White paper

Optimal Cardiac CT imaging with ZeeFree

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Introduction

This publication provides a brief overview on the working principle of ZeeFree, a detector width-independent algorithm that provides optimal cardiac images with reduced misalignments usually originating from patient breathing or other means. It can be applied to retrospective ECG-gated spiral and prospective ECG-triggered sequence acquisitions.

Its performance is illustrated by clinical examples followed by a brief discussion on how it could be integrated into a Cardiac CT protocol and what to look out for in the patient workflow to enable optimal results.

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The state of Cardiac CT

Challenges of Cardiac Imaging

Cardiac computed tomography (CT) imaging has come a long way and many advancements throughout the years have paved the way to the current impressive image quality that is routinely achieved in cardiac exams around the world. Today, cardiac CT has become a primary tool for assessment of cardiovascular diseases due to its robustness and clinical benefits outlined by many clinical trials such as the SCOT-HEART and ISCHEMIA Trials, among others [1, 2].

However, imaging the heart, a constantly moving organ, has always been a challenge. Those challenges are related to the organ itself, the patient, or the equipment at hand and can result in any number of artifacts from various sources.

Motion artifacts arising from the heart itself can be reduced with high native temporal resolution. Dual Source technology provides just that by offering speeds that are twice as fast as a single source CT scanner.

Artifacts originating from patient breathing, movement, or adjacent cardiac cycles have remained evasive. Increasing the detector width can potentially reduce these, but this has initiated a new debate, namely "what is the optimal detector width?" Wide detectors inherently bring with them their own challenges and issues [3].

ZeeFree is a solution to tackle this issue and provide optimal cardiac image quality without introducing the aforementioned limitations. ZeeFree is a flexible solution that works independently of the detector width used to acquire the data.

Clinical perspective

Over the past two decades, cardiac computed tomography (CT) has transitioned from being a promising alternative non-invasive imaging technique to a Class I recommendation for the non-invasive assessment of individuals with a low to intermediate pre-test probability of coronary artery disease (CAD), as outlined in the 2019 guidelines from the European Society of Cardiology (ESC) [4].

In the most recent update to the American Heart Association (AHA) Chest Pain Guidelines in 2021, cardiac CT's role in the clinical management of patients with suspected CAD was further solidified, with coronary computed tomography angiography (CTA) being endorsed as the primary imaging modality [5].

The strength of cardiac CT lies in its ability to enable a comprehensive evaluation of not only coronary arteries but also other cardiac structures, including chambers and valves. Consequently, CTA provides high-resolution images detailing coronary arteries, plaque characteristics, and stenosis severity, and employs advanced post-processing software techniques.

A contributing driver of this evolution is the engineering found behind unique Siemens Healthineers technologies such as Dual Source and Photon Counting CT, which, since its beginning, had a very strong focus on cardiovascular imaging.

In recent years, advanced software algorithms are also of increasing importance on the CT scanner side. Most notably, Advanced Model-based Iterative Reconstruction (ADMIRE) for image reconstruction and myExamCompanion for clinical workflow have demonstrated that modern software algorithms are capable of further enhancing CT scanner performance beyond hardware-based approaches.

The ZeeFree algorithm represents the latest software innovation that complements the strong hardware enablers for cardiac imaging within CT scanners.

Technical perspective

The most crucial aspect of cardiac CT is freezing cardiac motion in each individual image. This is the prerequisite that needs to be met to successfully realize sharp visualization of small-scale anatomical structures, enabling diagnosis, stenosis assessment, and plaque quantification. While this is routinely supported by beta-blocked patient heart rate control, hardware-guaranteed high native temporal resolution is still the most reliable solution for this key aspect of cardiac CT [6].

As a consequence of this base requirement, the subsequent realization of a scan acquisition and image reconstruction in a fully ECG-synchronized fashion leads quite naturally to the most commonly used modes of a prospective ECG-triggered sequence and a retrospective ECG-gated spiral. Both have their individual merits in their application, often chosen for each patient individually and hence personalized.

In either case, it is common for an acquisition performed over the complete cardiac examination range to be distributed over multiple cardiac heart cycles. Typically, between 3 to 9 heart cycles are needed, depending on scanner model and length of the examination range, which can easily be up to 20 cm, as is the case of bypass patients [7].

