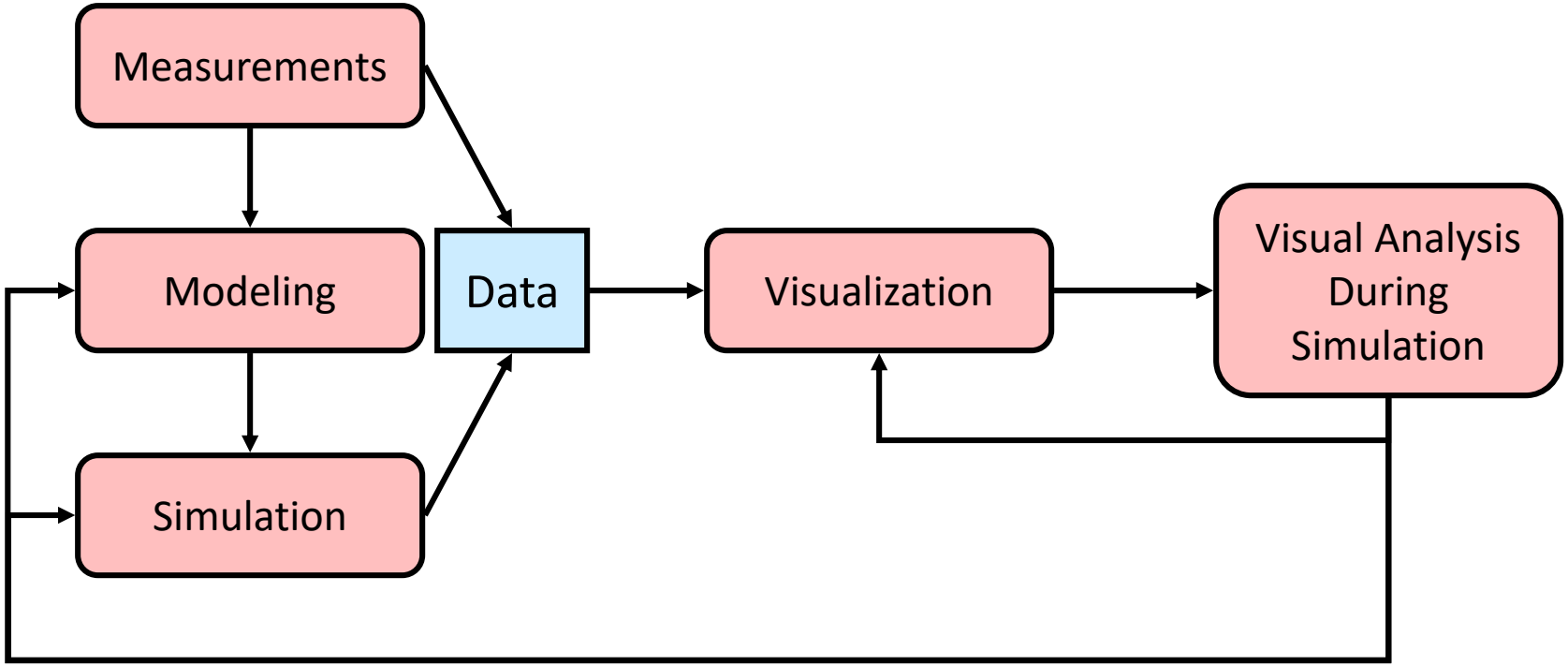
Non-Interactive Visualization



Interactive Visualization as Post-Process

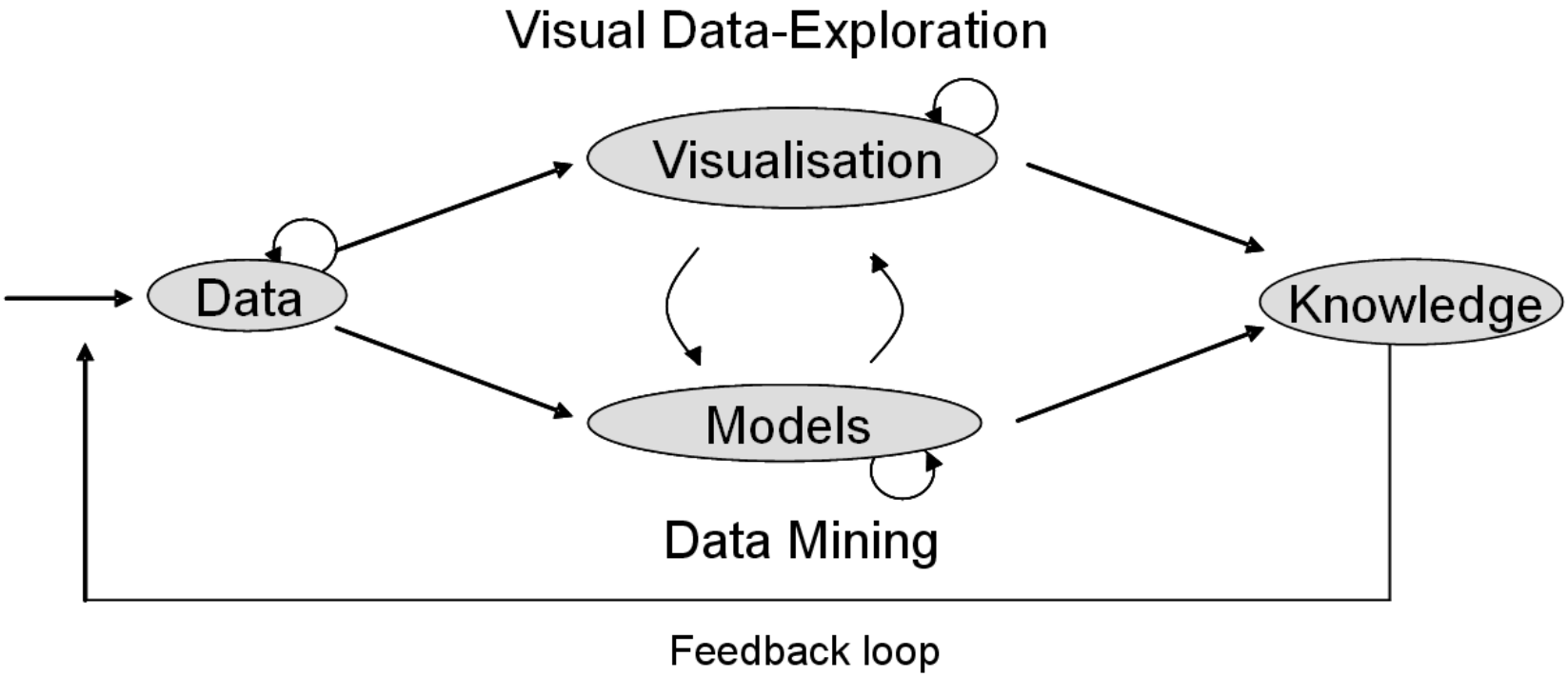


Computational Steering



Visual Analytics

- Source: Keim et al. 2008



Section 6.4:
Example System 1: Pathline

Pathline

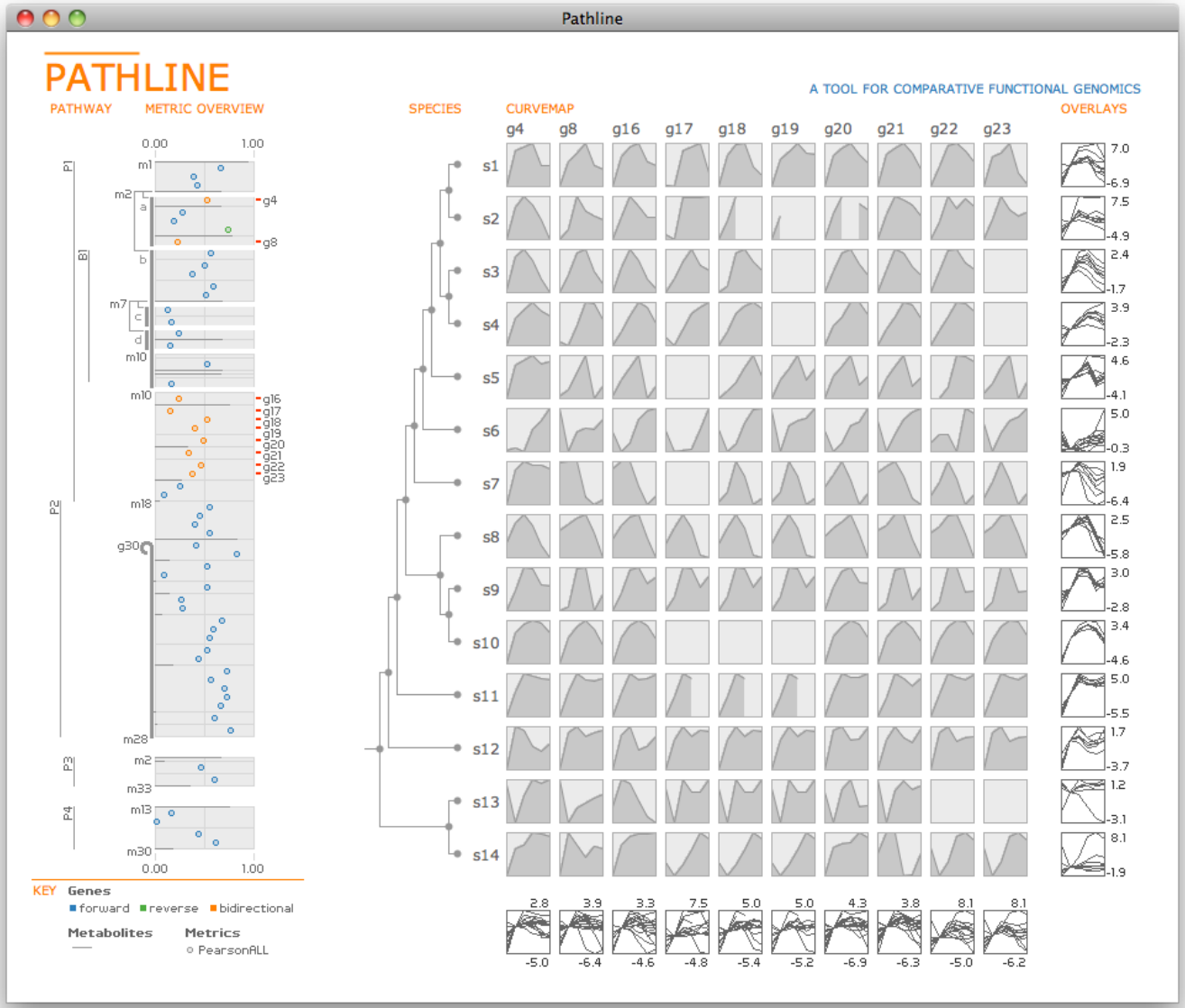
- Design study by [Meyer et al. 2010]
- **Comparative functional genomics**
  - How do gene regulation and metabolite levels in pathways evolve over time and across species?
- **Specific data:** 14 species of yeast
  - **Activity** of 6000 genes and **levels** of 140 metabolites at six points in time
  - **Metabolic pathways:** Directed graph (nodes: metabolites, edges annotated with genes)
  - **Similarity scores:** Similarities between time series measured by Pearson / Spearman correlation
  - **Phylogenetic relationship:** Tree (leaves: species) that shows differentiation of the species

