

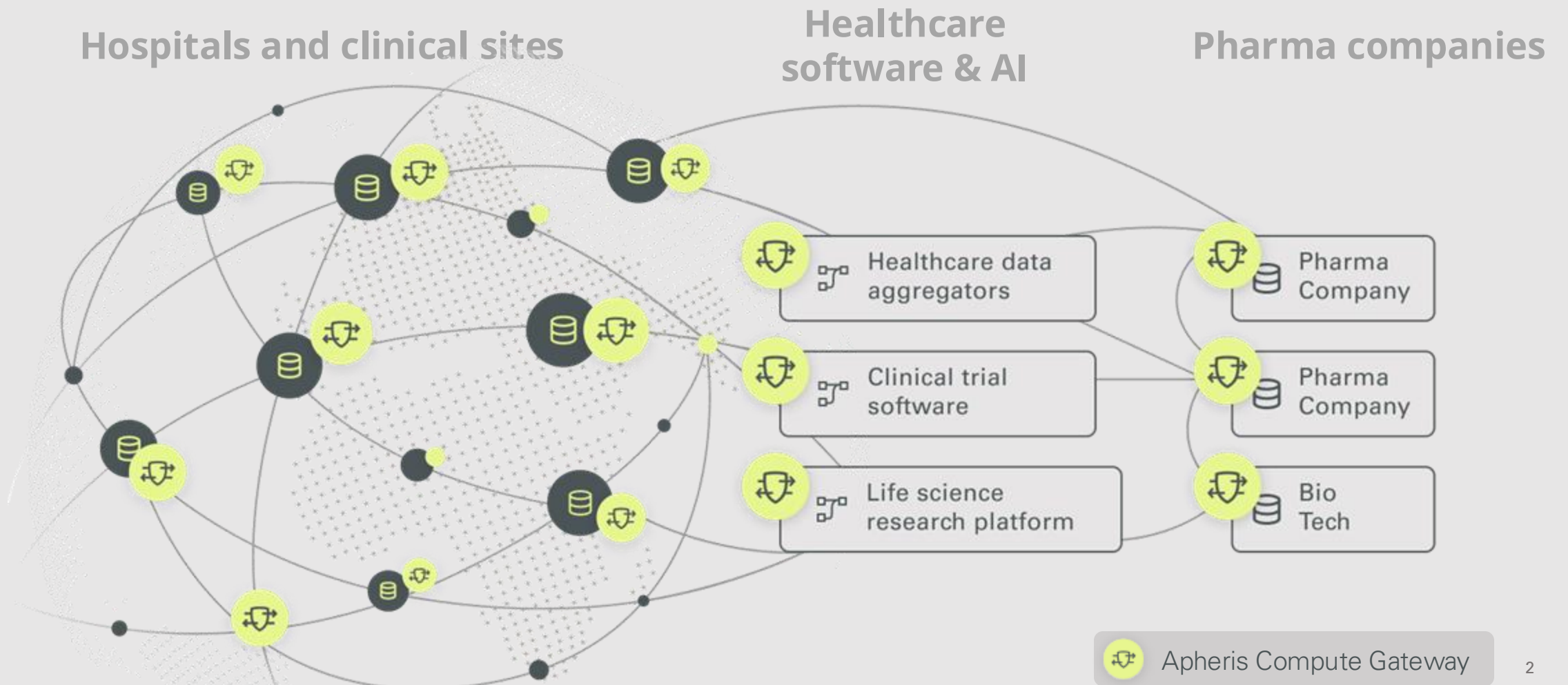


Federated data collaboration in BioPharma leveraging NVIDIA FLARE and BioNeMo