When the individual image stacks of images are combined into a complete series, patient breathing during the acquisition can on rare occasions lead to image misalignments between the stack boundaries, which present as stair-step or misalignment artifacts in the final series [8, 9].

One solution is to acquire the full cardiac volume quickly within one heartbeat using either high-pitch spiral (Flash mode) or increasing the detector width to cover the whole organ.

Wide detector technology has been embraced by various vendors to tackle the issue of stack artifacts. Today there are various detector widths available on the market:

- 2, 4, 8, 14, 16 cm (General Electric Healthcare)
- 4, 8 cm (Philips Healthcare)
- 2, 4, 8, 16 cm (Canon Medical Solutions)

However, only the 16 cm detectors can address this issue as a normal human heart is ~ 12 to 14 cm in length, and many scans go beyond 16 cm due to bypass or other cardiovascular indications. Unfortunately increasing the detector width introduces its own set of challenges due to physics complications.

Disadvantages of wide detectors include and are not limited to:

- Increased X-ray scatter and potential introduction of cupping or hypodense artifacts [10, 11]
- Heel effect: non-uniform dose and image quality (IQ) in the z-direction [12, 13]
- Trade-off: resolution vs. power
- Cone-beam artifacts [13]

Scanning with a 16 cm detector width is always a compromise between whole-organ imaging and various disadvantages [3].

Another solution to tackle the artifacts issue is ZeeFree technology, which can be implemented on a broader range of scanner detector widths from 2 cm to 6 cm and beyond. This has the potential to provide a robust solution for optimal cardiac imaging without introducing the issues of wide detectors.

ZeeFree is a detector-independent feature aimed at these cases with a dedicated scanner reconstruction algorithm, which reduces the misalignments present in the underlying acquired data, yielding a corrected optimal image series.

ZeeFree – Technical principle

Figure 1a illustrates an ECG-triggered sequence acquisition, which covers the heart in three consecutive steps. As indicated in the illustration, the acquisition is performed in an overlapping fashion to accommodate the 3D cone beam nature of a multi-slice CT scanner. While the individual amount of overlap depends on the system geometry, a typical value found in most 128-slice systems is 10%.

If patient breathing occurs during the scan acquisition, as illustrated, the stacks of data are misaligned and discontinuities can arise in the cardiac anatomy and most critically in the vessel structures.

Two established reconstruction options are currently available for cardiac sequence and spiral acquisitions. The "Standard" reconstruction utilizes all available data at each image position at the selected cardiac ECG phase, independent of its heart cycle origin. This results in a stack of images that is appealing due to its smooth contrast transition between the individual stacks because the available data in the overlap area is mixed. This reconstruction is ideally suited for the best image quality assuming that the individual stacks are perfectly aligned and no misalignment has occurred. In case of a misalignment in the acquisition data, a standard reconstruction will result in an averaging and smearing of individual structures in the transition zone, depending on its strength and the scale of the misalignment. Such an effect can subsequently hamper the diagnostic interpretability of the images.

The alternative "TrueStack" reconstruction mitigates some of these issues by making it very clear to the user "if and where" a misalignment has occurred. It is therefore the ideal option for determining with high certainty if a misalignment is present in the data and often points to the root cause of the misalignment. While in most cases patient breathing is involved, indicated by misalignment in the pulmonary vessels or the sternum, a misalignment artifact can also occur purely from the combination of adjacent cardiac cycles with very different heart rates with no associated pulmonary vessel misalignment.

The reconstruction underlying TrueStack is simple in that only one additional rule is employed in the process: Each primary axial thin slice image is only allowed to be reconstructed from data of a single cardiac cycle. This leads to the effect that overlapping data in the transition area is partially discarded, because each image is derived completely from only one of the two candidate heart cycles. The transition therefore occurs instantaneously from one image to the next, right in the middle of the data overlap area. The illustration below on the right indicates this behavior, which leads to very sharp steps in coronal or sagittal views, making it easy to identify misalignments, if present. However, TrueStack might sometimes be difficult to interpret.

