

EuroVis 2015

The EG / VGTC
Conference on
Visualization



25 - 29

May



Cagliari / Sardinia / Italy

Card Sorting Techniques for Domain Characterisation in Problem-driven Visualization Research

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KU Leuven, Belgium

KU LEUVEN



STADIUS

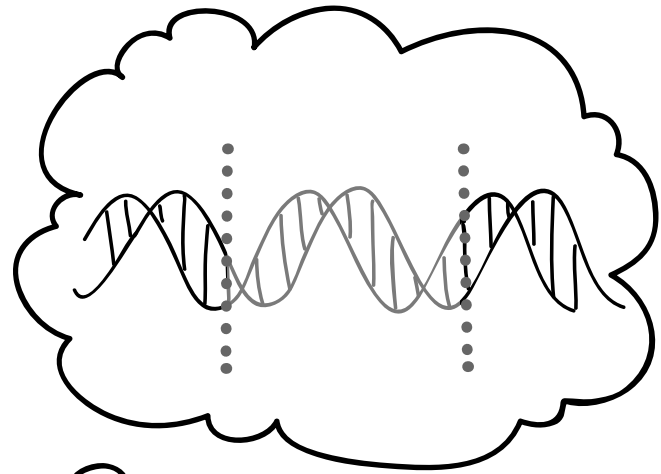
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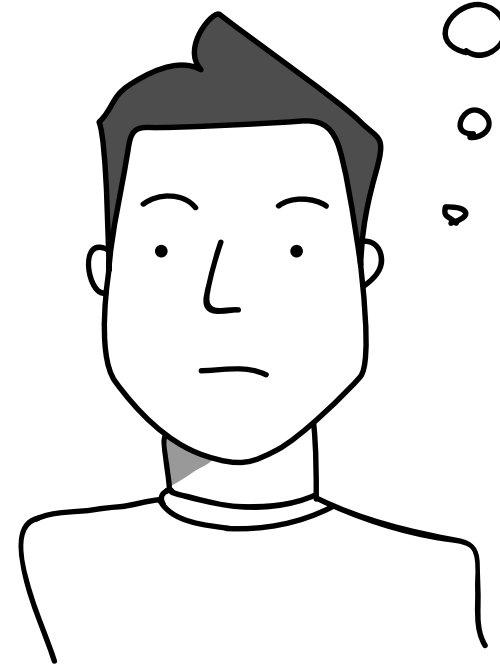
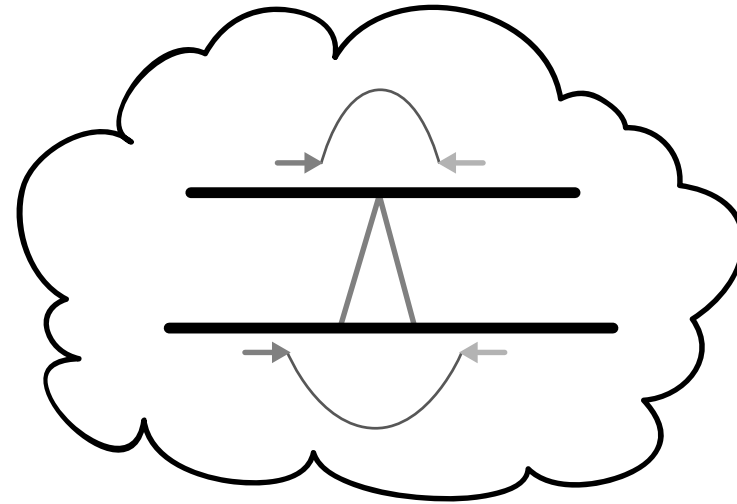
Domain characterization is not easy.