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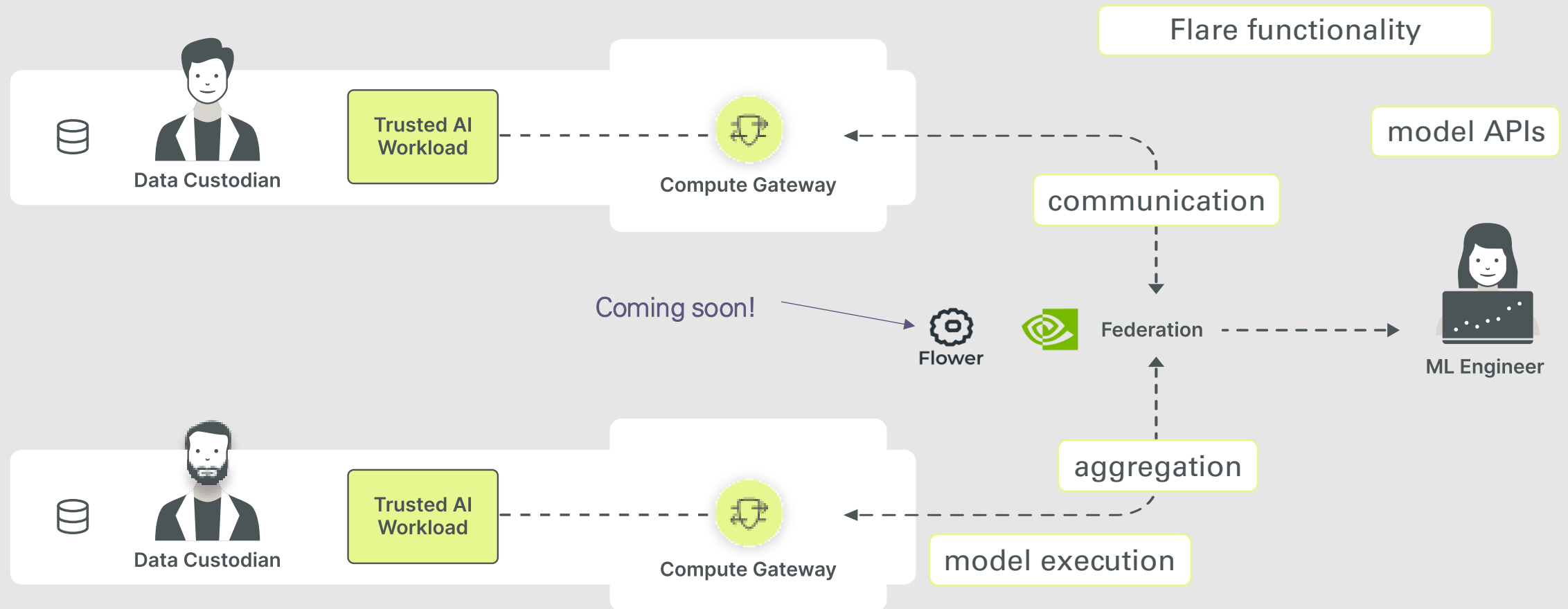
First, a few words about Apheris.

