

# Machine learning with ontologies

## Semantic similarity

- We want to use *background knowledge* in ontologies to
  - ▶ determine similarity between classes,
  - ▶ instances,
  - ▶ and entities with ontology annotations

# How to measure similarity?

- semantic similarity measures similarity between classes
- semantic similarity measures similarity between instances of classes
- semantic similarity measures similarity between entities *annotated* with classes
- $\Rightarrow$  reduce all of this to similarity between classes

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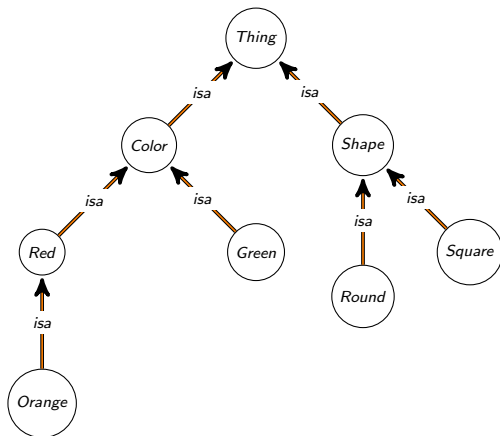
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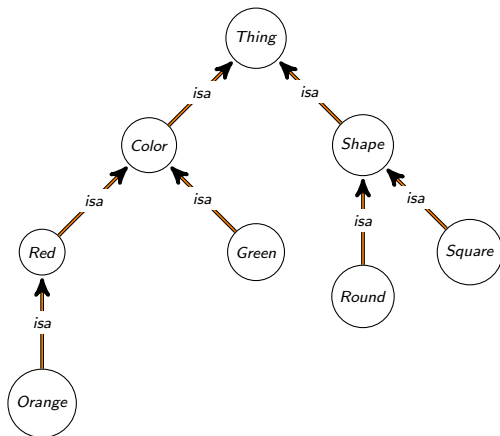
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- $sim$  is a *normalized* similarity measure if it has values in  $[0, 1]$

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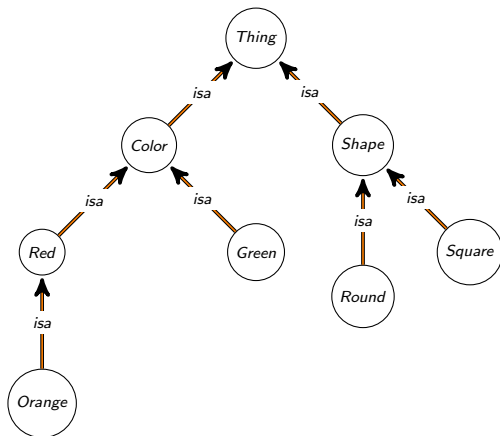


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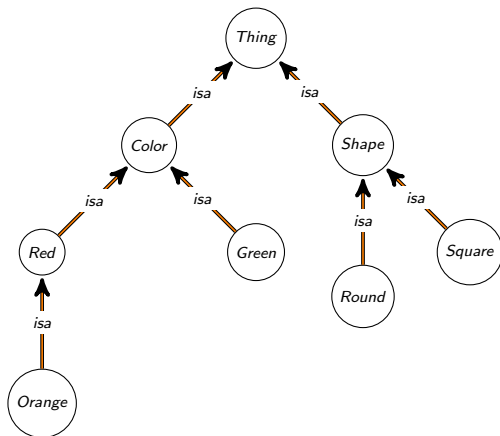
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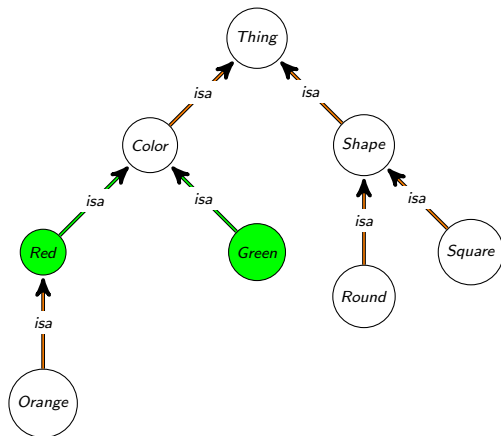
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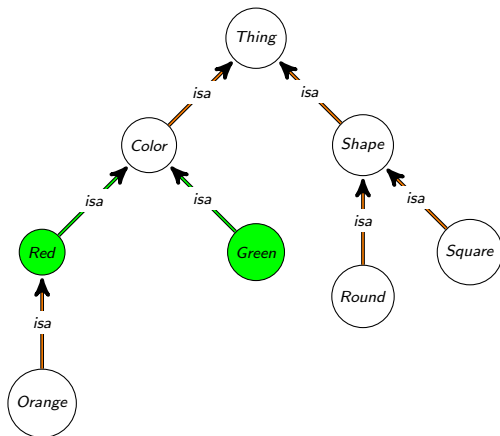
- distance on shortest path (Rada *et al.*, 1989)
- $dist_{Rada}(u, v) = sp(u, isa, v)$
- $sim_{Rada}(u, v) = \frac{1}{dist_{Rada}(u, v) + 1}$