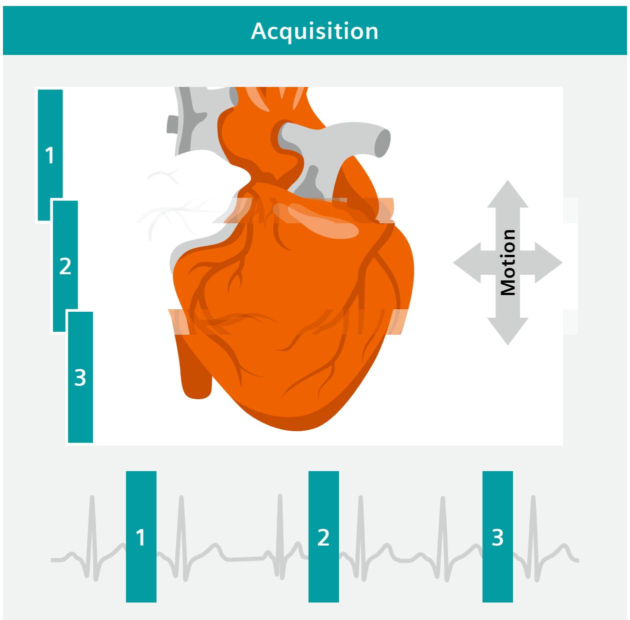

Figure 1a: ECG-triggered acquisition, covering the heart in three consecutive steps

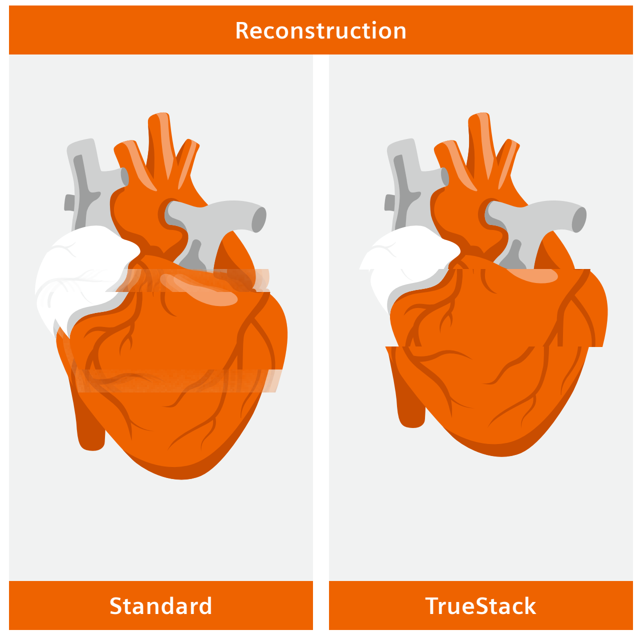

Figure 1b: Cardiac CT acquisition and reconstruction options

The ZeeFree Algorithm

The algorithm can be broken into three individual steps: A non-rigid registration applied separately to each stack transition followed by a vector field interpolation and resampling and a final "user" reconstruction vector field application step.

The first non-rigid registration step is independently performed for all transitions of the entire acquisition based on a pair of stack images in each case (illustrated by stack A and B in Figure 2). The overlapping data allows for the selection of a single image from stack A and B at the same image position in the middle of the overlapping area (dotted green line). The level of misalignment between the images I_A and I_B can be expressed by their absolute HU value difference $|I_A\text{-}I_B|$.

The images I_A and I_B define a joint 2D plane, which allows for the definition of a 3D vector field, resulting in the mapping of a two-dimensional grid into a 3D volume space. The two stacks A and B are then subjected to a demon-type registration algorithm [14, 15], based on this vector field model, which describes the image transformation as a joint vector field with opposing signs for the images from stack A and B, minimizing the root mean squared of the difference of the images I'_A and I'_B. The illustration below on the right illustrates this approach, which can be summarized in layman's terms as "create images I'_A and I'_A with pixels from somewhere else in a way that they are pretty much the same when finished."

The respective petrol and orange arrows in the figure indicate the "optimized source location" from where values are pulled into images I'_A and I'_B.

The registration algorithm is designed for robustness and simplicity. The main control parameters are to update step length and spatial length of the regularization. Both are set to values that ensure smoothness and local rigidity of the resulting vector field, which preserves the morphology of small-scale structures (e.g., vessel diameter, plaque volumes, etc.).