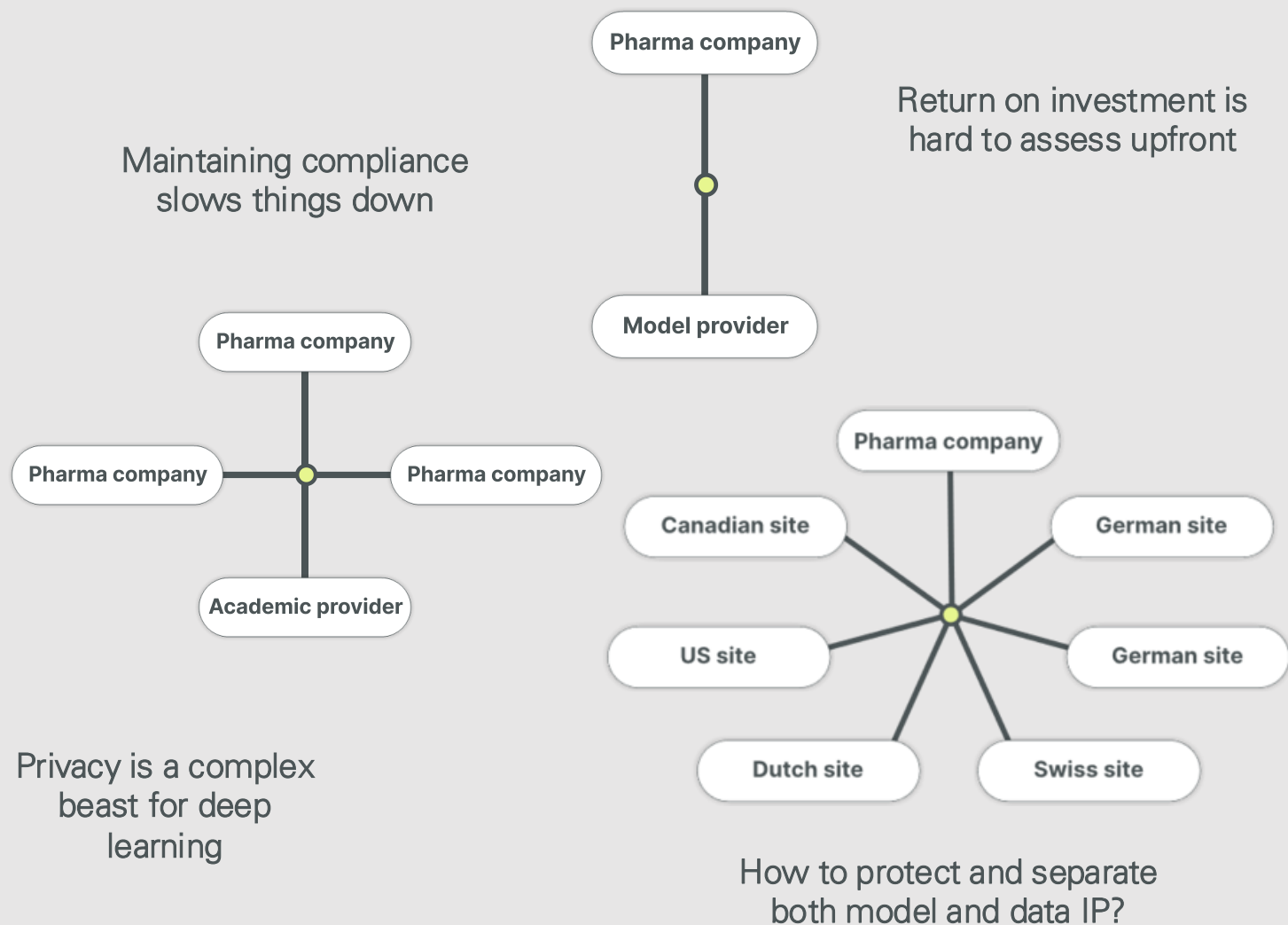
We safely connect models and data





We use NVFlare (and soon Flower-on-Flare) for a strong foundation on the federation side





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 Check for updates

Furthermore, although FL removes the option of stealing the data from a central database, it does not give any formal guarantees against re-identification⁴. Numerous studies have shown that it is possible to reverse engineer privacy-sensitive data from the model information that is shared in FL (see, for example, ref. 5). Thus, the term 'privacy-preserving' is not entirely appropriate for FL. The bottom line is that an ML model (or its parameters/gradients) trained on private data must itself be considered private data. Therefore, approaches such as differential privacy (for example, adding noise locally) remain needed, yet such approaches may represent a trade-off between data privacy and the utility of the models⁶. This trade-off arises in cases in

(AI) applications in medicine, protection regulations of Federated learning (FL) solution that can allow AI in the term 'federated' refers to a federation of participants multiple independent data, and then combine a central server. In this need to combine data in FL has turned out to using standard data format^{2,3}. However, FL is a technical considerations. We are concerned digital health, for example bodies, to use FL as a sufficient acknowledged tant ethical and practical those deploying it. In this FL should be coupled w

- Is federation truly privacy preserving?
- Accuracy, bias and fairness
- Transparency and explainability