# How to measure similarity?



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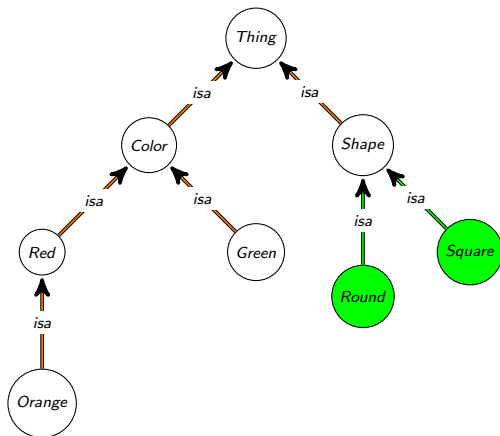
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- distance on shortest path
- $\text{distance}(\text{green}, \text{red}) = 2$
- $\text{sim}_{\text{Rada}}(\text{green}, \text{red}) = \frac{1}{3}$



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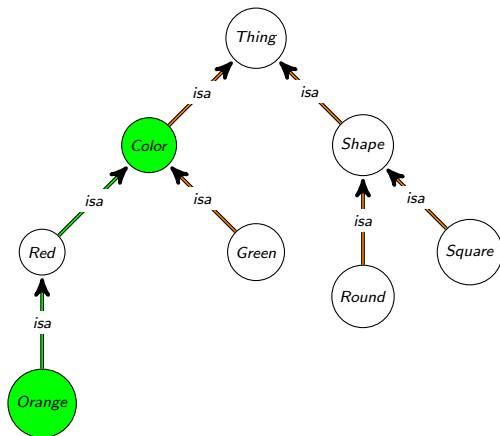
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- *density* of a branch in the ontology
  - ▶ number of siblings
  - ▶ information content
- account for different edge types
  - ▶ non-uniform edge weighting

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- ▶  $\sigma(x) = f(A(x))$  (for ancestors  $A(x)$ )

- ▶  $\sigma(x) = f(D(x))$  (for descendants  $D(x)$ )

- ▶ many more, e.g., Zhou et al.:

$$\sigma(x) = k \cdot \left(1 - \frac{\log |D(x)|}{\log |C|}\right) + (1 - k) \frac{\log \text{depth}(x)}{\log \text{depth}(G_T)}$$



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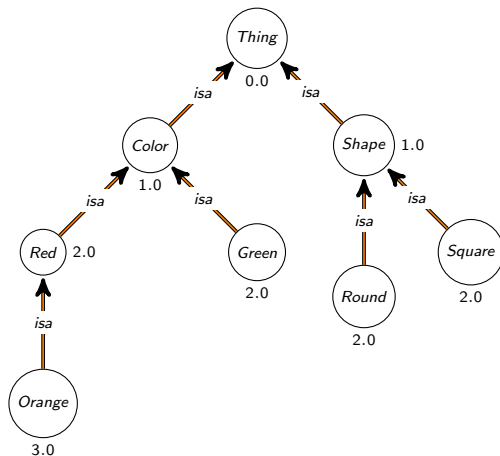
- ▶  $\sigma(x)$  defined as a function of instances (or annotations)  $I$