The above-described registration step is derived from images that were independently reconstructed in the background with a set of fixed parameters to exclude a potential influence of user-specific settings (e.g., reconstruction kernel, slice thickness, matrix size, iterative strength, etc.) on the registration result. Therefore, a resampling to the final matrix size and pixel spacing of the "user" reconstruction is performed. In addition, a distance-weighted interpolation for all images of the entire volume between the individual vector fields from all stack transitions of the acquisition is performed. This interpolation step contains a Gaussian smoothing operation, which can be interpreted as a relaxation of the "tension" in the vector field over the distance.

The third step for the final ZeeFree images is derived from hidden "user" reconstructions, which are resampled by means of the final vector field as described above. It is interesting to note that ZeeFree images share the same base characteristics as TrueStack images, because there is no mixing of data in the overlapping zone and each axial image contains the same amount of data and therefore exhibits the same image noise. The same applies to the stack transition in terms of contrast enhancement, which is also immediate from one image to the next at the middle overlap z-position location of the images I_A and I_B.

In a recent publication, ZeeFree algorithm demonstrated significant reduction of non-diagnostic coronary segments. [16]

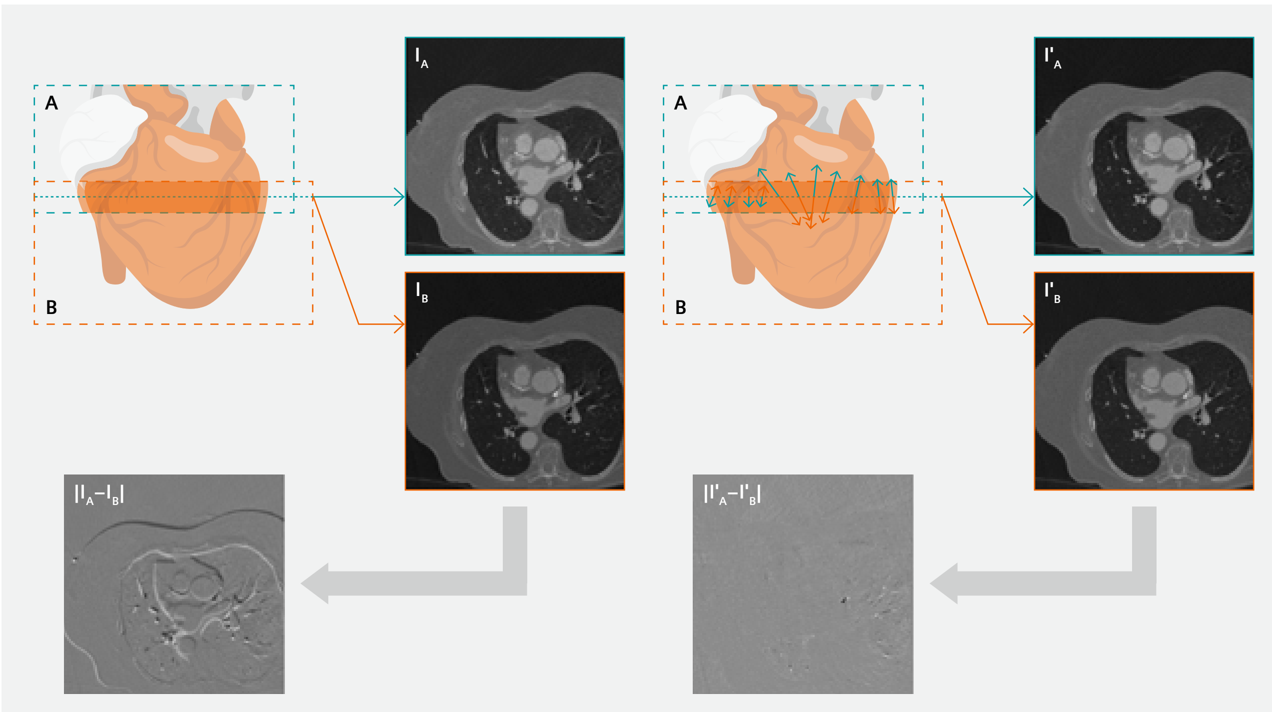

Figure 2: Break-down of the ZeeFree Algorithm

Clinical cases

Figure 3 is a Coronary CTA case acquired with a single-source CT scanner, SOMATOM X.ceed, in an prospective ECG-triggered sequence mode (64 × 0.6 mm, 80 kV, CTDI 3.4 mGy).

