

Breakout Session 2: Track B

ASTOR: Alliance Standardized Translational 'Omics Resource

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A-STOR

Alliance Standardized Translational Omics Resource

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A-STOR: Background

- Challenges for clinical trial high dimensional data
 - Correlative 'omics are an integral part of clinical trials
 - NCTN/GDC/dbGAP are definitive repositories
 - Data are decentralized & often deposited years after sequencing
- **ASTOR: Goals**
 - Stable, secure, **scalable storage** for multi-omics data from Alliance trials
 - **Accessibility** to approved investigators for more rapid and robust analysis including secondary analyses and meta-analyses
 - **Rapid correlative turnaround** enhances trial design, grants, and publications
 - **Data harmonization** to facilitate meta-analyses
 - **Portal for analyses**

A-STOR: Workflow & Structure

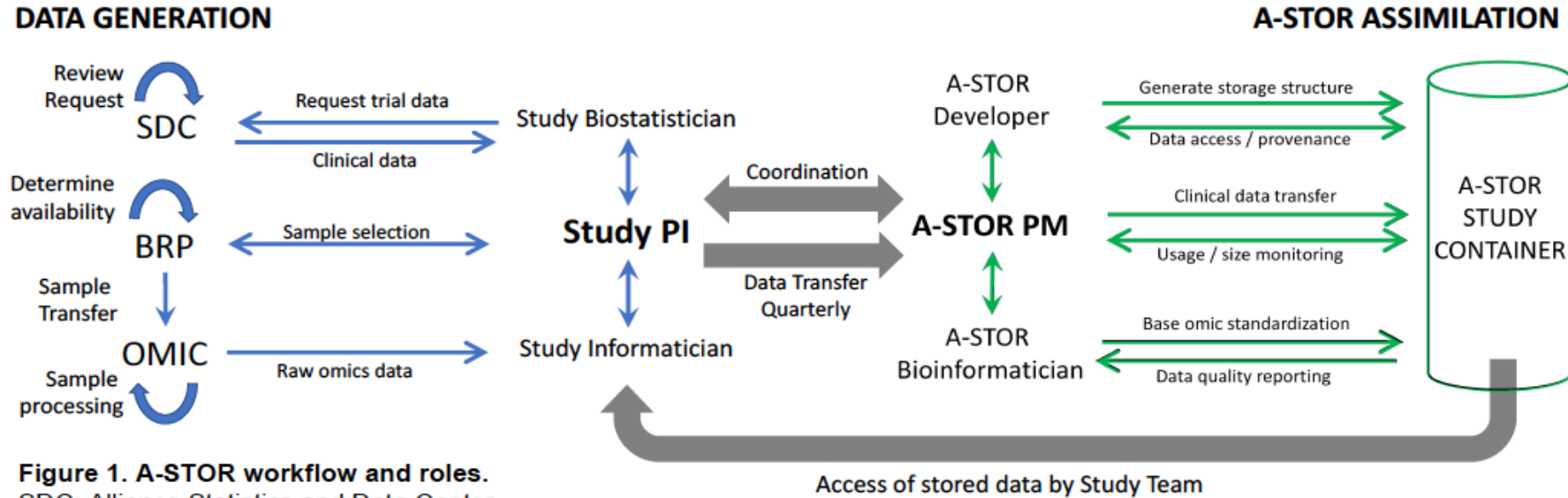


Figure 1. A-STOR workflow and roles.

SDC: Alliance Statistics and Data Center

BRP: Alliance Biorepository

PM: Project Manager

OMIC: Designated Sequencing Core

PI: Principal Investigator

Governance: ASTOR 'Manual of Operations'

- Regulatory: Confirmation of consent, deidentification, HIPAA compliance
- Approvals: MOU to deposit data, User rights/responsibilities
- Data use/standards: FAIR principles, inter-operability, end-to-end provenance

A-STOR: Workflow & Structure

Consolidated directory structure: 'Put it all together'

- Diverse data types: DNaseq, RNAseq, SNP, path images, ctDNA
 - Flexible storage: Raw (fastq), aligned (BAM), processed (vcf, maf), variant results
- De-identified clinical data: Minimal (not full) clinical data + study docs

