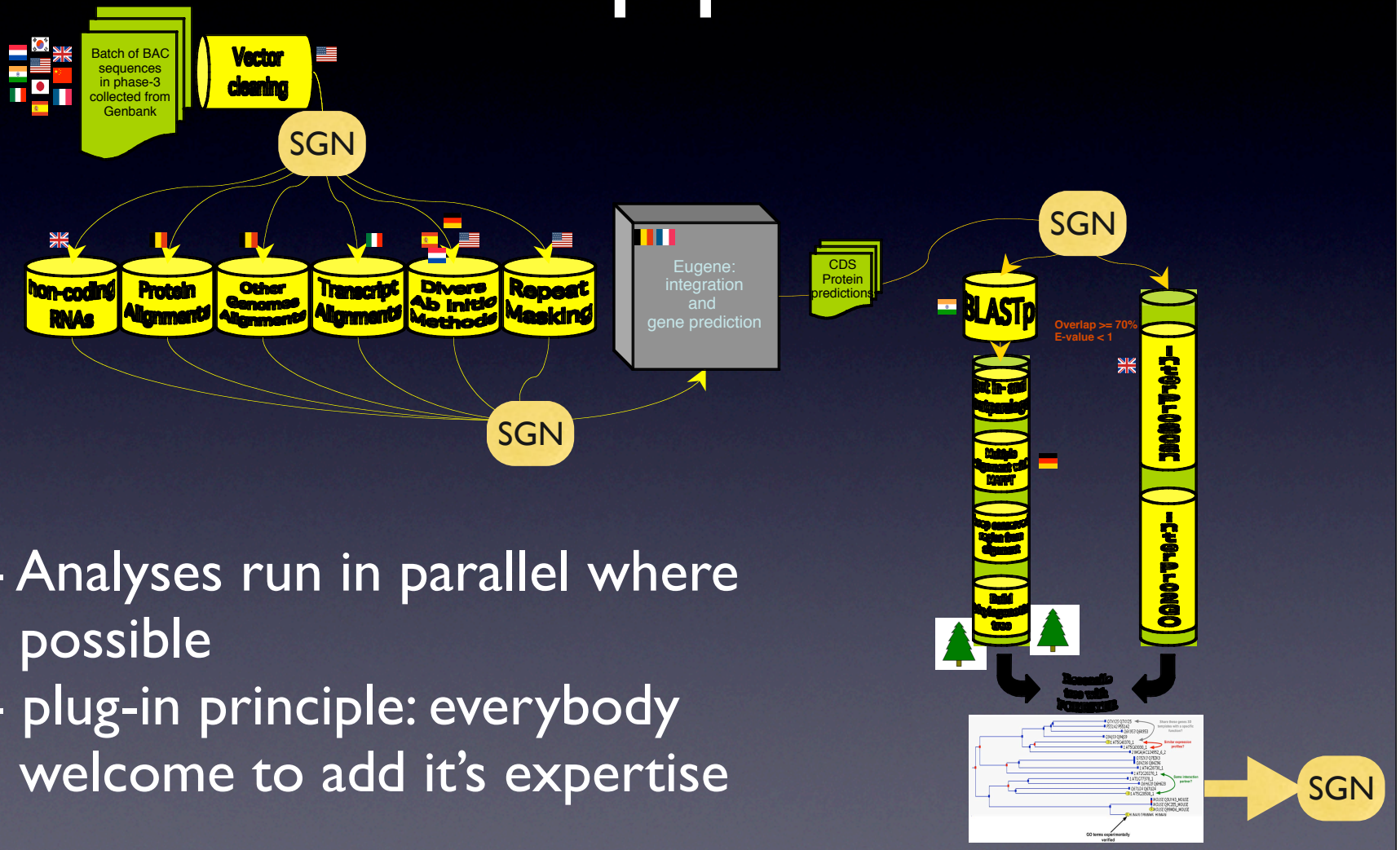
iTAG

Stephane Rombauts

iTAG, why?

- aim
  - high quality
  - homogeneous
  - state of the art tools
  - include all SOL members, divide the work

iTAG pipeline



- Analyses run in parallel where possible
- plug-in principle: everybody welcome to add it's expertise

iTAG members:

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pipeline v000

- on phase-3 BACs only
- exchange format is GFF3,
- Eugene adapted to take also GFF3 as input
- data repository at SGN
- all the steps towards v001 are in place
  - only thing to do still is to train eugene to a fully Tomato Eugene

training set

- procedure on 229 BACs:
  - with a not fully trained eugene, make a prediction using all available extrinsic data
  - generated gene structures were pre-selected by script from Daniel (428 genes selected)
  - results are on the itag-wiki
  - manual final QC on selected models

QC of structures

- QC involves alignments with ESTs, proteins from SWISS-PROT, and NR
  - 172 BACs with 428 genes to check
  - BACs from chr01-04 done (±)
    = 54 BACs with 183 genes that passed QC
    (3.4 genes/BAC)
  - not all selected genes are actually good, while not-selected genes could be added after minor correction, so QC is really needed.
  - main problem are split and truncated genes

future plans

- finish QC for training set
- train eugene
- run pipeline v000
- switch to v001
- prepare websites to distribute data
- put annotation in GenBANK, update of the BACs (contact resp. BAC-owners!!)

people involved in Gent

- Jeffrey Fawcett
- Stephane Rombauts
- Yves Van de Peer