Challenges

1. Domain-specific knowledge
2. Exploratory tasks
3. Establish a shared understanding of the domain problem and analysis needs
4. Foster creative thinking



vis designer



domain expert

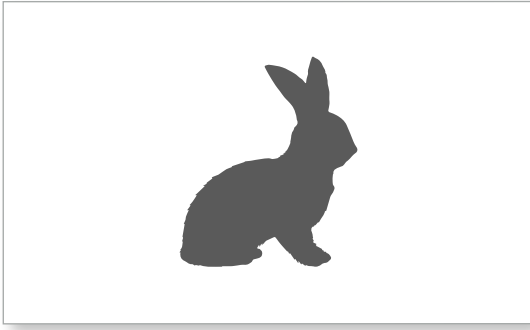
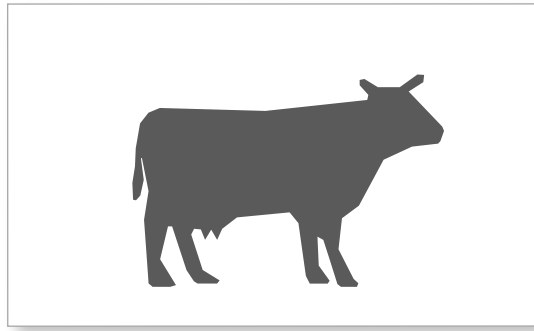
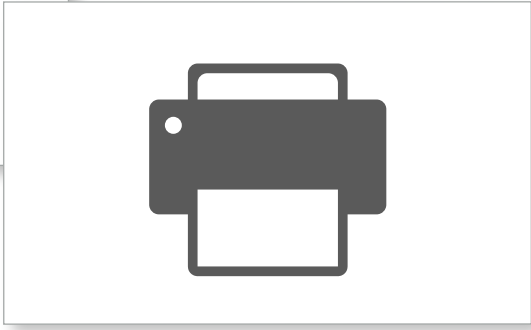
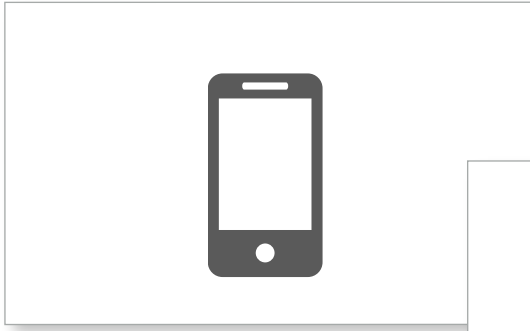
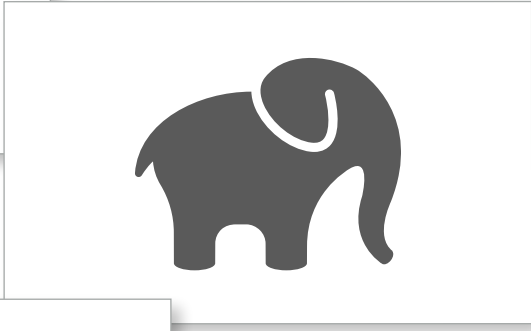
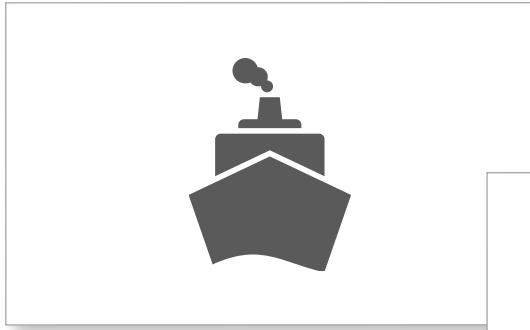
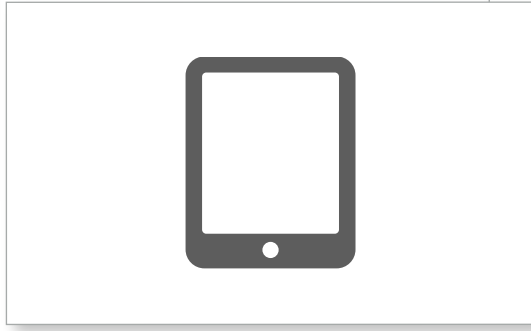
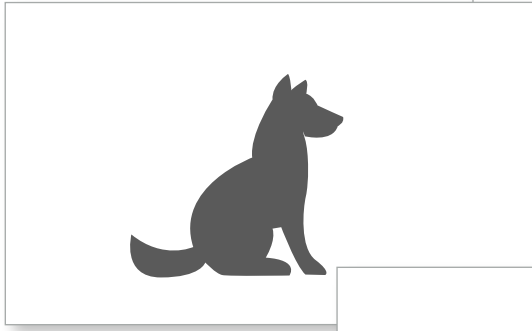
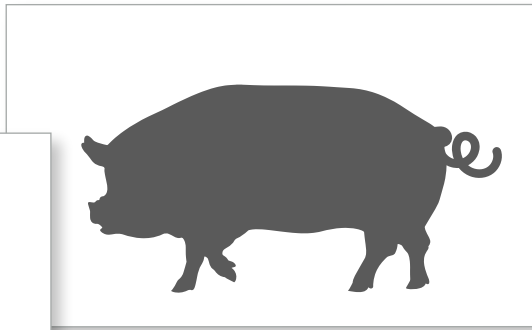
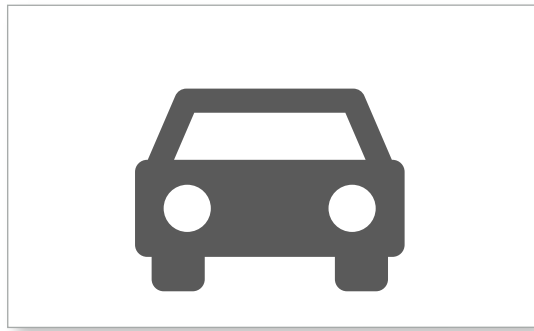
Card sorting