CALGB40601

Settings Manage Monitor 1 Visualize

+ Add Data New Folder New Workflow Start Analysis

SEARCH SCOPE: Entire project | NAME: Any | ID: Any | MODIFIED: Any

CALGB40601 > cBioPortal

| Name | Type | Size |
|---------------------------|--------|------------|
| case_lists | Folder | |
| data_clinical_patient.txt | File | 30.83 KiB |
| data_clinical_sample.txt | File | 184.27 KiB |
| meta_clinical_patient.txt | File | 145 bytes |
| meta_clinical_sample.txt | File | 143 bytes |
| meta_mutation.txt | File | 286 bytes |
| meta_study.txt | File | 253 bytes |
| mutations.maf | File | 1.61 GiB |

A-STOR: AI/ML Readiness

Overarching Goals Addressed:

- **Stable, secure, scalable storage for multi-omics data from Alliance trials**
- **Accessibility to approved investigators for more rapid and robust analysis**
 - Support primary study team with analyses and meta-analyses
 - Secondary analyses by Alliance investigators before 1^o publication
- Correlative turnaround enhances trial design, grants, and publications
- **Data harmonization to facilitate meta-analyses**
- Portal for analyses

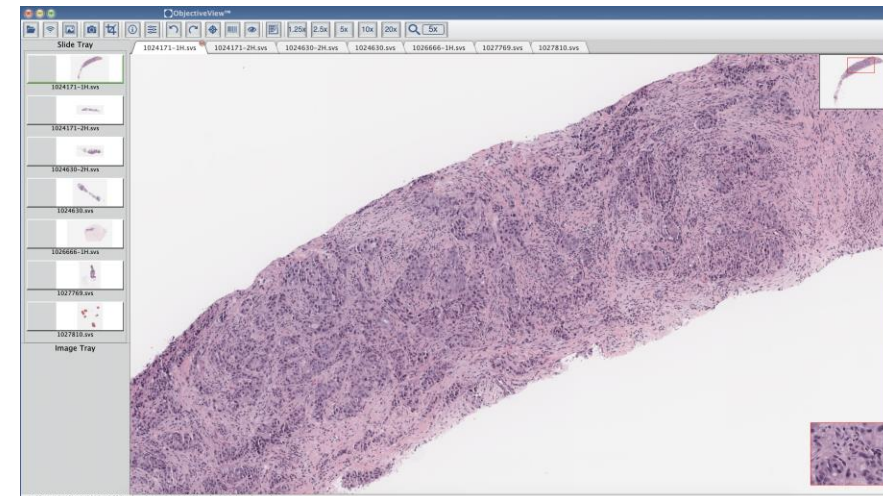
ASTOR AI/ML Readiness

- AIM 1: To expand and optimize ASTOR to facilitate AI/ML research
 - Expand studies in ASTOR: **2300pts → >17,000 pts | 10Tb data → >100Tb data**
 - Focus on digital pathology images

| Trial ID | Cancer | Unique Patients (n) | SNP | DNaseq | RNAseq | DigPath | Other |
|--------------|----------|-------------------------------|-----|--------|--------|---------|----------------|
| AFT-05 | Breast | 2558 | | X | X | X | |
| CALGB 40101 | Breast | 2015 | X | | | X | |
| CALGB 9741 | Breast | 2005 | | | | X | |
| CALGB 80405 | GI | 1512 | X | X | X | X | X (NanoString) |
| CALGB 80702 | GI | 1040 | X | | | | X (ctDNA) |
| A031201 | GU | 989 | X | | | | |
| A011106 | Breast | 857 | | X | X | X | |
| CALGB 90401 | GU | 827 | X | | | | |
| A0131501 | GU | 702 | | X | X | X | |
| CALGB 40502 | Breast | 661 | X | | X | X | X (CTC) |
| CALGB 70604 | Myeloma | 656 | X | | | | |
| CALGB 50303 | Lymphoma | 550 | | | | X | |
| A031202 | GU | 545 | | X | | | X (ctDNA) |
| AFT-38 | Breast | 518 | | X | | | X (ctDNA) |
| AFT-04 | Breast | 488 | | | X | X | |
| CALGB 90601 | GU | 456 | X | | | | |
| CALGB 40603 | Breast | 389 | | X | X | X | |
| CALGB 80303 | GI | 374 | X | | | | |
| CALGB 40601 | Breast | 265 | | X | X | X | |
| A031902 | GU | 56 | | X | X | | |
| TOTAL | | 17,463 Unique Patients | | | | | |

