OWL visual depiction

OWL

KEY

A
≡
B
A equivalent to B

italics 'primitive' class

bold class with equivalence axioms

substitution of equivalent classes (aka unfolding)

MAPK cascade

≡

intracellular cascade

MAPKKK activity

≡

intracellular cascade

kinase activity

MAPKK activity

≡

intracellular cascade

kinase activity

kinase activity

MAPK activity

'MAPK cascade'

≡

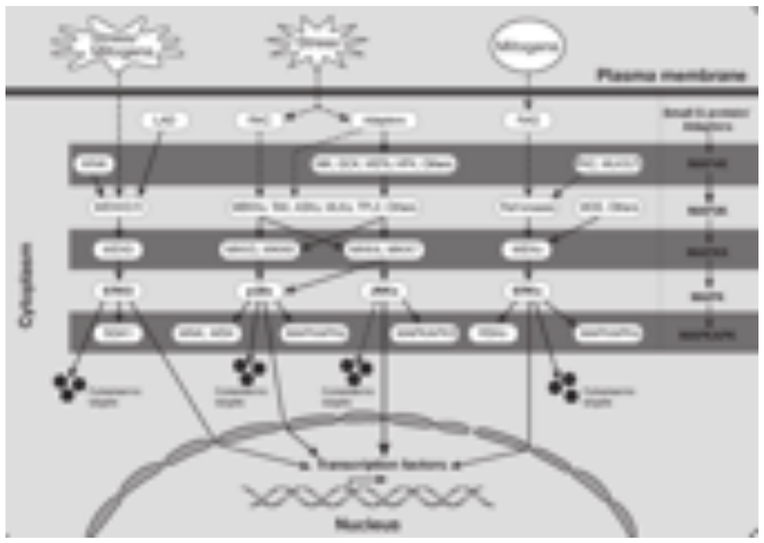
'intracellular cascade'
AND starts_with SOME
'MAPKKK activity'

≡

'intracellular cascade'
AND starts_with SOME
(*'rp s/t kinase activity'* AND
initiates SOME
'MAPKK activity')

≡

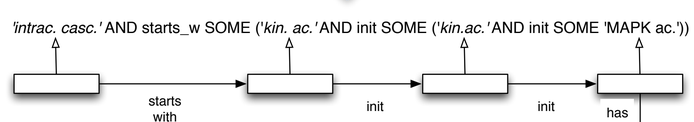
'intracellular cascade'
AND starts_with SOME
(*'rp s/t kinase activity'* AND
initiates SOME
(*'kinase activity'* AND
iniates SOME
'**MAPK activity**'))



Here we have unfolded the black box 'MAPK cascade' to it's equivalent computable description in terms of primitives. We can also do the same for subclasses like 'JNK cascade'. However, the resulting structure is still very general. If we want to describe a particular MAPK cascade in a particular context we need to 'fill in the blanks' - i.e. for every kinase activity in the chain, we can specify what

≡

'intrac. casc.' AND starts_w SOME (*'kin. ac.'* AND init SOME (*'kin.ac.'* AND init SOME 'MAPK ac.'))



refine

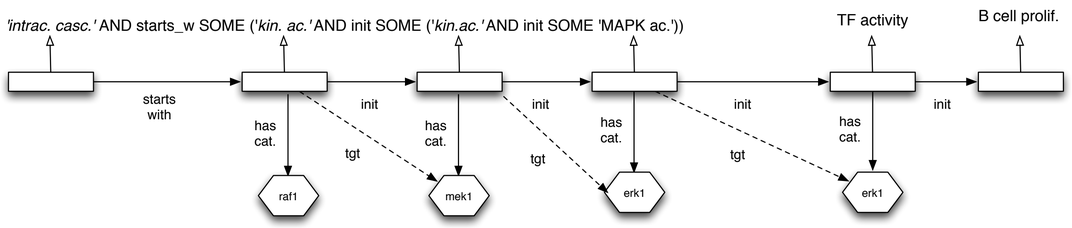
'blank nodes' - equivalent to pre-coordinated class

'intrac. casc.' AND starts_w SOME (*'kin. ac.'* AND init SOME (*'kin.ac.'* AND init SOME 'MAPK ac.'))

refine

manifesting a particular instance of the MAPK cascade
- filling in one blank node
- input is constrained

'intrac. casc.' AND starts_w SOME (*'kin. ac.'* AND init SOME (*'kin.ac.'* AND init SOME 'MAPK ac.'))



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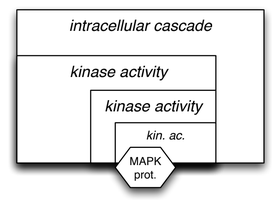

≡

'intracellular cascade'
AND starts_with SOME
(*'rp s/t kinase activity'* AND
initiates SOME
(*'kinase activity'* AND
iniates SOME
('kinase activity AND
has_input SOME
'MAPK protein')))