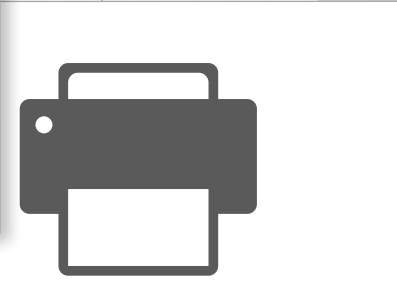
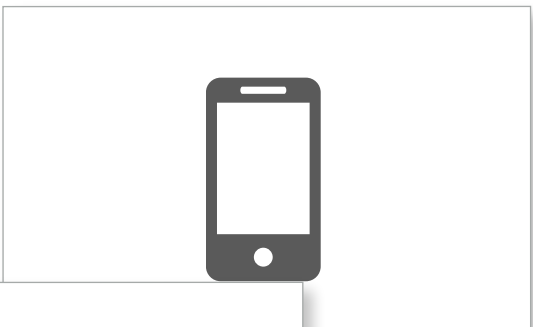
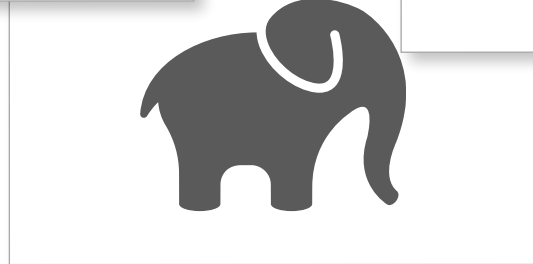
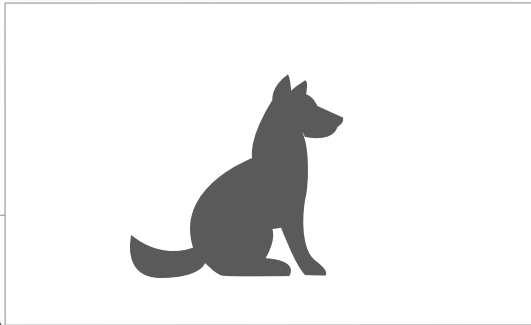
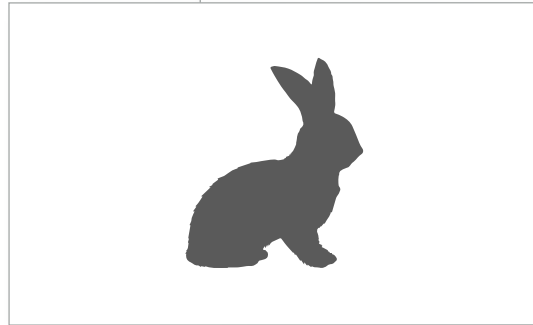
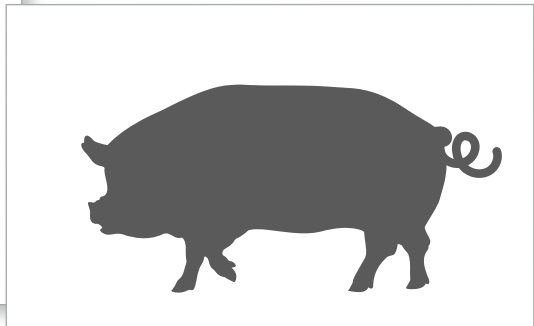
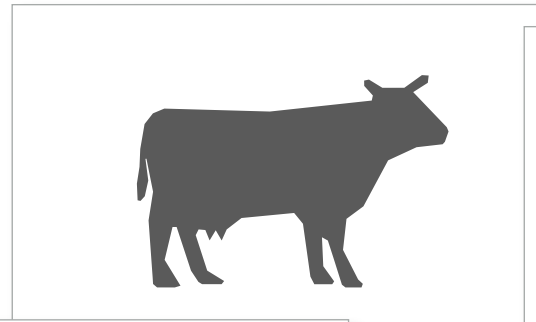
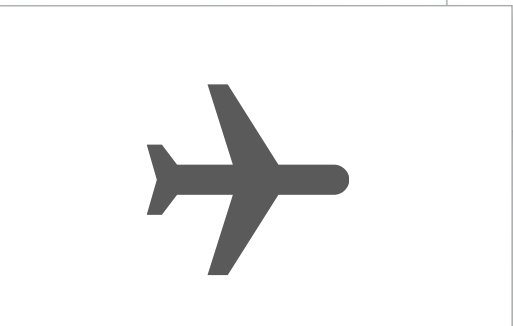
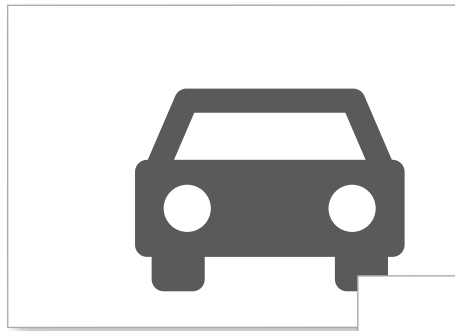
Related works in VIS