Discover: Task Abstraction

- **High-level task:** Find commonalities and differences between species in the activation patterns of genes and metabolite levels
  - At which point in evolution were specific cellular processes and regulatory mechanisms introduced?
- **More specific tasks:**
  - Look for trends in a set of time series for a gene / metabolite across species
  - Look for trends across genes / metabolites in a set of time series within a species
  - Compare time series to find specific features (e.g., timing of peaks, clusters of time series etc.)

Design: Overview of System

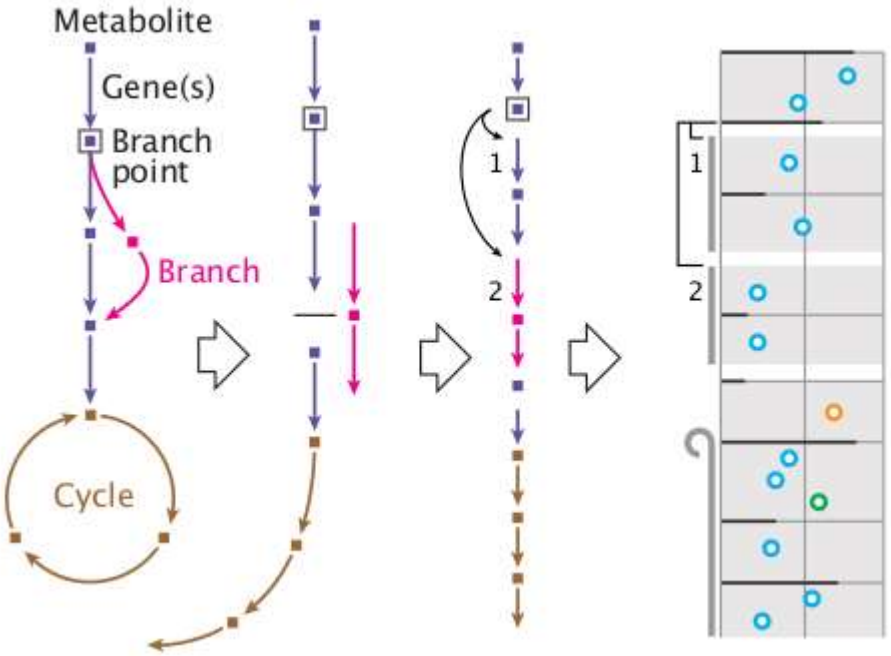
- **Two main views:** Linearized Pathways vs. Curvemap
- Can select genes for analysis in curvemap



Images from [Meyer et al. 2010]