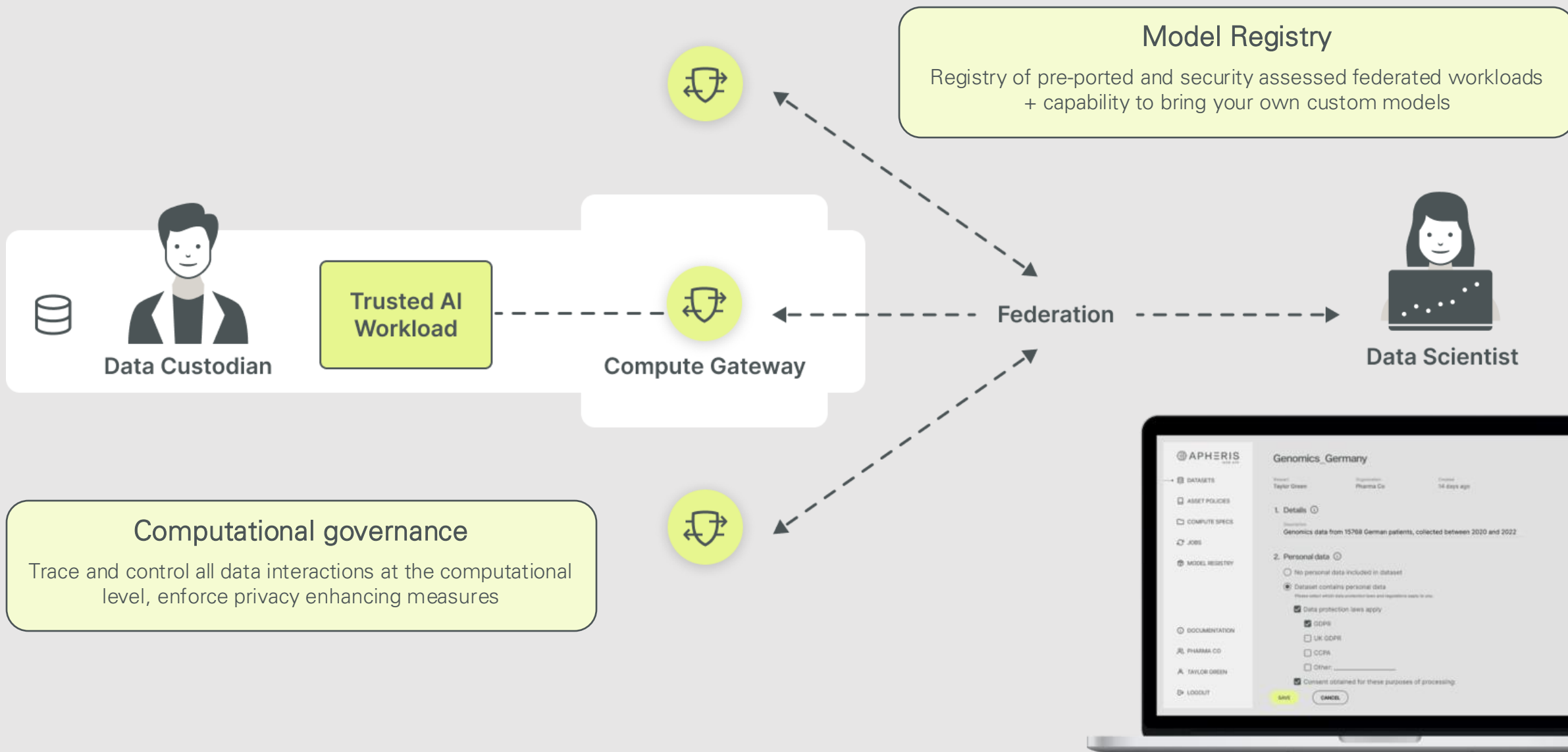
The fact that sensitive data are not transferred to a central point in FL mitigates certain privacy concerns regarding data transfer and allows organizations to avoid administratively burdensome data transfer agreements, but it does not relieve the data holders from their data protection responsibilities¹. Ethical and legal justifications for data collection and sharing are still needed (that is, patient consent or research exemptions), and data holders remain responsible for implementing governance and technical measures to securely protect the data locally on the nodes (for example, appropriate access control and encryption). Indeed, because this responsibility is spread out over multiple partners instead of being allocated to a central

Why privacy preserving?