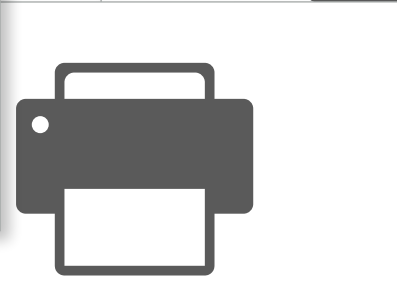
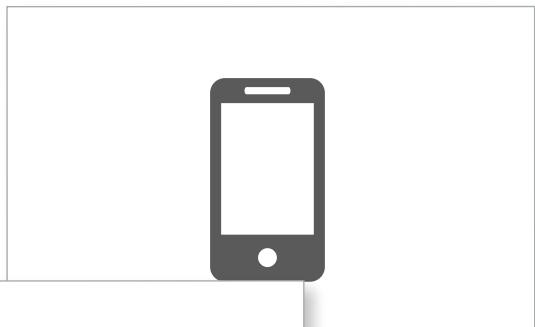
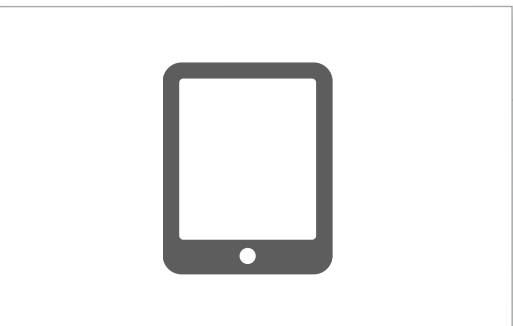
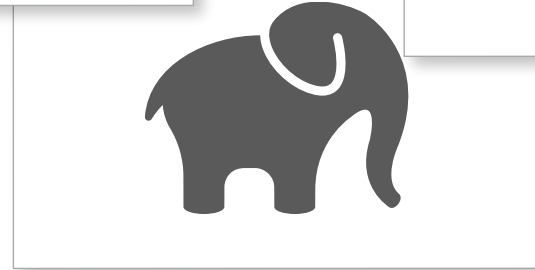
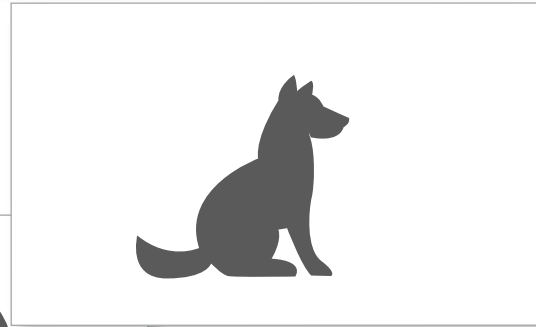
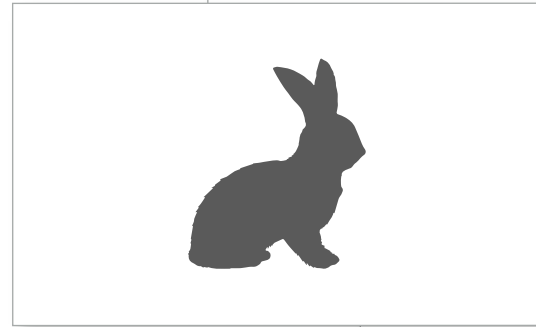
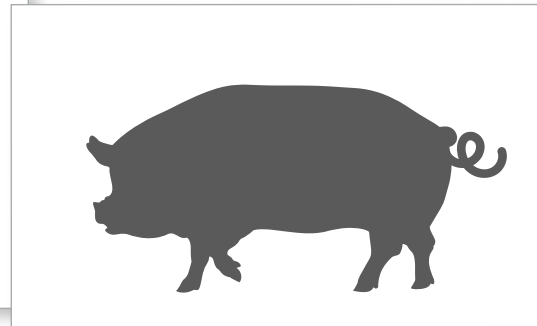
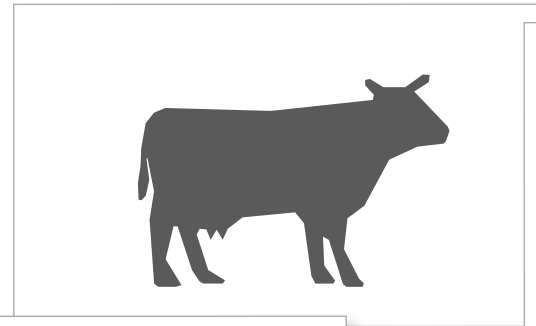
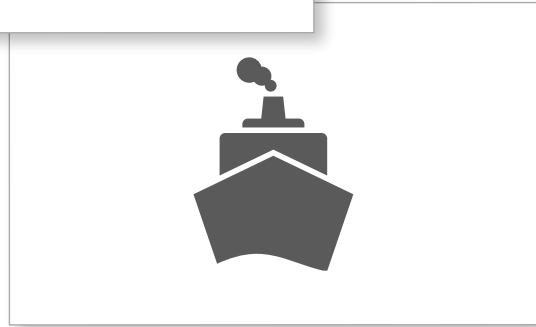
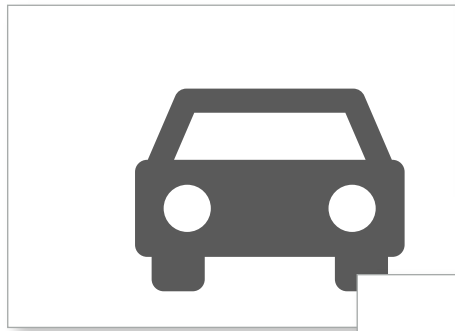
- [1] D. Lloyd and J. Dykes, “Human-centered approaches in geovisualization design: Investigating multiple methods through a long-term case study,” *IEEE Trans. Vis. Comput. Graph.*, vol. 17, no. 12, pp. 2498–2507, 2011.
- [2] S. McKenna, D. Mazur, J. Agutter, and M. Meyer, “Design activity framework for visualization design,” To Appear *IEEE TVCG (Proc. InfoVis)*, vol. 20, no. 12, pp. 2191–2200, 2014.