Design: Linearized Pathways

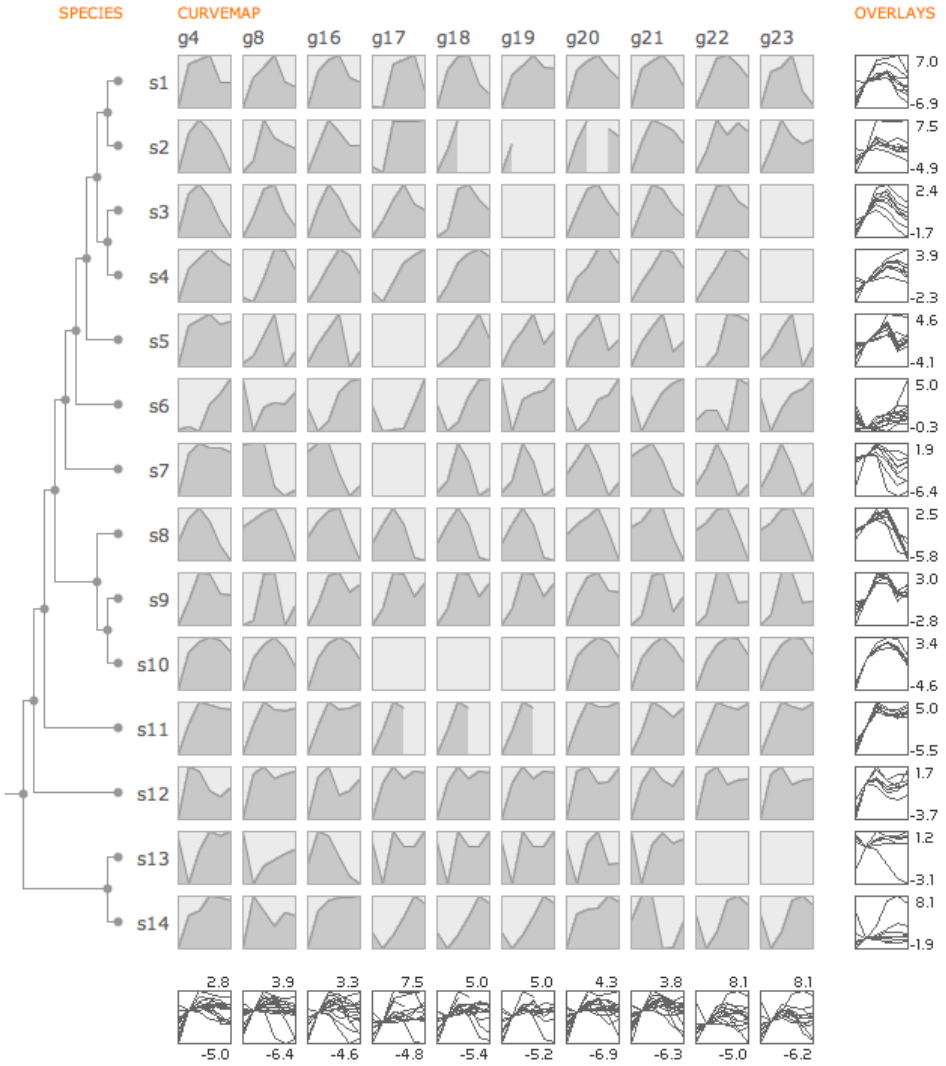
- **Goal:** Emphasize quantitative values along pathways, pathway topology is secondary
  - Unroll loops, disconnect and reinsert branches
  - Gaps indicate branches
  - Only include relevant genes / metabolites
  - Query user in case of ambiguities
  - Lines encode similarity scores of metabolites
  - Circles encode genes
  - Color indicates direction
  - Different pathways shown below each other



Images from [Meyer et al. 2010]

Design: Curvemap View

- **Matrix view,** curves in cells show protein expression / metabolite levels over time
  - Better than heat maps
- **Min/max normalization** per cell to make shape obvious
- **Aggregate views** for each row / column for more detailed comparison (incl. absolute levels)
- **Phylogenetic tree** shows how species relate



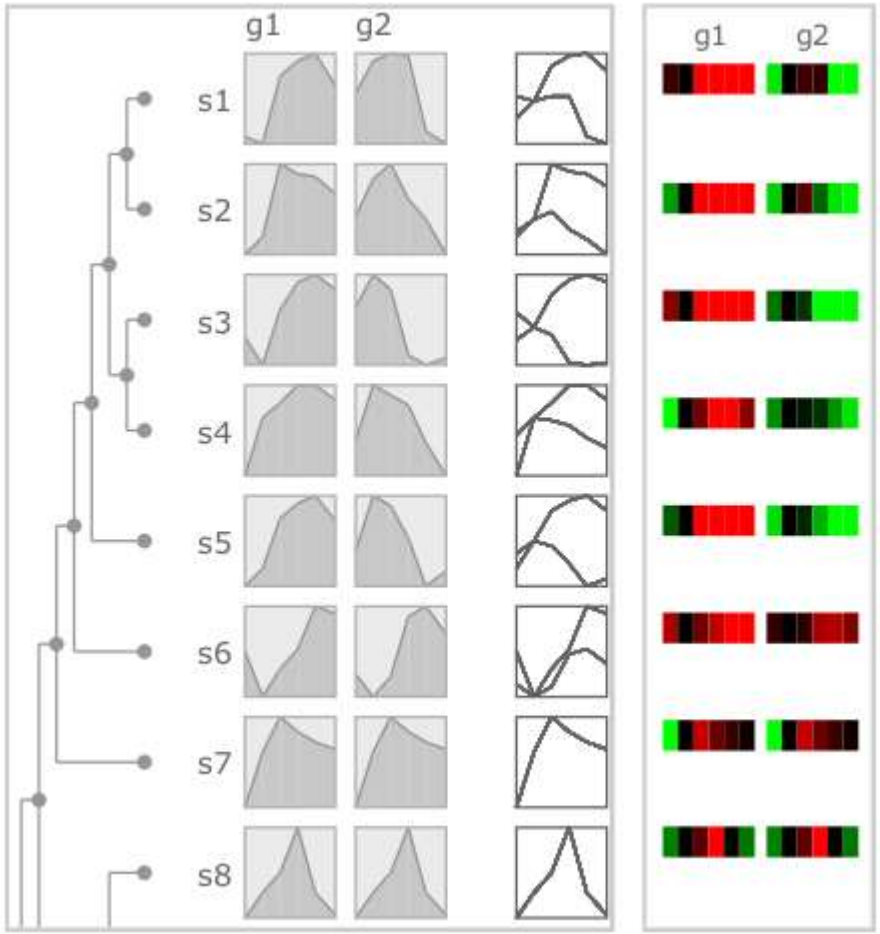
Images from [Meyer et al. 2010]