While the patient's heart rate was a regular sinus rhythm, clear signs of breathing are observed over the entire examination range of 17 cm, clearly identified in the TrueStack reconstruction.

As can be seen in the outer CPR panels (RCA left, LAD right) and the coronal and sagittal views, the ZeeFree algorithm reduces and corrects the misalignment.

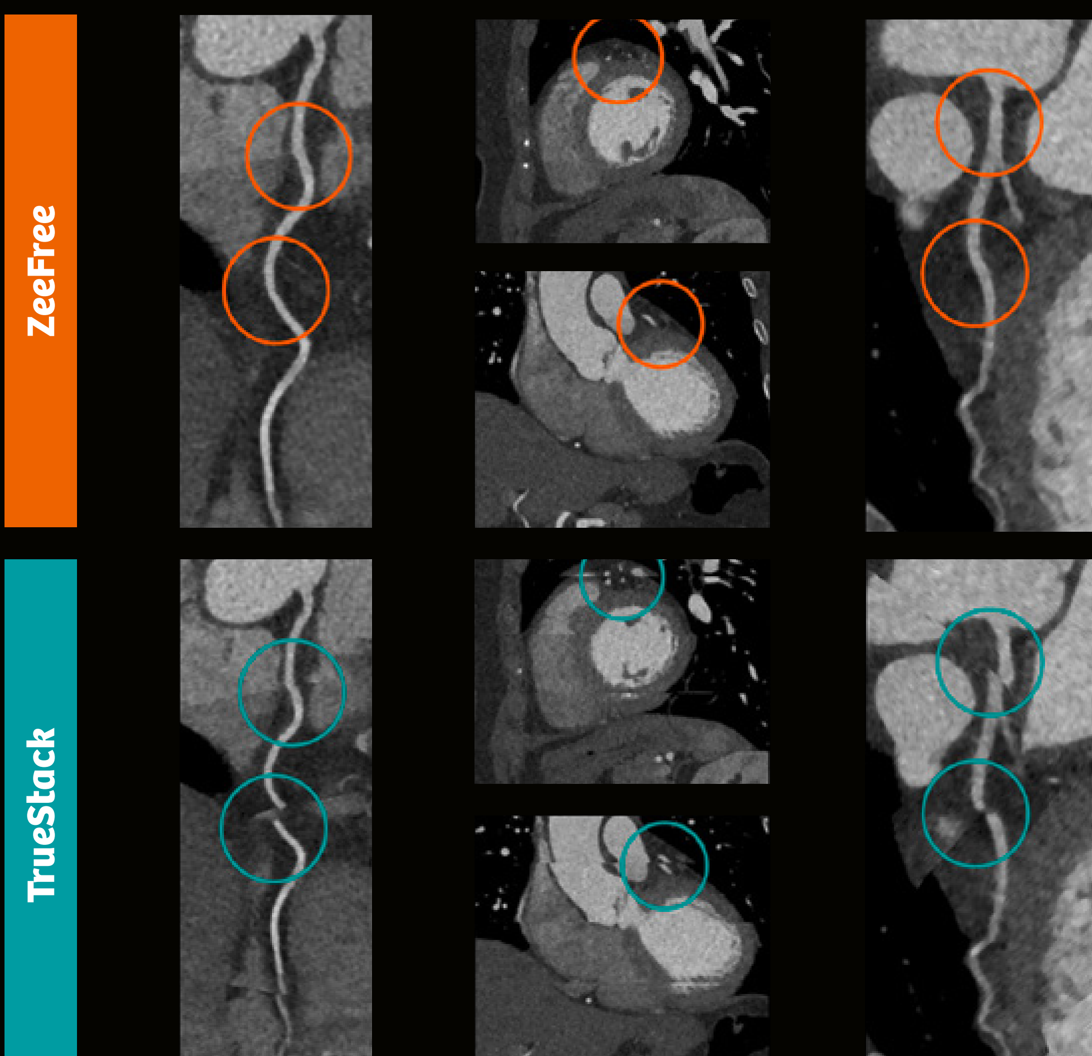

Figure 3: Coronary CTA acquired with SOMATOM X.ceed
Courtesy of Diagnostikum Linz, Linz, Austria

In Figure 4 is a similar case acquired with the new Dual Source CT scanner, SOMATOM Pro.Pulse. In this case, the misalignments can be seen in both the LAD and the RCA, mimicking a soft plaque stenosis. ZeeFree enabled the morphology to be seen as intended. The combination of high temporal resolution with ZeeFree results in optimal cardiac images at any heart rate.