More in CS and HCI

see our paper...









Transportations



Animals



Technology



Drinks

Card sorting

1. *Open* card sorting

- ♦ goal: to elicit tacit categorisation of items
- ♦ generative

Technology

Transportations

Animals

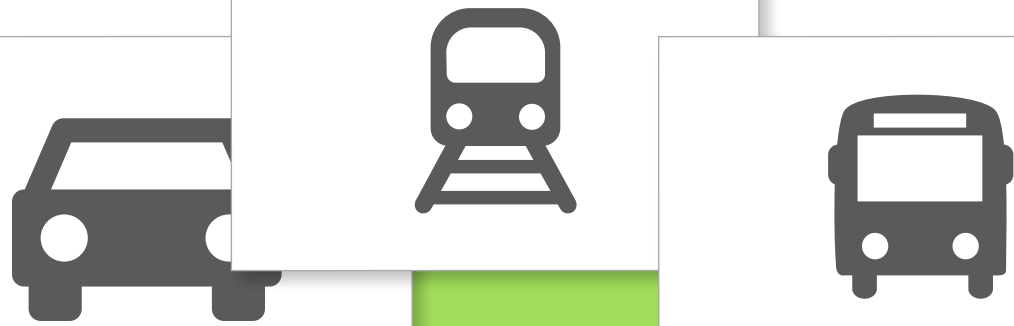
Drinks

Transportations

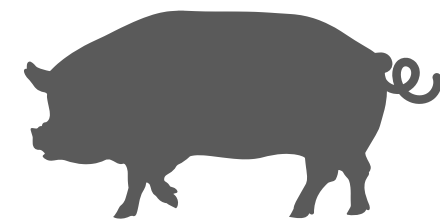
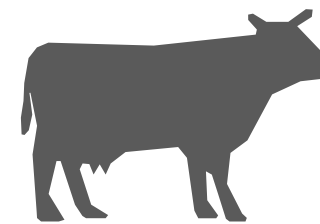
Animals

Technology

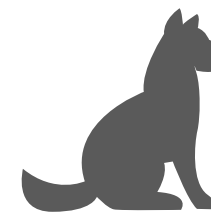
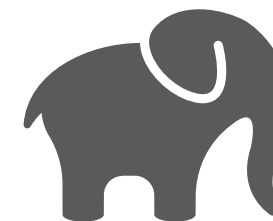
Drinks



Transportations



Animals



Technology



Drinks



Card sorting types

1. *Open* card sorting

- ♦ goal: to elicit tacit categorisation of items
- ♦ generative

2. *Closed* card sorting

- ♦ goal: to evaluate the assignment of items to categories
- ♦ evaluative

Step 1: Preparation

Step 1: Preparation

inquiry-based cards

Are there any disrupted or deleted genes?

mic
calized?

ic and
le?

samples?

tion:

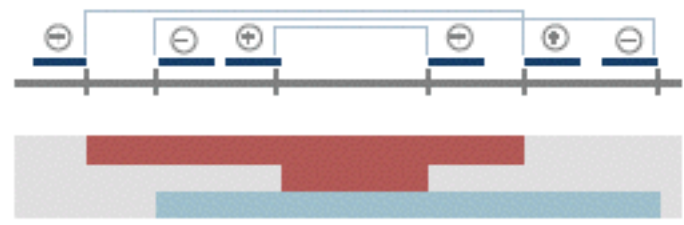
Step 1: Preparation

inquiry-based cards

| | |
|---|-----------------|
| Are there any disrupted or deleted genes? | mic calized? |
| | |
| | ic and le? |
| | |
| samples? | tion: |
| | |
| | |

picture cards

complex



new visual encoding ideas

Progressive rearrangements model

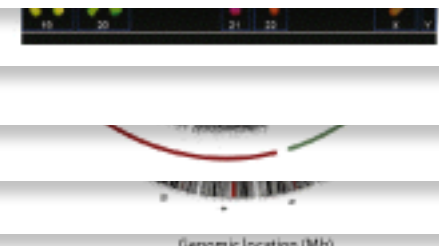
Germline
A B C D E F G H I J

Tandem duplication CDEF
A B C D E F C D E F G H I J

Inversion EFGH
A B C D E F C D H G F E I J

Deletion EI
A B C D E F C D H G F J

Tandem duplication BC
A B C B C D E F C D H G F J



Genomic location (Mb)

from literature

Step 1: Preparation

inquiry-based cards

Q1

omic
calized?

ic and
le?

samples?

tion:

picture cards

V1

new visual encoding ideas

Progressive rearrangements model

Germline
A B C D E F G H I J

Tandem duplication CDEF
A B C D E F C D E F G H I J

Inversion EFGH
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Deletion EI
A B C D E F C D H G F J

Tandem duplication BC
A B C B C D E F C D H G F J

Genomic location (Mb)

from literature

Step 2: Execution

1. open card sorting by yourself
2. repeat with the same/different cards with the same/different user
 - ♦ “front-line analyst” vs. “gate keeper” [Sedlmair et al. 2012]

Step 3: Analysis

1. careful observation during the sorting exercise
2. analysis of criteria and categories (open)
3. analysis of assigned cards (open/close)

Case study

- Structural variations of human cancer genome
- user: computational biologists

| | 1 | 2 | 3 | 4 |
|--------|----------|---------|---------|---------|
| who: | designer | user | user | user |
| type: | open | open | closed | closed |
| cards: | inquiry | inquiry | inquiry | picture |

| | 1 | 2 | 3 | 4 |
|--------|----------|---------|---------|---------|
| who: | designer | user | user | user |
| type: | open | open | closed | closed |
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| cards: | inquiry | inquiry | inquiry | picture |

Genomic
Resolution

Genome

Chromosome

Segment

Feature

M. Meyer, T. Munzner, and H. Pfister, "MizBee: A multiscale synteny browsers," in IEEE Transactions on Visualization and Computer Graphics, 2009, vol. 15, no. October, pp. 897–904.

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|--------|----------|---------|---------|---------|
| who: | designer | user | user | user |
| type: | open | open | closed | closed |
| cards: | inquiry | inquiry | inquiry | picture |

Process

Primary
Analysis

In depth
Analysis

Impact
Validation

| | | | | |
|------|----------|------|------|------|
| | 1 | 2 | 3 | 4 |
| who: | designer | user | user | user |

chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr20 chr21 chr22 chrX

10Mb

147570160

158494016

147765232

9753436bp

158298944

ID:215



Structural Variation deletion inversion probable-inversion tandem-duplication distal-duplication complex

P

| | 1 | 2 | 3 | 4 |
|--------|----------|---------|---------|---------|
| who: | designer | user | user | user |
| type: | open | open | closed | closed |
| cards: | inquiry | inquiry | inquiry | picture |

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Genomic
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Chromosome

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Feature

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|--------|----------|---------|---------|---------|
| who: | designer | user | user | user |
| type: | open | open | closed | closed |
| cards: | inquiry | inquiry | inquiry | picture |

Genomic Resolution

Genome

How does the pattern of structural variation compare between the reference genome and tumour sample?