Implement

- **Interaction:**
  - Mousing over genes / metabolites in pathview shows names and numerical values
  - Clicking on them adds them to curvemap
  - Mousing over species / gene / metabolite highlights its curve in overlay plots

Deploy: Case Study 1

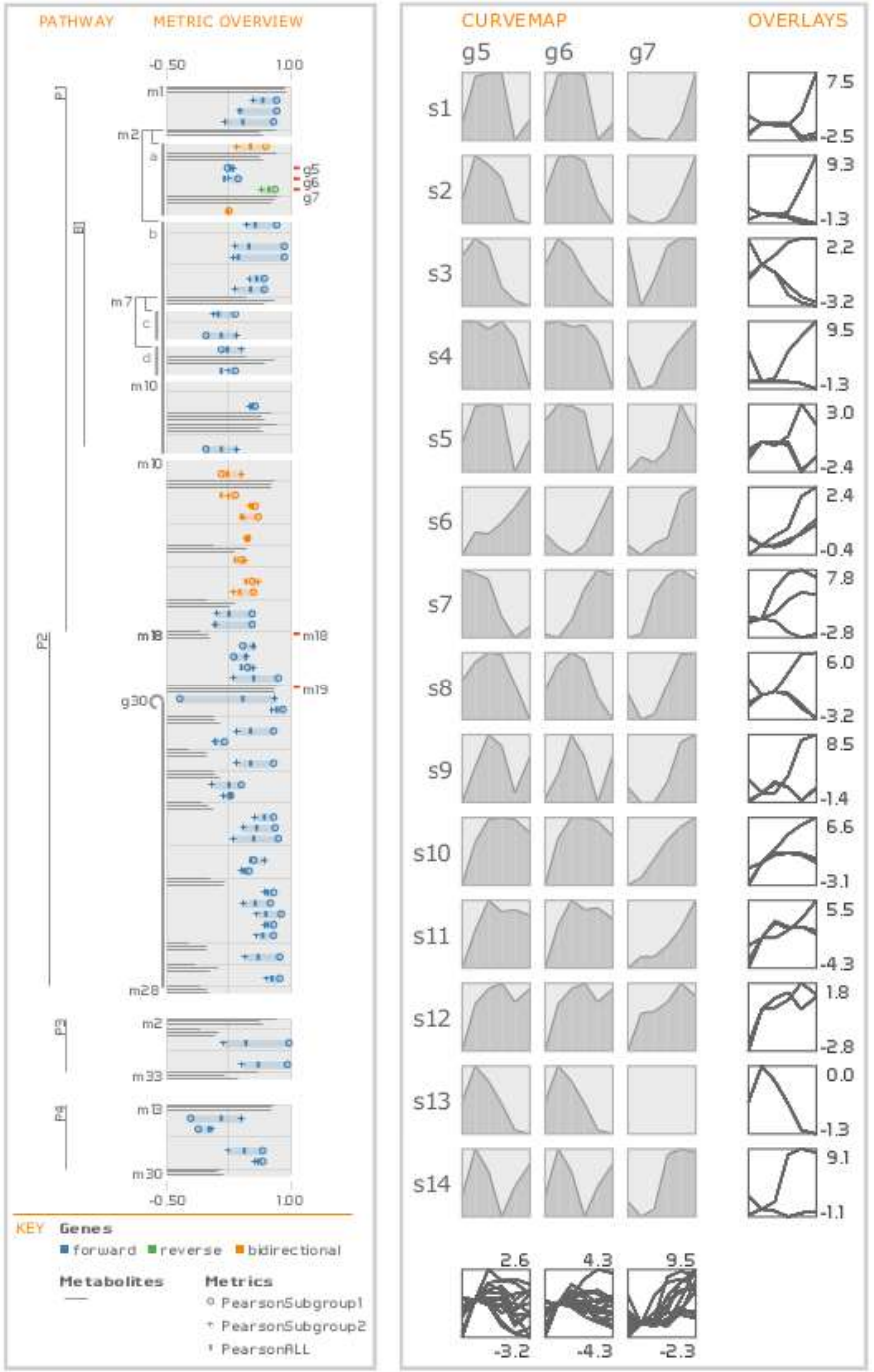
- Investigate **whole-genome duplication**
  - g1/g2 are duplicates in s1-s7
  - Curvemap clearly shows how different regulation mechanisms have evolved
  - Heat maps make it much more difficult to see this



Images from [Meyer et al. 2010]

Deploy: Case Study 2

- **Pathway analysis** (left)
  - Clear trend of reduced similarity in metabolites along the pathway
  - Trend suddenly reversed between m18 and m19
- **Gene-level analysis**
  - g5 and g6 strongly coupled, but time course varies across species
  - Discovered previously unknown gene duplication event in s7