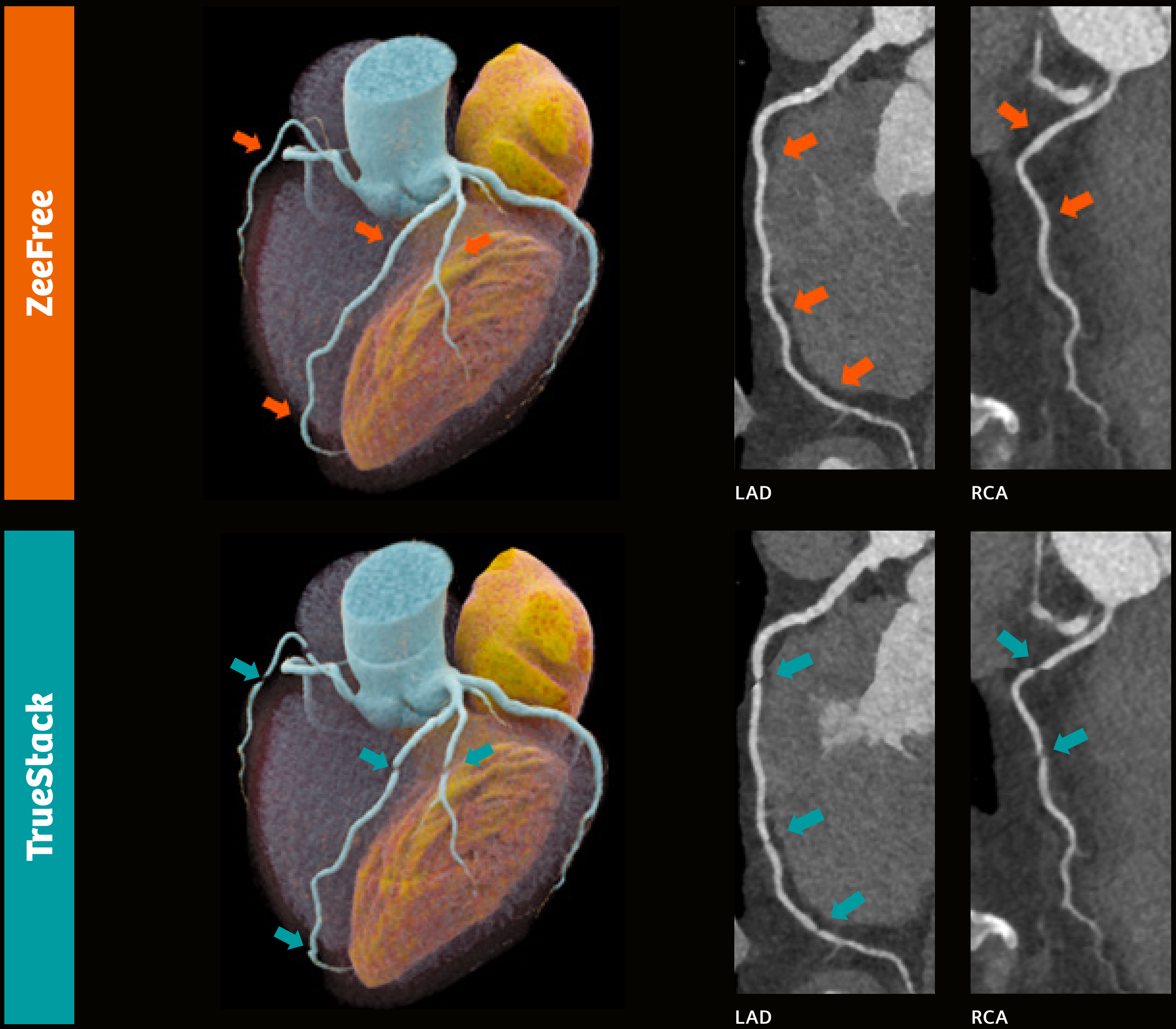

Figure 4: Coronary CTA acquired with the Dual-Source CT SOMATOM Pro.Pulse
Courtesy of Morges Hospital, Morges, Switzerland

Figure 5 illustrates a cCTA case acquired with a NAEOTOM Alpha in a Quantum HD Cardiac sequence mode (120 × 0.2 mm, 120 kV).