mit bias in models trained on pooled data, it is even more difficult when learning is distributed and each 'node' sees only its own data". Bias is often caused by the under-representation of (minority) populations in the source data, or by limited access to specific variables for these groups. Although this, too, is not a problem unique to FL, it can in some cases be exacerbated by FL. For example, the FL training process can contribute to bias when the different local models are combined ('fused') using a weighted average: if larger datasets are weighed more highly during the fusion, bias in those datasets is amplified. Another issue arises when certain types of data are not used in the global model because only specific centers have them. If only the



We solve for trust between collaborating parties





<https://build.nvidia.com/explore/healthcare>

We benefit from the BioNeMo suite and its integration with Flare



AlphaFold 2

Predicts the 3D structure of a protein from its amino acid sequence.



MolMM

Controlled generation, finding molecules with the right properties.



MegaMolBart

Molecular generator

DiffDock

Predicts the 3D structure of how a molecule interacts with a protein

ESM2

Generates embeddings of proteins from their amino acid sequences

ESMFold

Derivative of ESM2; predicts the 3rd structure of a protein from it's amino acid sequence

ProteinMPNN

Predicts amino acid sequences for protein backbones

RoseTTAFold

Generates protein backbones for protein binder design



Job approval

```

jupyter demo_esm2 Last Checkpoint: 14 seconds ago

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JupyterLab Python 3 (ipykernel)

ESM2 Multi-task Downstream Finetuning on the Apheris platform

[1]: import json
import warnings

from pathlib import Path
from typing import Literal
from pydantic import BaseModel, Field

import wandb

import apheris
from apheris import compute, job, datasets, models
from apheris import job as job_cli

warnings.filterwarnings("ignore")

[1]: apheris.login()

[1]: datasets.list_datasets(slug_contains="esm")

[1]: models.list_models(name_contains="apheris")

We create a ComputeSpec that defines
• the model,
• the datasets, and
• hardware specs of server and clients

[1]: compute.set_ignore_limits(True)
compute_spec = compute.ComputeSpec(
    model={
        "id": "apheris-model-bionemo",
        "version": "0.0.5"
    },
    dataset_ids=[
        "esm2-downstream-scl-1_gateway-1_org-1",
        "esm2-downstream-scl_gateway-2_org-2"
    ],
    client_n_cpu=8,
    client_n_gpu=1,
    client_memory=32000,
    server_n_cpu=1
)

```

Job execution

```

jupyter demo_esm2 Last Checkpoint: 24 minutes ago

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JupyterLab Python 3 (ipykernel)

[15]: 'running'

[16]: job.wait_until_job_finished(
    compute_spec_id=compute_spec_id,
    job_id=job_id,
    timeout=3600
)

You provided the job ID f38104b4-984f-4286-a5a6-0a3c67beb7c4.

[17]: job_cli.list()

[1]: job.logs()

Now that training has finished, we can download the results and explore them.

[1]: download_path=Path.home() / "esm_finetune_result"

job.download_results(
    job_id=job_id,
    compute_spec_id=compute_spec_id,
    download_path=download_path
)

We deactivate the compute spec to shut down all machines and stop costs for running cloud infrastructure.

[1]: compute.deactivate(compute_spec_id=compute_spec_id)

[1]: import subprocess
from wandb.cli.cli import sync

wandb_path = download_path / "workspace" / "wandb"
for f in wandb_path.rglob("*.wandb"):
    subprocess.call(["wandb","sync", str(f), "--project", "apheris-bionemo-scl"])

[1]: compute.get_status(compute_spec_id=compute_spec_id)