ASTOR AI/ML Readiness

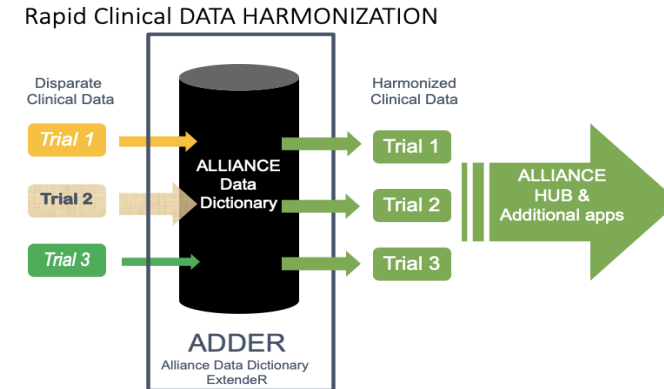
- AIM 1: To expand and optimize ASTOR to facilitate AI/ML research
 - Expand studies in ASTOR: **>17,000 patients, >100Tb data**
 - Focus on digital pathology images
 - Significant interest from academic and commercial partners
 - Leadership by Mark Watson/BSSR – vision to scan slides results in powerful data



By end 2025, ASTOR plans to host >45,000 digital H&E images

ASTOR AI/ML Readiness

- **AIM 2: Test and implement Alliance Data Dictionary ExtedeR (ADDER) for trial clinical and adverse event data harmonization**
 - Develop a unified clinical & AE data dictionary and data dashboard

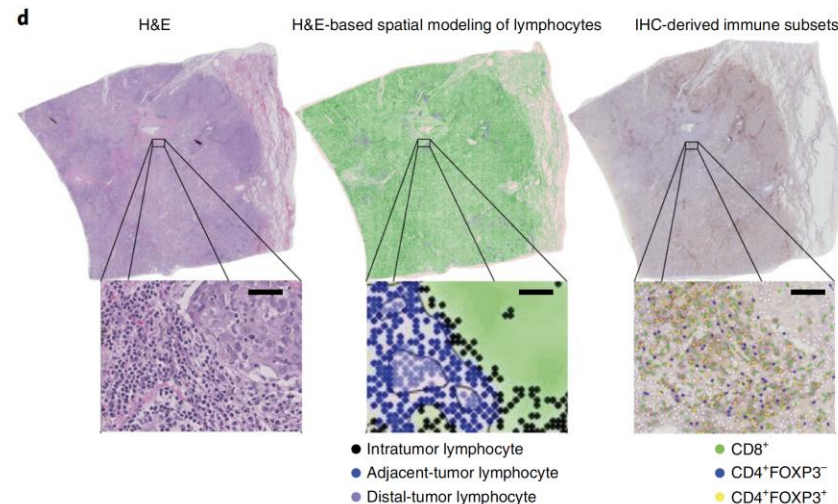


Example: ASTOR Data Dictionary v1.1

| DATA ELEMENT Common Name (Based on) | DATA CLASS | DATA ELEMENT Common Name | Provenance / Source Text? | Definition | CDASH/SDTM Variable | CDASH Note | mCODE Data Element |
|-------------------------------------|--------------------|--------------------------|---------------------------|--|---------------------|---|--------------------|
| title | PROTOCOL/TRIAL | Short Title | SDMC | Study title | TS_TSVAL_TITLE | Study identifier not title or protocol number | |
| protocol_number (PK) | PROTOCOL/TRIAL | Protocol Number | SDMC | Alliance Protocol Number | STUDYID | | |
| disease_site | | | SDMC | PENDING | | | |
| start_date | PROTOCOL/TRIAL | Start Date | SDMC | Protocol activation date | TS_TSVAL_SSTDAT | | |
| end_date | PROTOCOL/TRIAL | End Date | SDMC | Last Patient Last Visit. | TS_TSVAL_SENDAT | | |
| principal_investigator_name | PROTOCOL/TRIAL | PI | SDMC | Alliance Study Chair | TS_TSVAL_SCHAIR | | |
| navigator_status | PROTOCOL/TRIAL | | BBR | | | | |
| ppid (PK) | PARTICIPANT | PPID | | Alliance Participant ID | USUBJID | | patient-9 |
| sex | PARTICIPANT | Sex | SDMC | Sex, as determined by the | DM_SEX | | patient-3 |
| ethnicity | PARTICIPANT | Ethnicity | SDMC | Ethnicity, as entered in OPEN | DM_ETHNIC | | patient-14 |
| country | PARTICIPANT | Country | SDMC | Country of Residence, as ente | SC_SCORRES_CNTRYRES | | |
| race | PARTICIPANT | Race | SDMC | Race, as entered in OPEN | DM_CRACE | | patient-13 |
| trial_protocol_number (FK) | | | | Link patient to trial | | | |
| id (PK) | | | | Uuid to link encounter to patient? | | | |
| height_inches | PARTICIPANT | Height at Registration | SDMC | Participant Height at | VS_VSORRES_HEIGHT | | |
| weight_lb | PARTICIPANT | Weight at Registration | SDMC | Participant Weigh at | VS_VSORRES_WEIGHT | | |
| registration_date | PARTICIPANT | RegistrationDate | SDMC | Participant (First) | DS_DSSTDAT_REGRAND | | |
| trial_arm | PROTOCOL/TRIAL | Arm | SDMC | Participant (First) | CARM | | |
| disease_code | PARTICIPANT | Disease Code | | | | | |
| nci_medra_disease_code | PARTICIPANT | NCI MedDRA Disease Code | SDMC | NCI MedDRA Disease Code at | SUPPMH_QVAL_MHDSXCD | | |
| ecog_performance_status | | ECOG PS at Registration | SDMC | ECOG Performance Status at | IRS_RSORRES_ECOC101 | | patient-17 |
| participant_mrn (FK) | | | | Link patient to trial encounter | | | |