In the TrueStack reconstruction, the misalignments can be appreciated in cVRTs, axial and orthogonal views of the CPRs. The stacks run right through the LAD, mimicking stenosis in the mid LAD segments and making confident diagnosis more challenging. As can be seen at the top half, ZeeFree provides optimal cardiac images even in challenging cases with ultra-high resolution as well.

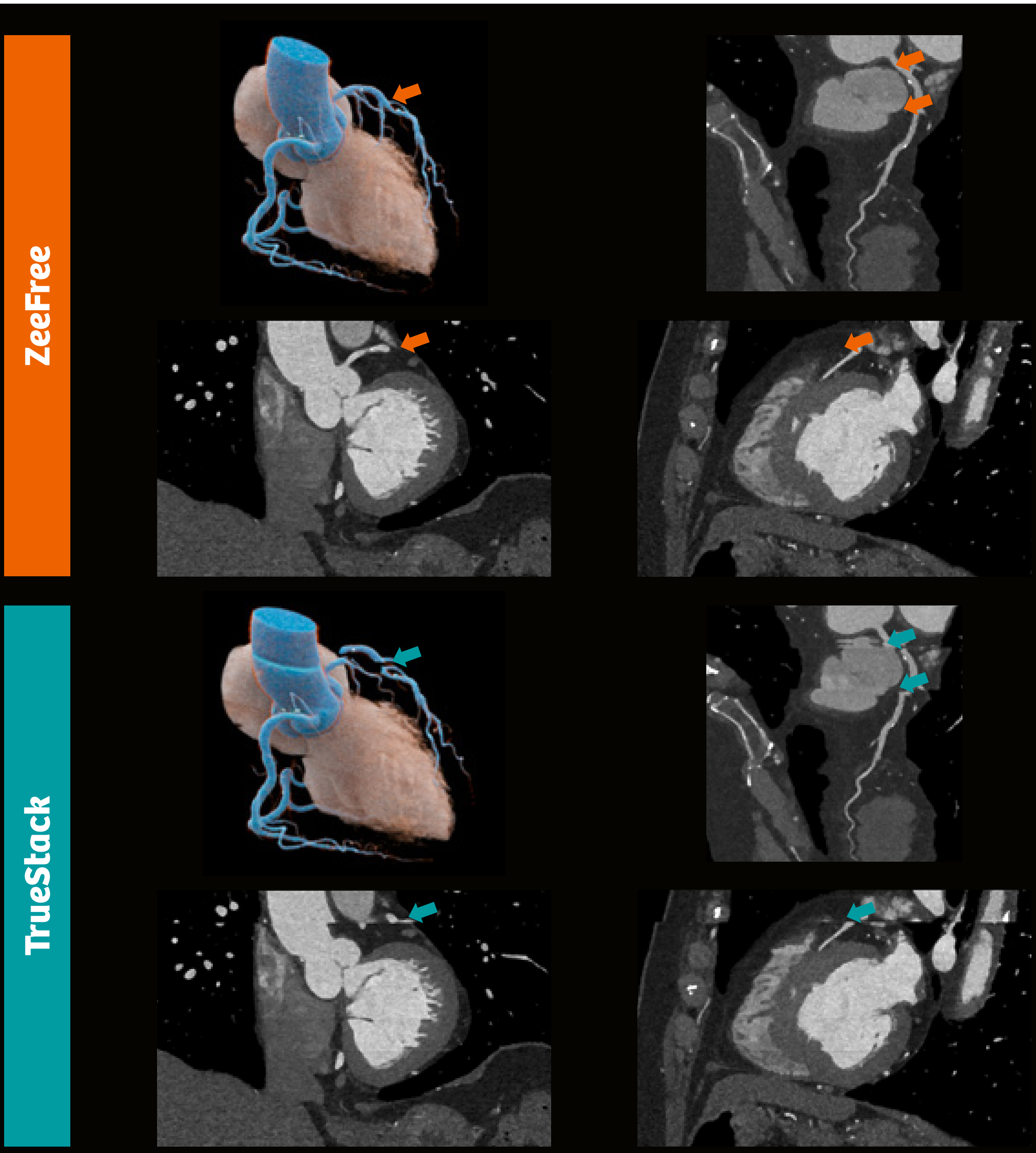

Figure 5: Coronary CTA acquired with the Dual Source Photon-counting CT NAEOTOM Alpha
Courtesy of Mühlenkreiskliniken, Minden, Germany