```



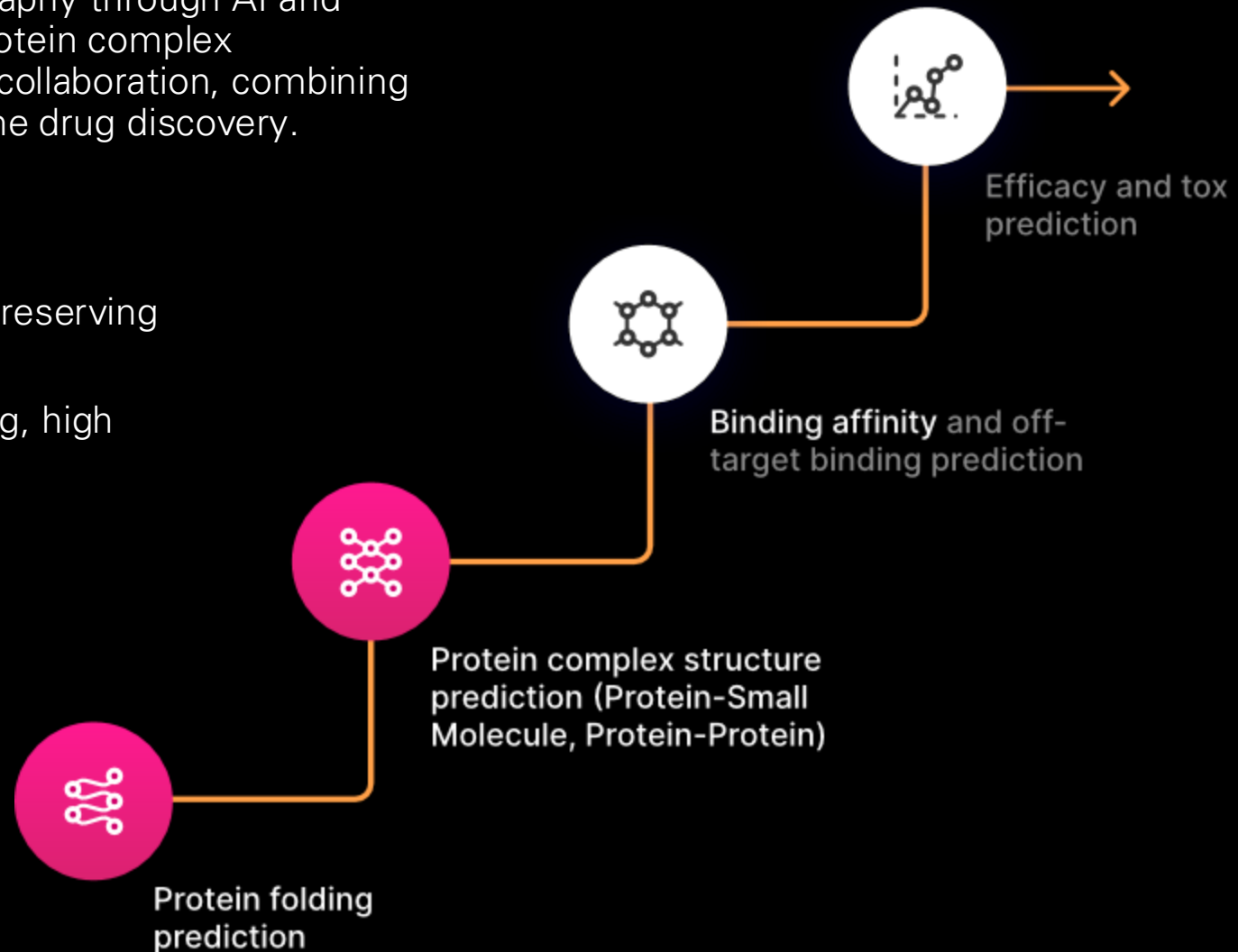
Powering the AISB Consortium to Revolutionize AI Drug Discovery

Apheris provides the tech layer for the Artificial Intelligence Structural Biology (AISB) Consortium, an unprecedented collaboration among AbbVie, Boehringer Ingelheim and Johnson & Johnson aimed at transforming AI drug discovery. State-of-the-art AI models will be trained and evaluated on unique data from multiple biopharma companies without exposing proprietary information.

