CLUE - the situation

- CLUE is designed to work on final RTRA ($\rightarrow$ RecoTrack) and RVER ($\rightarrow$ RecoVertex).
- RSEG information available in CLUE, but not useful as input to analysis code.
- RTRA not usable on data right now.
- Particle id. should completly be done in ARTE.
- To work on MC, a (rough) particle id. is needed.
- Particle id. for MC is needed most urgent to start programming analysis code.
- CLUE tasks:
  - find secondary vertices,
  - identify decay chains,
  - determine kinematic quantities,
  - proper treatment of clones,
  - comparison with MC.

Infrastructure

- We expect that many people will work on analysis code in the near future.
- HERA-B analysis software homepage:

  `http://www.mpi-hd.mpg.de/herab/clue`

  - entry point to other analysis software pages,
  - collection of documentations & examples,
  - maintenance by a group of persons possible.
- Tagging software homepage will be created in Munich.
- Mailinglist for software development:

  `clue@mhb10.mpi-hd.mpg.de`

  - efficient communication
  - to join, write **T.Glebe@mpi-hd.mpg.de**
  - install/maintain mailinglist @ DESY?

Analysis software: How about reproducability?

- Which code versions are used?
- Which parameters are used?
- What are their values?
- Which scripts are used?

Versioning

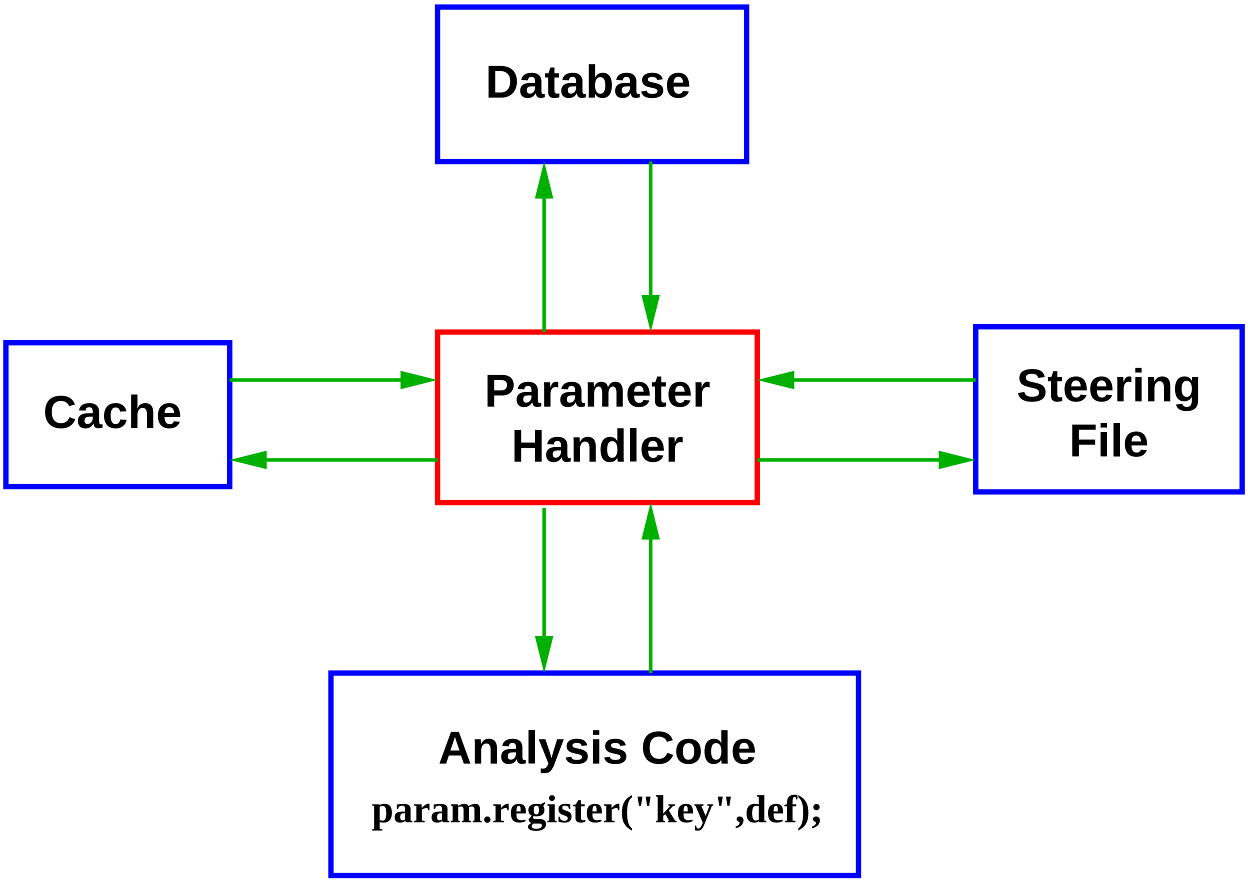
Analysis code will be available as a collection of shared libraries. They can be loaded dynamically at runtime. Thus we need:

- ☛ version number for each library
- ☛ version number available inside library
- ☛ routines to print/store version numbers
- ☛ automatic version number update if repository is modified
- ☛ after recompilation new version number available in library

xcvs can do the job

Analysis Profile

- Can we bundle all parameter settings that lead to a certain physics result?



- A draft of the implementation exists.

- Implementation will be CLUE independent.

Analysis Pseudo Code

```
void usevnt() {

  clueGetEvent();

  GObjArray<PatternMatch*> jpsiCandEE;
  ...
  Kinematic::find_jpsiEE(param, event, jpsiCandEE);
  ...
  if(Tag::tag(param, tagme, event) == CLUE_SUCCESS) {
    cout << "successfull tag" << endl;
  }
  ...
}
```

Open Questions

- Which `namespace` domains should we forsee?
  - Particle_Id ($\rightarrow$ ARTE)
  - Kinematic
  - Vertexing
  - Tag
  - ...
- How do analysis routines exchange their results?
  - individual, user defined lists
  - a single global list ($\rightarrow$ ARTE Table)
  - pointer to particles or container
- Do we have to extend `PatternMatch`?
- Analysis concepts in other experiments?
- Was anything forgotten up to now?

Next Steps

- Set up some infrastructure (WWW, repository).
- Learn more about CLUE & ROOT interna.
- Start with (simple) particle id code for MC.
- Make RTRA being useful for data.
- Clarify existing CLUE $\leftrightarrow$ ROOT problems.
- Improve documentation of CLUE.
- Collect (working) CLUE examples.
- Improve / add vertexing code in CLUE.
- Continue diskussion on open questions.
- Start implementation of a first analysis task.