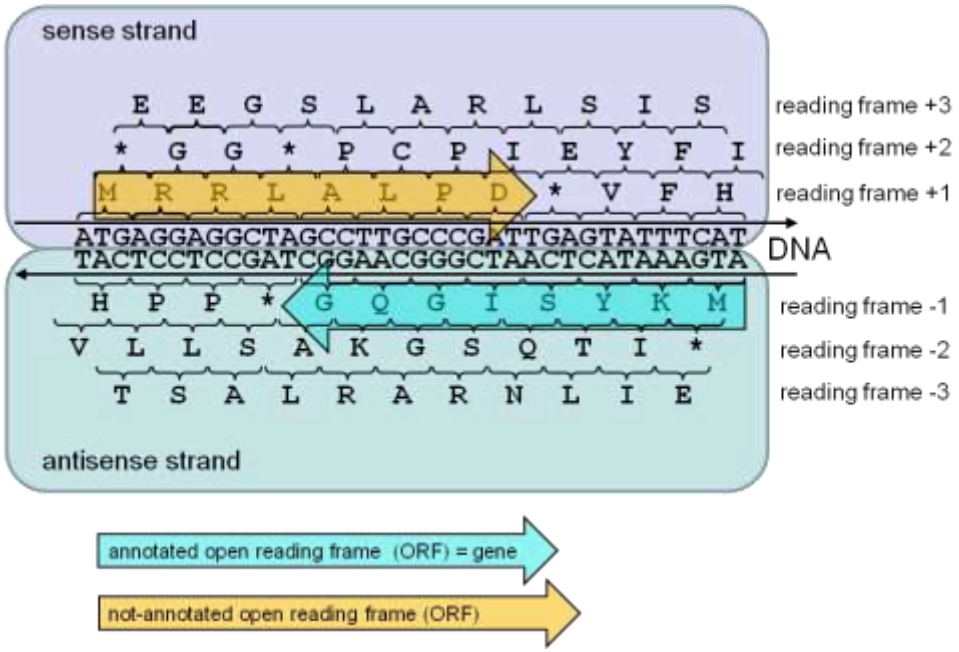


Images from [Meyer et al. 2010]

Section 6.5:
Example System 2:
Overlapping Gene Detection

Task: Discover Overlapping Genes

- Framework by [Simon et al. 2011]
- DNA double strands give rise to six reading frames:



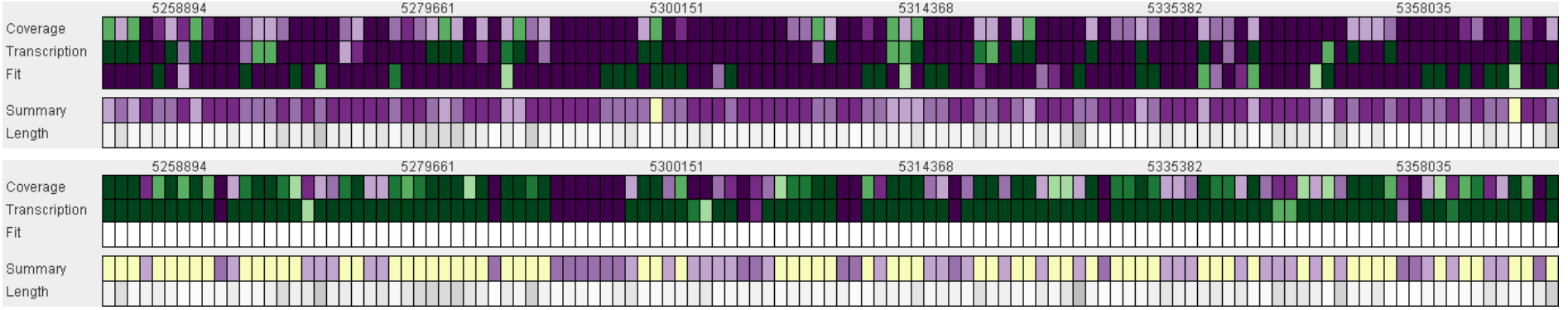
Images from [Simon et al. 2011]

- **Task:** Based on DNA & RNA sequencing, discover locations where genes overlap (e.g., sense and antisense strand encode different proteins)