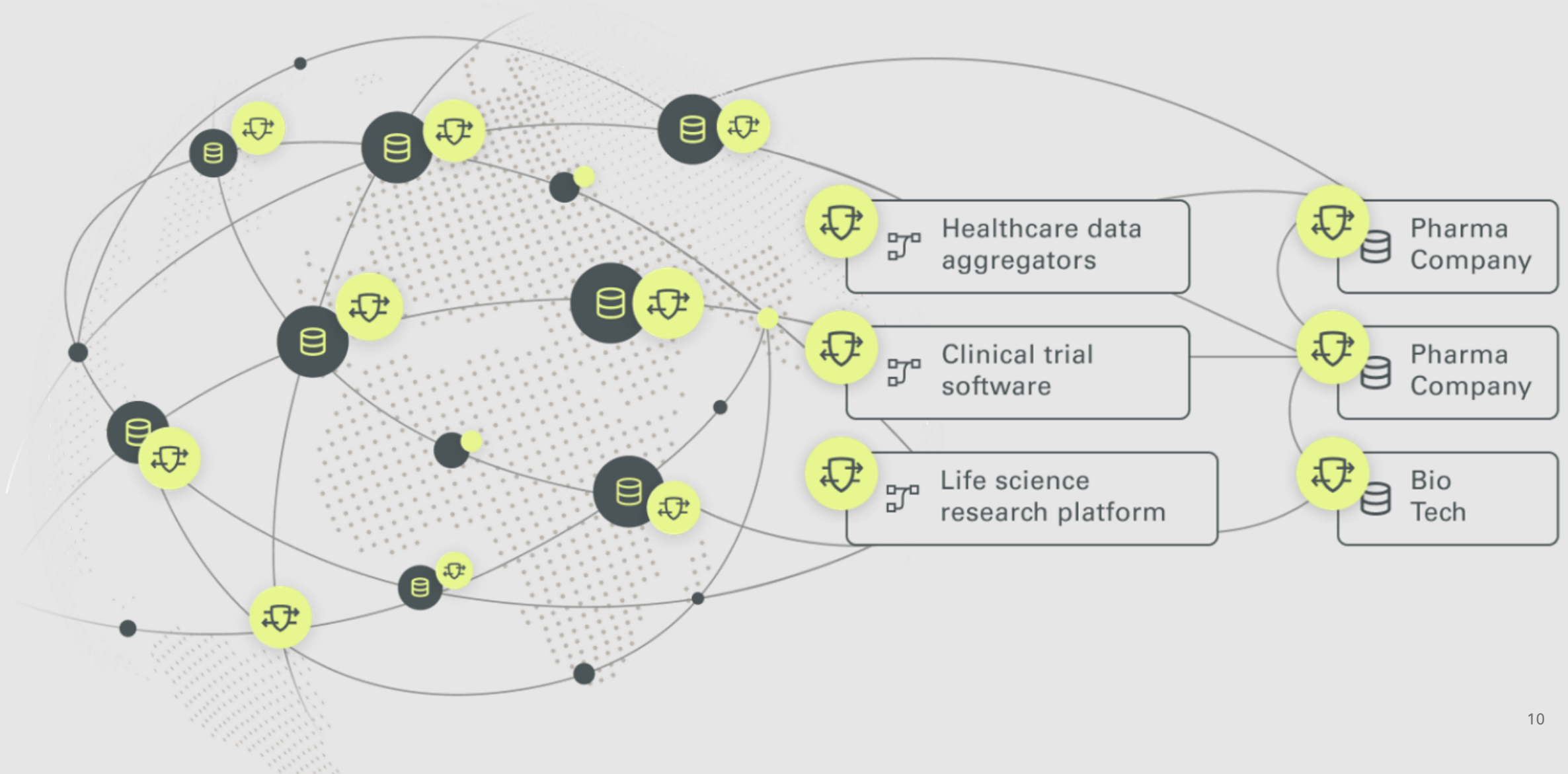

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The AISB Consortium aims to leverage secure, federated learning to ensure both data privacy and AI model performance – with the ultimate goal of accelerating the application of AI in molecule design by achieving precision akin to X-ray crystallography through AI and machine learning in predicting protein complex structures. Our vision thrives on collaboration, combining our collective expertise to redefine drug discovery.

- Data available for training while preserving confidentiality/IP
- Infrastructure (Federated Learning, high performance compute)
- Leading edge AI algorithms
- Partnership between pharma and tech



A combination of data, models, federated computing and governance can join the data-modeller network up





Thanks for listening

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