- ▶ note: the number of instances monotonically decreases with increasing depth in taxonomies

- ▶ Resnik 1995:  $e/C_{\text{Resnik}}(x) = -\log p(x)$  (with  $p(x) = \frac{|I(x)|}{|I|}$ )

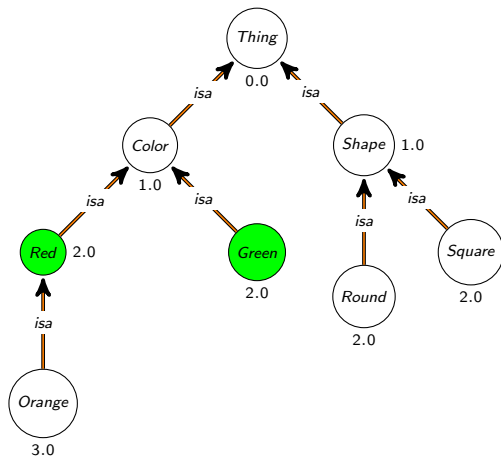
- ▶ in biology, one of the most popular specificity measure when annotations are present

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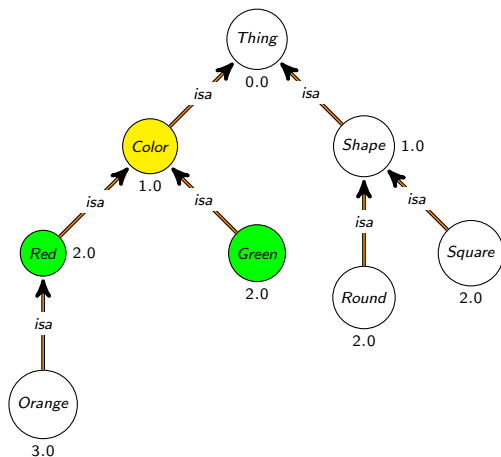
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similarity between  $x$   
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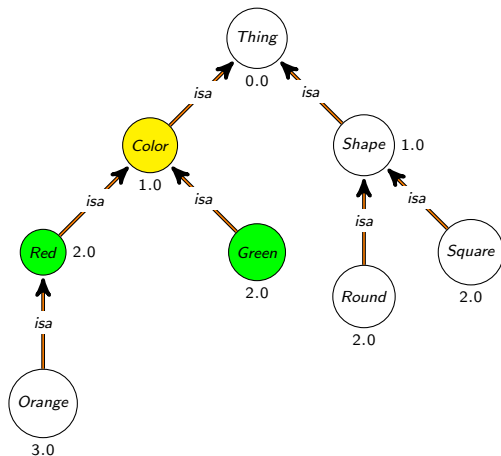
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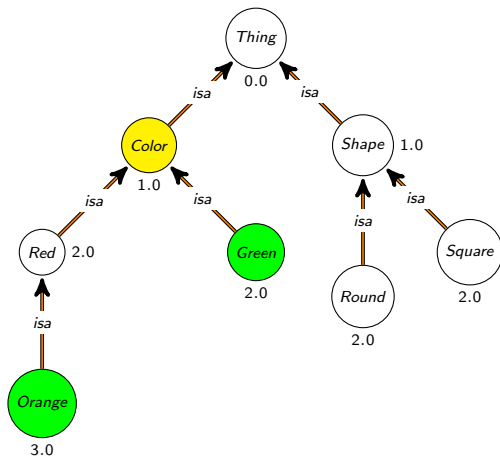
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- $$\text{sim}_{\text{Resnik}}(\text{Green}, \text{Red}) = 1.0$$