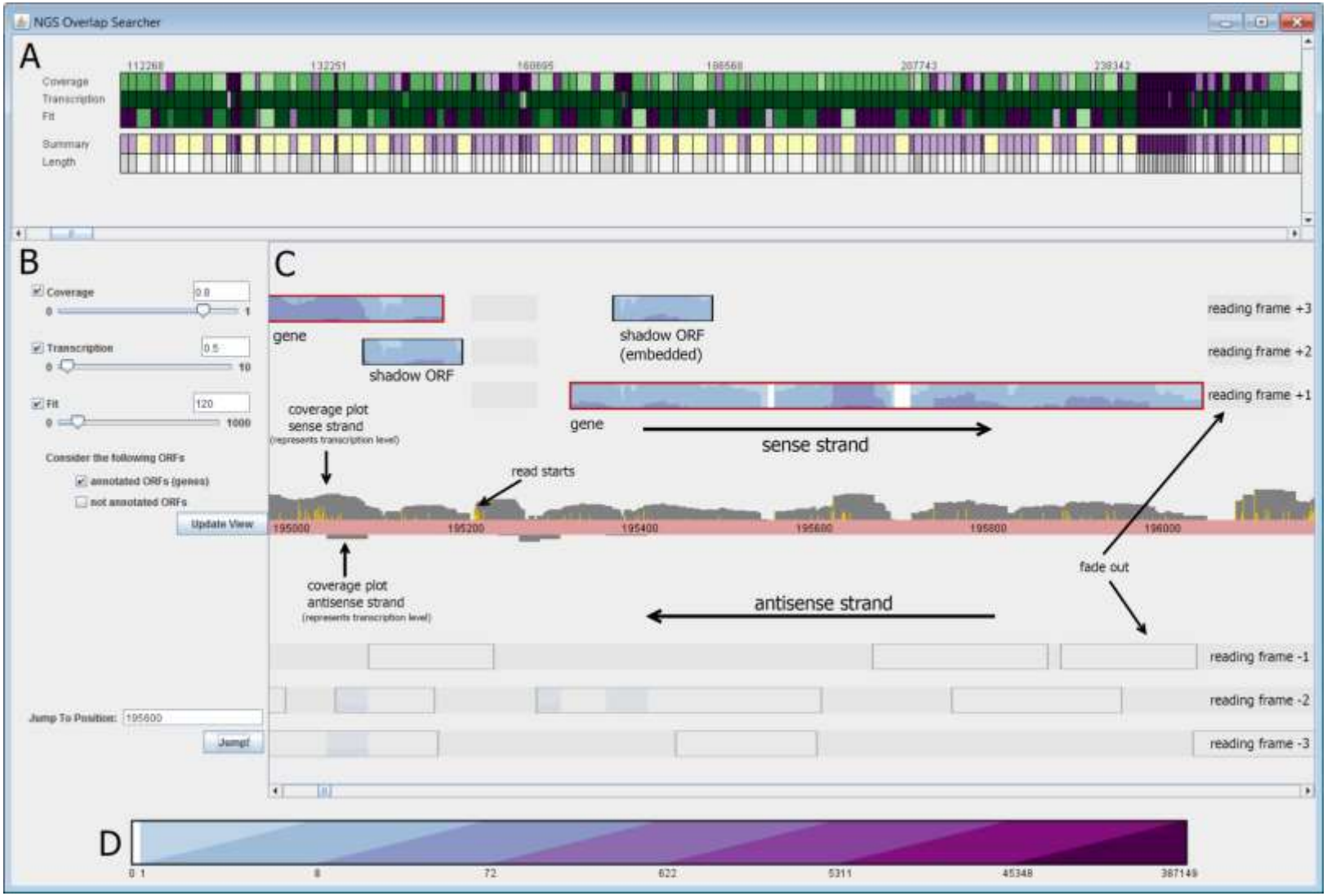
User-Defined Filters

- **Challenge:** Huge amount of data (2-200 Gbp) and open reading frames (ORFs), noisy data
  - Fully automated analysis impossible
  - Fully manual analysis impossible
- **Filter** ORFs based on three criteria:
  1. **Coverage:** Percentage of bases that has been counted at least once
  2. **Transcription:** Average counts per basis
  3. **Fit:** Difference between ORF and transcript lengths

Images from [Simon et al. 2011]