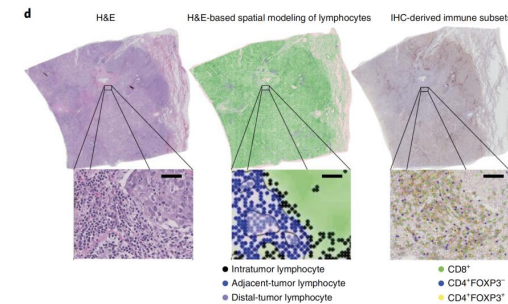
ASTOR AI/ML Readiness

- **AIM 3: Pilot implementation of ASTOR and ADDER to develop a multi-modal ML-based neoadjuvant chemotherapy response predictor using pooled data from two phase III clinical trials.**
 - TNBC Neoadjuvant Chemotherapy: CALGB 40603 and BrighTNess
 - Integration of RNAseq and digital pathology
- **AI Algorithm Deployment & Unit Testing**
 - **Digital Pathology Algorithms:**
 - Geospatial immune variability algorithm (Abdul-Jabbar, et al *Nat Med*2020)
 - Open source, QuPath-based tumor infiltrating lymphocyte



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 - **RNAseq:**
 - Harmonization/reprocessing of RNAseq via standard STAR-Salmon pipeline
 - Deployment of immune deconvolution algorithms + immune signatures
 - **AI/ML Implementation:** Implementation of dockerized platforms on Ohio Supercomputer Center 'Ascend' cluster cluster devoted entirely to intensive GPU processing (NVIDIA A100 80GB GPUs)



ASTOR AI/ML Readiness: Deliverables

- **Example Approved Projects:**

- **Aim 1 (Multi-trial Data):** Kalari (Mayo MN) – RNAseq predictor for TNBC; Steckline (Kansas) – DDIR and neoadj chemo response; Rajagopal (NCI) – germline:somatic interaction; Magbanua (UCSF) – CTCs and RNAseq to predict breast cancer outcomes
- **Aim 2 (ADDER):** Lustberg (Yale) – Meta-analysis of CIPN prediction
- **Aim 3 (Image Analysis):** Vater (Ohio State) – Image/RNAseq TILs classification; Chumsri (Mayo FL) – TLS and outcomes; Howard (UChicago) – AI-based pathology image subtyping and predictors

