

S6E2 | How can AI make coagulation smarter

*with **Dr. Bas De Laat**, General Director at the Synapse Research Institute.*

*Interviewed by **Karine Carrière**, Global Product Line Manager at Stago*

Artificial intelligence is rapidly transforming laboratory medicine. In this Meet the Expert conversation recorded at ISTH 2026, Dr Bas de Laat shares his perspective on how A.I. can improve decision-making, enhance data interpretation, and help laboratories unlock the full value of coagulation testing.

Before we dive in, could you briefly introduce yourself and tell us what challenges led you to bring AI into coagulation?

My name is B. De Laat. I studied Medicine and have a PhD in Hemostasis and Immunology, and I am Head of the Synapse Research Institute in Maastricht. We work on everything from basic research to prototype assays. Through the development of these prototype assays and clinical studies, we became involved in artificial intelligence. We introduced AI into our laboratory about seven years ago in response to several challenges we were facing.

You started from a very concrete challenge in coagulation: the limitations of current diagnostic approaches. How did artificial intelligence help address these challenges in antiphospholipid syndrome diagnosis?

My background is in antiphospholipid syndrome (APS). I have been working on it since 2001, and I completed my PhD in this field. On paper, the diagnosis of APS seems straightforward. You have diagnostic criteria, antiphospholipid antibodies, and clinical criteria. If antiphospholipid antibodies are detected in the blood and the patient presents the appropriate clinical criteria, such as venous thrombosis or pregnancy morbidity, the diagnosis can be made. However, in practice, it is not that simple. Diagnostic criteria differ between manufacturers. A patient who tests positive for APS in one center using a particular assay may not necessarily test positive in another center using a different manufacturer's test.

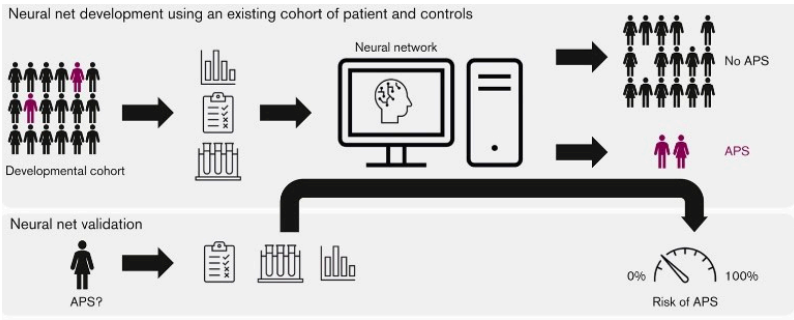
Another challenge is that the assay that best supports APS diagnosis is the lupus anticoagulant test. However, patients with APS are often treated with vitamin K antagonists (VKAs), which can interfere with lupus anticoagulant testing and make interpretation difficult. As a result, we looked for alternative assays. My background also includes thrombin generation, so we evaluated thrombin generation in several patient populations to determine whether this test, which can detect prothrombotic states such as APS, could also serve as a diagnostic marker.

If I understand correctly, this was mainly about combining multiple parameters?

We evaluated thrombin generation and observed increased thrombin generation, higher peak values, and increased prothrombin conversion, all of which are associated with a prothrombotic state. However, there was considerable overlap between APS patients, healthy controls, and other patient populations. When such overlaps exist, the test cannot be used reliably as a diagnostic assay.

We initially applied conventional statistical approaches to see whether multiparametric analyses could separate these populations without overlap. Unfortunately, this was not sufficient.

We then turned to artificial intelligence. We explored neural networks and trained several members of our institute to work with them.



Romy M. W. de Laat-Kremers, et al. Blood Adv (2024) 8 (4): 936–946.

By combining thrombin generation parameters with thrombodynamics, which is currently a thrombin generation add-on not yet available on the market, we were able to diagnose APS with 100% accuracy in the first cohort and 92% accuracy in a second multicenter cohort.

How did this improve the performance of the diagnostic model?

When patients were receiving VKA treatment, the multiparametric AI approach allowed us to diagnose them correctly without relying on lupus anticoagulant testing.

In addition, combining conventional parameters with AI-derived information further improved diagnostic accuracy for antiphospholipid syndrome.

This means that patients can be diagnosed accurately even while receiving anticoagulant therapy.

That's very interesting. It shows how complex biological data can be transformed into a powerful diagnostic tool. What is also fascinating is that you are using artificial intelligence not only to improve the interpretation of biological data but also to develop new diagnostic tools themselves. Could you explain how you use artificial intelligence to develop antibodies at Synapse?

Artificial intelligence is increasingly impacting every aspect of laboratory work, including antibody development.

In the past, we generated antibodies by immunizing mice. More recently, we have immunized llamas to obtain single-chain antibodies, or nanobodies, which can offer advantages over conventional IgGs.