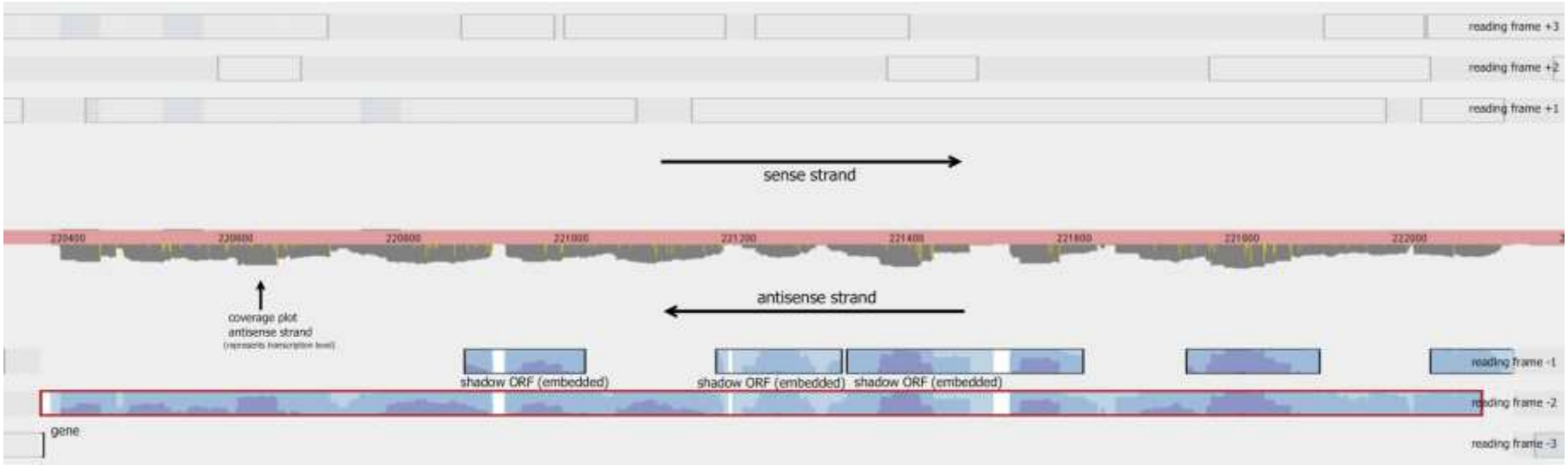


Visual Analytics Framework



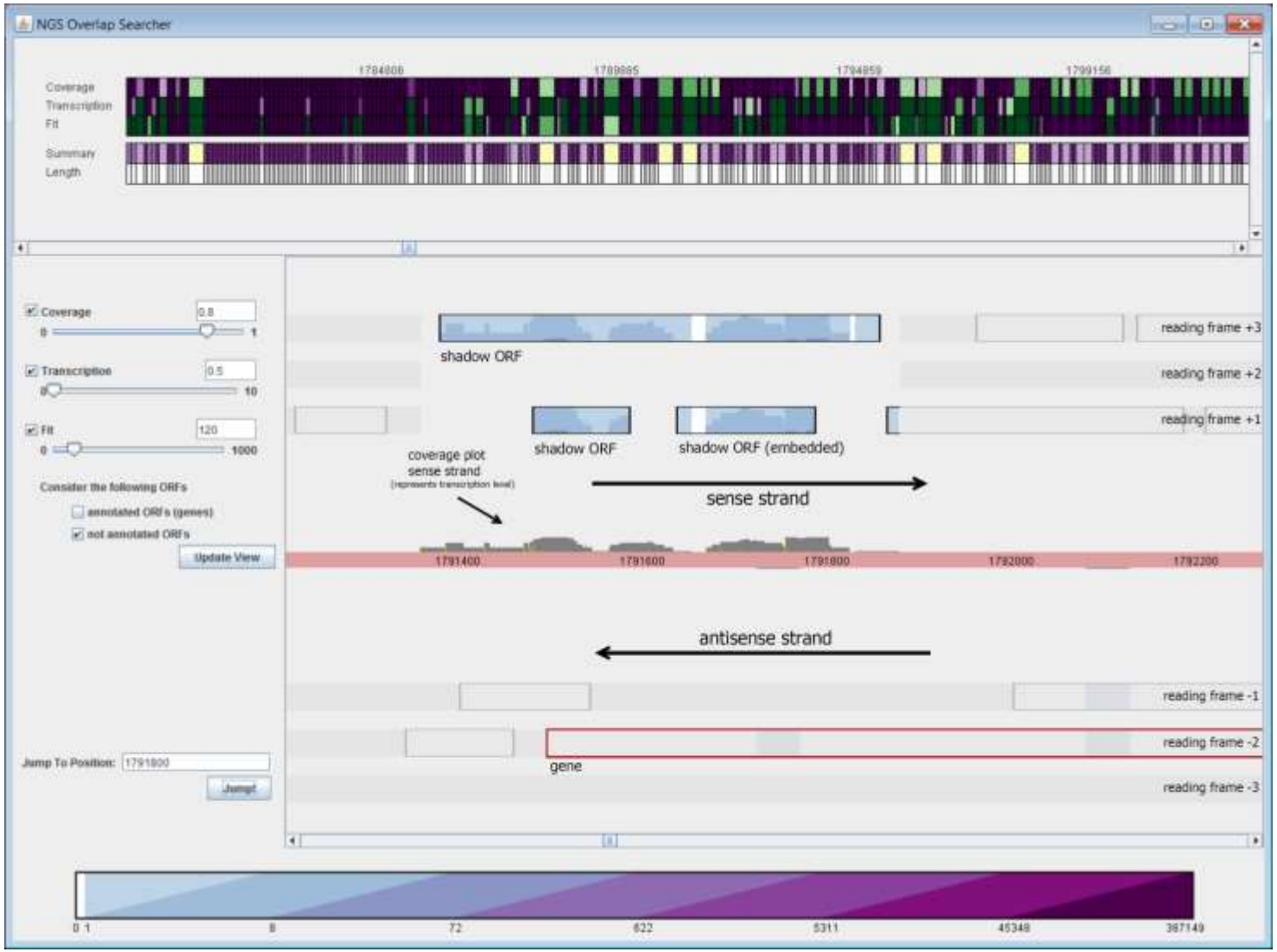
Images from [Simon et al. 2011]

Example Result 1: Known Gene



Images from [Simon et al. 2011]

Example Result 2: Pot. Overlapping Gene



Images from [Simon et al. 2011]

Summary of Chapter 6

- Topics of **Chapter 6** were:
  - Visualization Design Process
  - Classification of Marks and Channels
  - Visualization Pipelines
  - Example Systems: Pathline / OLG Detection
- **Concludes first part of lecture:** How to use visualization for data analysis

References

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- Simon et al., **Visual Analysis of Next-Generation Sequencing Data to Detect Overlapping Genes in Bacterial Genomes,** BioVis 2011