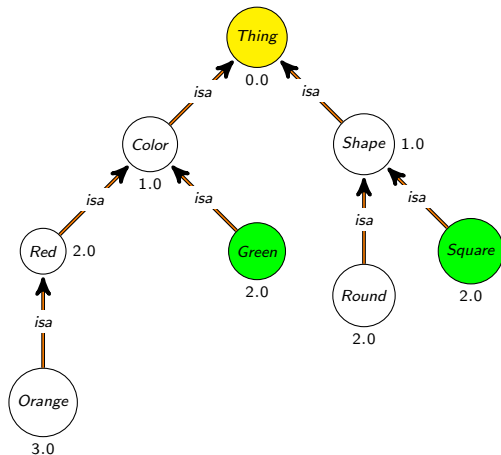
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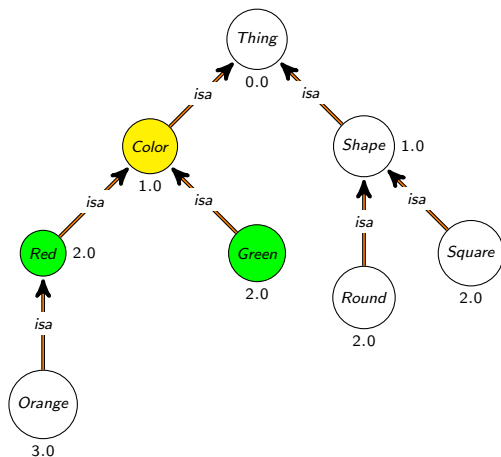
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similarity between  $x$  and  $y$  is the information content of the *most informative common ancestor*
- $sim_{Resnik}(Square, Orange)$   
0.0

# How to measure similarity?

- (Red, Green) and (Orange, Green) have the same similarity
- need to incorporate the specificity of the compared classes



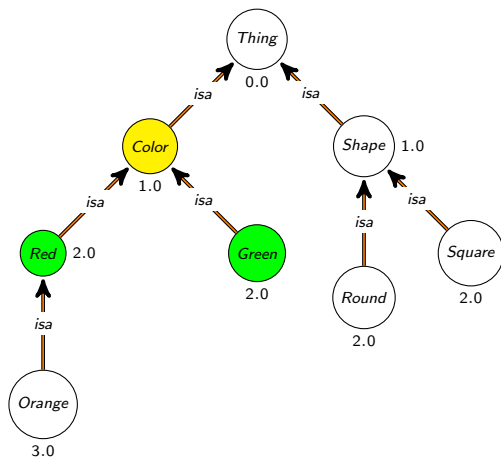
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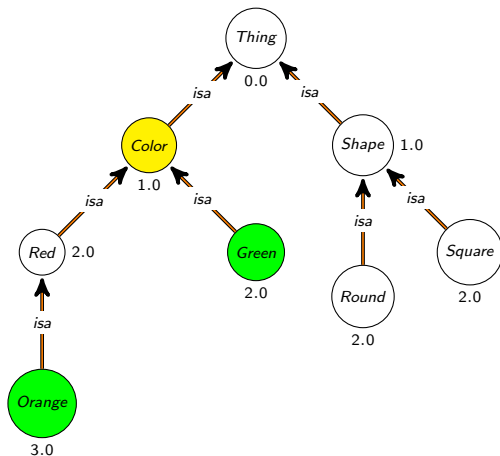
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$$sim_{Lin}(x, y) = \frac{2 \cdot IC(MICA(x, y))}{IC(x) + IC(y)}$$

- $sim_{Lin}(Green, Orange) = 0.4$

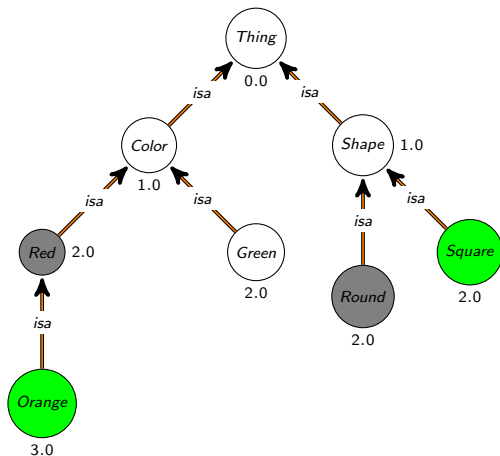
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- many(!) others:
  - ▶ Jiang & Conrath 1997
  - ▶ Mazandu & Mulder 2013
  - ▶ Schlicker et al. 2009
  - ▶ ...