Last year, we started developing antibodies de novo. With de novo antibody generation, animals are no longer required. This is beneficial for animal welfare, and it also reduces costs.

Several companies provide dedicated software platforms, but there are also open-source programs available. Using these programs, researchers can load a target protein, most of which have known structures available through PDB files and specify the region where antibody binding is desired.

The software then generates multiple antibody candidates. Researchers can select the most promising ones, produce them, and test whether they bind as expected.

You mentioned lower development costs, but where do you see the greatest benefits: cost, speed, performance, or all three?

I would say speed, above all.Traditionally, it takes around six months to obtain an antibody, from immunization through affinity maturation and validation. Today, we can complete the process in approximately eight weeks, from design to finished antibodies. This saves significant time and money.

Many companies are already using these approaches. Major pharmaceutical companies often use commercial platforms. For example, Chai Discovery works with Pfizer, providing integrated software and laboratory workflows for antibody production.

However, if a company already has laboratory capabilities, open-source programs can be just as effective and sometimes even outperform commercial solutions.

I believe this will benefit both the scientific community and companies like STAGO.

Do you think this is a real game changer for the development of diagnostic tools?

Absolutely. At Synapse, we often say that de novo antibodies are like Lego bricks. Once you have the antibody sequence, you can modify it in many different ways.

You can create antibodies that recognize two different epitopes or even two different proteins. You can also attach additional molecules. For example, we recently developed anti-DOAC nanobodies capable of reversing the activity of Rivaroxaban, Apixaban, and Edoxaban.

Using AI, we improved these antibodies and further engineered them into multivalent proteins. This has major implications for therapeutic applications, which is why companies such as Pfizer, Takeda, and Eli Lilly are interested in this field.

For diagnostic companies like ours, these technologies will accelerate development and help create more specific reagents that reach the market more rapidly. That is our objective.

If we step back and summarize our discussion, artificial intelligence is not only improving patient diagnosis but also helping us combine biological data more effectively and enhance the tools behind it. Is that correct?

Yes, AI represents an entirely new era with almost unlimited possibilities. At the same time, that is also one of its challenges.

For example, with current software, we can generate new antibodies every day. In the past, when we immunized a llama, we might obtain around ten candidate nanobodies. Today, we can generate a hundred nanobodies in a single day.

That is exciting, but it also means we must become much more selective, because all of these candidates still need to be produced and validated. The process is faster, but it requires greater focus and prioritization.

Where do you think artificial intelligence brings the greatest value today in practice? And what are the main limitations we should keep in mind?

The greatest value is speed. As individuals, we each have a single brain. With artificial intelligence, it is as if you suddenly have hundreds or even thousands of brains working simultaneously. The computational power is far greater.

The main limitation is data quality. We often say: "garbage in, garbage out." If you train an AI model using poor-quality data or an inappropriate patient population, the resulting algorithm may appear successful in one cohort but fail entirely when tested in another.

The same applies to antibody development. When antibodies are generated through animal immunization, we can perform counterselection to ensure specificity for a given epitope. With de novo antibody generation, there is always a possibility of unintended binding to other epitopes.

Therefore, careful validation remains essential. Fortunately, current software can estimate the likelihood of such off-target interactions.

Regarding intellectual property, when you use artificial intelligence, who owns the resulting innovation?

You mean who owns intellectual property rights? When using commercial AI platforms such as Chai or others, ownership is typically governed by licensing agreements. These solutions are often expensive and primarily intended for pharmaceutical applications.

However, if you use appropriately licensed open-source software, you generally retain ownership of the intellectual property.

This is particularly attractive for organizations like ours. Commercial solutions can

be extremely costly, whereas open-source alternatives provide greater flexibility and ownership opportunities.

Looking ahead, do you see opportunities for artificial intelligence to improve stroke risk prediction through more comprehensive patient profiling?

Yes, we are currently working on programs focused on stroke risk prediction. This is more complex than APS because stroke risk depends on multiple parameters and cannot be assessed using thrombin generation alone. I believe better diagnostic methods and, hopefully, predictive approaches will emerge in the future.

We are currently involved in a study based on the Moli-sani cohort, which includes approximately 25,000 healthy volunteers from the general population. This cohort represents about 10% of the population of the Molise region in Italy. Within this cohort, we developed a model capable of predicting stroke risk over a ten-year period with a specificity of 98%. However, the model still needs to be validated in multiple independent populations. That is the main challenge. Collecting and measuring all these parameters in 25,000 individuals was extremely costly. Repeating the process for validation requires substantial resources. Nevertheless, I believe significant advances are coming in the field of stroke prediction.

About Dr. Bas De Laat



Dr. Bas De Laat is General Director at the Synapse Research Institute. His expertise is translational research as his background is Medicine with a PhD in hemostasis and autoimmunity.
Under his supervision Synapse develops new diagnostic methods in the field of hemostasis , and leads scientific studies from discovery up to market access.