Chromosome

How does the pattern of SV compare between the normal and the tumour samples?

Segment

What is the sequence of structurally altered region?

Feature

Are there any exonic deletion or duplications?

| | 1 | 2 | 3 | 4 |
|--------|----------|---------|---------|---------|
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Genomic Resolution

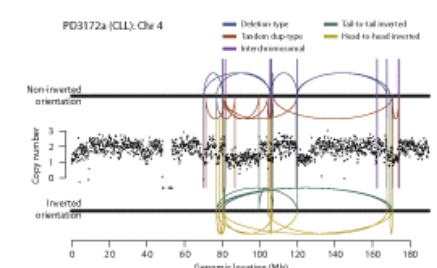
Genome

How does the pattern of structural variation

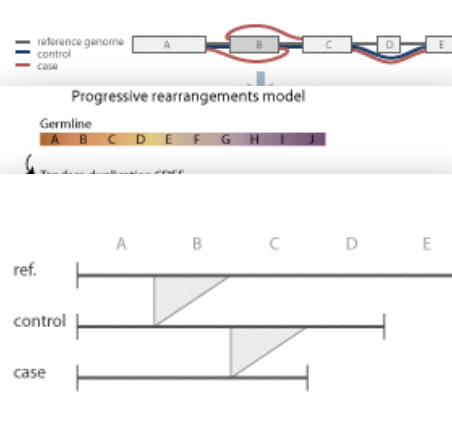


Chromosome

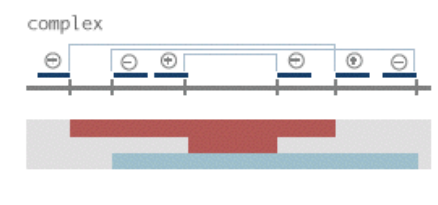
How does the pattern of SV compare between the

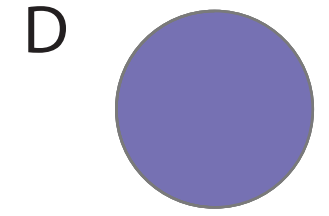
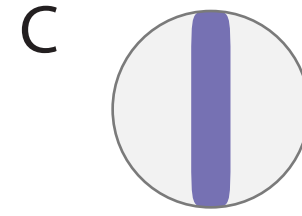
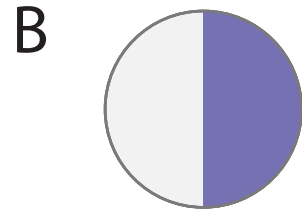
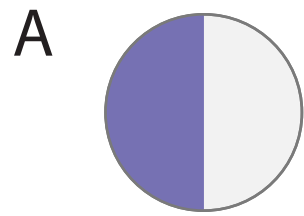


Segment



Feature

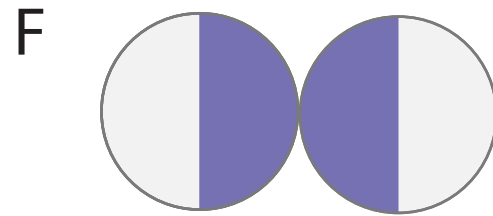
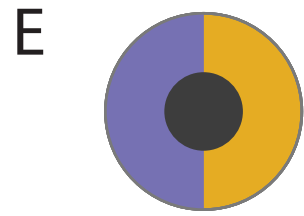




gene



SV event



gene



SV events



case

R. Sakai, M. Moisse, J. Reumers, and J. Aerts, "Pipit: visualizing functional impacts of structural variations.," *Bioinformatics*, vol. 29, no. 17, pp. 2206–7, Sep. 2013.

Take home message

1. Card sorting is a simple and flexible method.
2. Card sorting exercises can be *generative* or *evaluative*.
3. The distilling process of card preparation helps to understand the context as well as the relationships of analysis tasks.
4. Card sorting can be useful for the domain characterisation in a problem-driven visualization research.

Acknowledgements

Dept. of Oncology, KU Leuven

Matthieu Moisse

Joke Reumers

KU LEUVEN



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Thank you!