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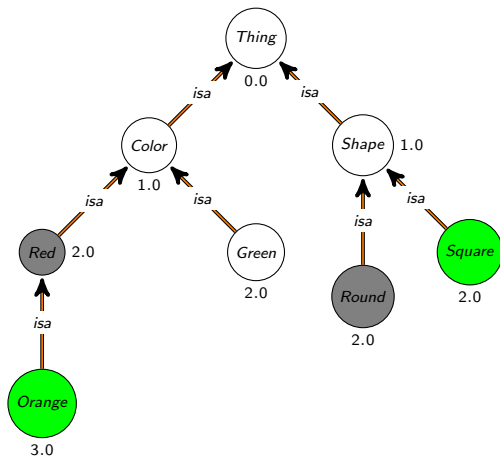
- we only looked at comparing pairs of classes
- mostly, we want to compare *sets* of classes
  - ▶ set of GO annotations
  - ▶ set of signs and symptoms
  - ▶ set of phenotypes
- two approaches:
  - ▶ compare each class individually, then merge
  - ▶ directly set-based similarity measures

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- similarity between a square-and-orange thing and a round-and-red thing

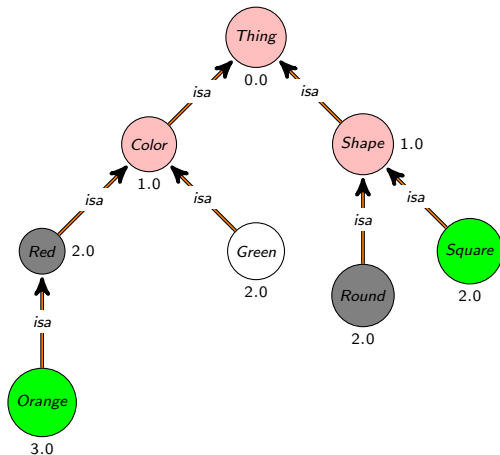
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- $simGIC(so, rr) = \frac{2}{11}$



# How to measure similarity?

- alternatively: use different merging strategies
- common: average, maximum, **best-matching average**
  - ▶ Average:  $sim_A(X, Y) = \frac{\sum_{x \in X} \sum_{y \in Y} sim(x, y)}{|X| \times |Y|}$
  - ▶ Max average:  $sim_{MA}(X, Y) = \frac{1}{|X|} \sum_{x \in X} \max_{y \in Y} sim(x, y)$
  - ▶ Best match average:  $sim_{BMA}(X, Y) = \frac{sim_{MA}(X, Y) + sim_{MA}(Y, X)}{2}$

# How to measure similarity?

- Semantic Measures Library:
  - ▶ comprehensive Java library
  - ▶ <http://www.semantic-measures-library.org/>
- R packages: GOSim, GOSemSim, HPOSim, LSAfun, ontologySimilarity,...
- Python: sematch, fastsemsim (GO only)

# Applications of semantic similarity

- no obvious choice of similarity measure
- depends on application
  - ▶ e.g., predicting PPIs in different organisms through similarity may benefit from a different similarity measure!
- different similarity measures may react differently to biases in data
- needs some testing and experience

# Applications of semantic similarity

## Recommendations:

- use Resnik's information content measure (normalized)
- use Resnik's similarity
- use Best Match Average
- use the full ontology
- classify your ontology using an automated reasoner before applying semantic similarity
  - ▶ although many ontologies come pre-classified
- $\Rightarrow$  but there are many exceptions
  - ▶ similar location  $\Rightarrow$  use location subset of GO
  - ▶ developmental phenotypes  $\Rightarrow$  use developmental branch of phenotype ontology