

Introduction

Harmonization is the process of minimizing the differences between CT protocols across different models. Task Group 309 describes harmonization as one of the primary goals of Protocol Management and Review. We will present some of the challenges to overcome in harmonizing CT protocols across scanner models.

Parameters

It is often possible to exactly harmonize the following parameters across models

- Recon series labels
- Autosend destinations
- Contrast timing
- Cardiac gating

The available values of the following parameters often cannot be exactly harmonized across scanner models.

- Tube voltage
- Helical pitch
- Detector configurations (NxT)
- Image thickness
- Gantry rotation times
- Manual tube current settings
- Minimum/maximum mA or mAs for AEC

For these, the job of harmonization is to ensure that the specified values are reasonably close to each other. Sometimes it is combinations of these values that should be harmonized. For example, for a CTA protocol it may be best to harmonize the table speed. Also, on GE scanners the tube current mA is a setting and mAs is derived; on Siemens and Phillips scanners, mAs is a setting and mA is derived.

The names, values, and behavior of the following parameters usually vary dramatically between vendors.

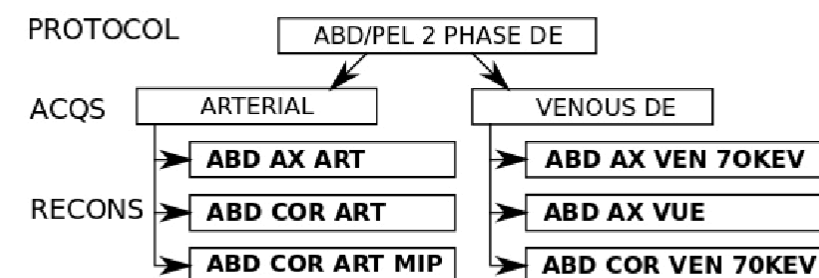
- Auto-mA settings
- Auto-kV settings
- Filter kernels
- Iterative reconstruction settings

For these parameters, the physicist must become familiar of the behavior of these settings; for example, knowing which filters on a GE scanner are the best match for given filters on a Philips scanner. Similarly, estimation of CTDI will depend on the behavior of the AEC, which varies from vendor to vendor and sometimes from model to model.

Protocol structure

Less commonly known is the variation in structure of the protocols from one model to another. The figures below illustrate the protocol structure for various scanner models, using an ABD/PEL 2 PHASE protocol as an example. Boxes containing BOLD text indicate the recon series that are sent to PACS.

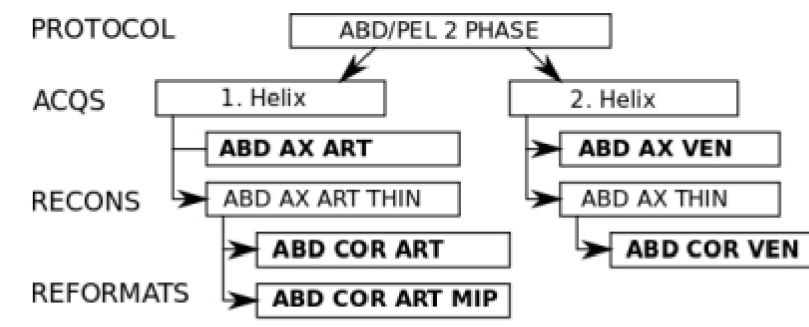
Siemens Somatom Force



The overall protocol structure of the Force is simple, with only 3 levels: Protocol, Acquisition, Reconstruction. Philips scanners with iPatient software have a similar structure; however, the Philips scanners require

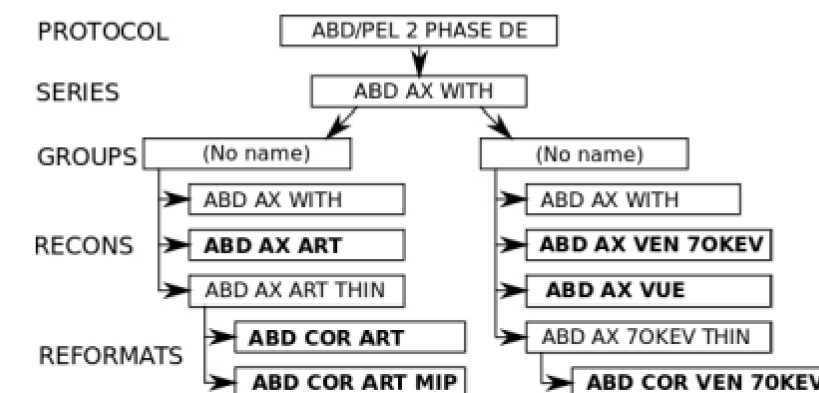
thin axial series in order to build high-quality coronals and sagittals while the Somatom Force does not.

Philips Brilliance



The Philips Brilliance scanners add another layer to the hierarchy: the “Reformat”. Sagittals, coronals, oblique, and MIP series are all Reformats and must be built from an axial series. The parent axial series are generally “thin” (<1mm thick) to allow adequate resolution in the reformats, and need not be sent to PACS.

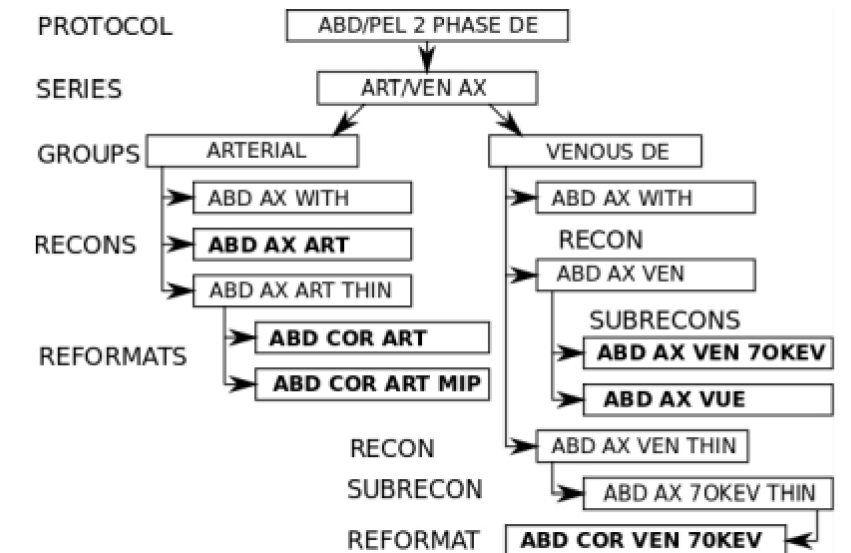
GE Discovery, Lightspeed, Optima



GE scanners using the Lightspeed user interface add another layer. Each acquisition is called a “Group”, and the groups are combined into “Series”. The first recon series in each group has the same name as the “Series” level. Another feature is that the reformats are

specified in DMPR files; a result is that if two reformat series in two protocols have the same name they must have the same thickness and interval.

GE Revolution



The Revolution user interface adds one more layer specific to dual energy protocols: the “Subrecon”. Parameters like image thickness and interval are specified at the Recon level, and dual-energy recon parameters are specified at the Subrecon level.

Conclusion

To effectively harmonize CT protocols across scanner models, it is important to understand which parameters can be exactly matched (series labels, etc.), which can be approximately matched (helical pitch, image thicknesses, etc.), and which are vastly different (auto-mA settings, filter kernels, iterative recon parameters). It is also important to understand the constraints imposed by the variation in protocol structures from one vendor to another, and even from one model to another from the same vendor.