Scan protocol and workflow

ZeeFree is not a post-processing feature at a workstation, instead it is a dedicated reconstruction algorithm working on the raw data. ZeeFree is a user-selectable option available in prospective ECG-triggered sequence and retrospective ECG-gated spiral acquisitions. It is selected from the reconstruction parameter panel **Physio Recon** under the label Stack Recon, which offers the choices **Standard, TrueStack,** and **ZeeFree.**

Protocol integration

Due to technical constraints, ZeeFree limits some parameter combinations, which one needs to consider during protocol setup. These are:

- Reconstruction kernel sharpness is limited to a maximum value of 60 (e.g., Bv60, ...)
- Extended Field of View (HDFOV) cannot be combined with ZeeFree.
- Metal Artifact Reduction (IMAR) cannot be combined with ZeeFree.

For the most optimal workflow, a tailored reconstruction setup might look as follows:

- **ZeeFree:** All primary axial thin slice series based on BestPhase. All in-line result series, e.g., Coronary vessel CPRs, VRT heart, etc.
- **TrueStack:** Multi-phase thin slice or thick slice series.

Use modified information as supplementary information only. For diagnosis, use unmodified images.

Breathing instruction

Figure 6 illustrates the limits of ZeeFree in terms of its reach for the non-rigid registration step, indicated by the dotted arrows, which are outside of the available image stacks. Through construction, as can be seen from the length of the arrows, the underlying problem is not symmetric and there is less "room" on the overlap side, which influences the workflow.

In case of an incomplete patient breathhold, a motion that follows the acquisition direction (middle) is beneficial because it leads to a doubling of structures, which the ZeeFree algorithm can detect, while the opposite motion direction (right) leads to a gap in the data and cannot be recovered.

Early experience therefore indicates a preferred combination of cranio-caudal acquisition and inspiration breathhold for optimal ZeeFree results – which represent the typical cardiac acquisition protocols today in clinical practice.

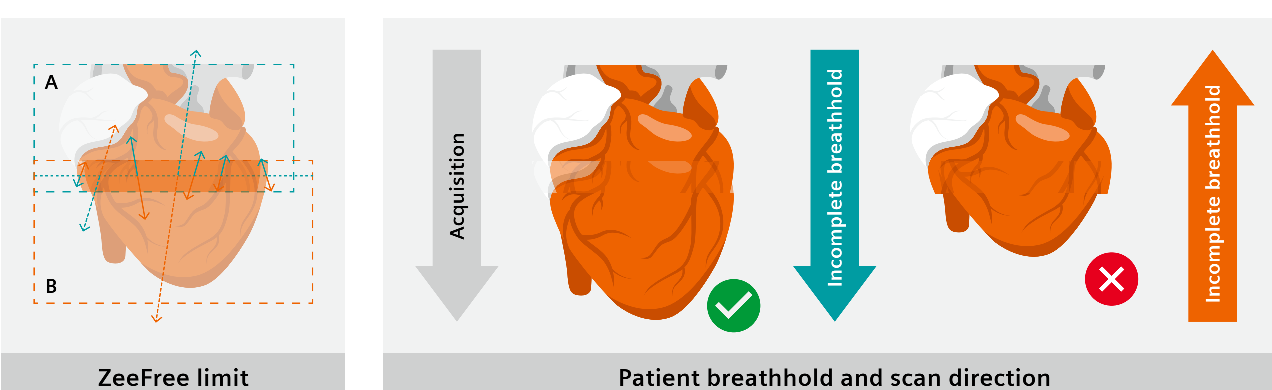

Figure 6: Optimal use of ZeeFree

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Abbreviations

CTA Computed Tomography Angiography
RCA Right Coronary Artery
LAD Left Coronary Artery

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[1] *Personalization of diagnosis, therapy selection and monitoring, after care and managing health.*

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