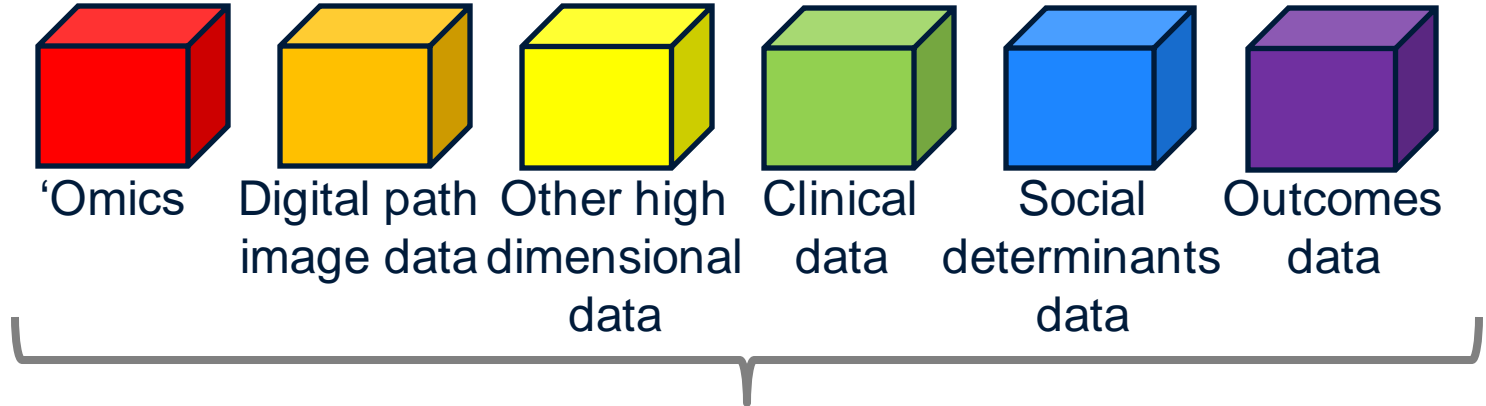
- **Publications:**

- Thompson KJ, Leon-Ferre RA, Sinnwell JP, Zahrieh DM, Suman VJ, Metzger FO, Asad S, Stover DG, Carey L, Sikov WM, Ingle JN, Liu MC, Carter JM, Klee EW, Weinshilboum RM, Boughey JC, Wang L, Couch FJ, Goetz MP, Kalari KR. Luminal androgen receptor breast cancer subtype and investigation of the microenvironment and neoadjuvant chemotherapy response. *NAR Cancer*. doi: 10.1093/narcan/zcac018. PMID: 35734391

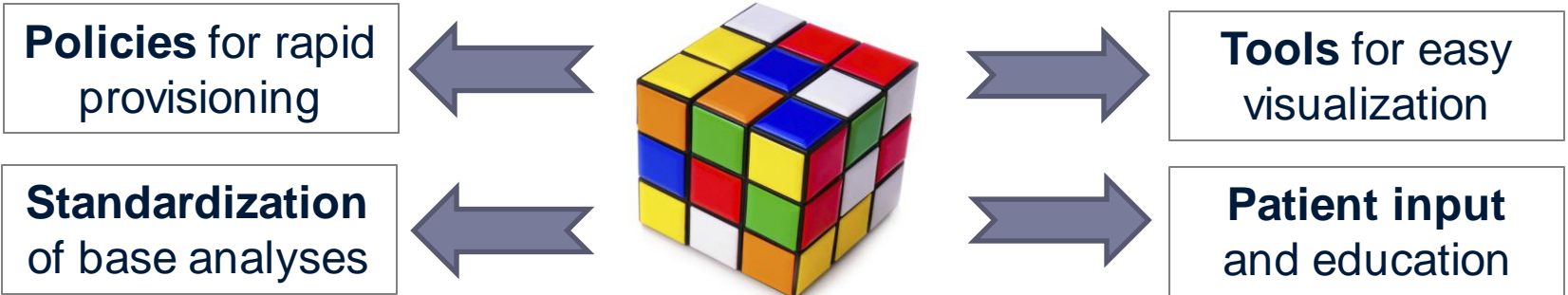
ASTOR: Innovation & Future Directions

- **First NCI NCTN cooperative group** to establish and operationalize a secure, cloud-based HIPAA-compliant repository for clinical and high dimensional data.
- **Harmonization** of 'omic and clinical/adverse event data across clinical trials.
- Coordination of **multiple distinct high dimensional data elements** for each patient (e.g. RNAseq, DNAseq, and digital pathology) facilitates AI/ML analyses beyond single modality efforts.
- **Deployment of tools to facilitate user accessibility** for non-informaticians and informaticians, including cBioPortal instances for individual trials.
- **Future Directions/Next Steps:**
 - Continue expansion of diverse data hosted and supported
 - User interfaces: cBioPortal, OpenSlide, immunogenomic tools
 - User feedback and input on trajectory

Future of Alliance Translational Research



ASTOR: Unified, expandible, secure



Thank You!

A-STOR

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Collaborators

ITSC: Chuck Perou

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PATIENTS.

Advocates

Patients who guide our research

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