

Table S1: Feature overview of published TMA management applications sorted by publication date

| Application name [Reference] | Supported features | | | | | | | | | | | | | | | | | | | | |
|---------------------------------|--------------------|-------------------|-----------------------|-----------------|-------------------------|------------------|-------------------------|-------------------------|---|--------------------|----------------|-------------------|------------------------|-------------------------|-------------------------|-----------------|---------------------|-------------------------|----------------------|----------------------|--------------------|
| | Clinical data | Tissue parameters | Multi species support | TMA layout data | Storage of donor images | Section tracking | Section quality control | Molecular analysis data | Storage of section and / or core images | Automated gridding | Manual Scoring | Automatic Scoring | Supported tissue types | Export as TMA-DES [1,2] | Export as MISFISHIE [3] | # of user roles | Relational Database | Controlled vocabularies | Browser based access | Platform independent | Publicly available |
| Bova <i>et al.</i> [4] | - | - | - | - | - | - | - | ✓ | - | - | - | - | any | - | - | 1 | ✓ | ✓ | - | - | - |
| Manley <i>et al.</i> [5] | ✓ | ✓ | - | ✓ | - | - | - | ✓ | ✓ | - | ✓ | - | 1 | - | - | 1 | ✓ | ✓ | - | - | - |
| TAD [6] | - | ? | - | ✓ | - | ✓ | - | ✓ | ✓ | - | ✓ | - | any | - | - | 1 | ✓ | - | ✓ | - | ✓ |
| Liu <i>et al.</i> [7,8] | ✓ | - | - | ✓ | - | - | - | ✓ | ✓ | - | - | - | any | - | - | - | - | - | - | - | - |
| Shaknovich <i>et al.</i> [9] | ? | ? | - | ✓ | - | - | - | ✓ | ✓ | - | ✓ | - | ? | - | - | - | - | - | - | - | - |
| Vrolijk <i>et al.</i> [10] | - | - | - | ✓ | - | - | - | ✓ | ✓ | ✓ | - | ✓ | any | - | - | - | - | - | - | - | - |
| CanSto [11] | ✓ | ✓ | - | ✓ | - | - | - | ✓ | ✓ | - | ✓ | - | 2 | - | - | 1 | ✓ | ✓ | - | - | - |
| TMAJ [12] | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | - | ✓ | - | any | - | - | 2 | ✓ | ✓ | - | ✓ | ✓ |
| Chen <i>et al.</i> [13,14] | ? | ? | - | ✓ | - | - | - | ✓ | ✓ | ✓ | ? | ✓ | any | - | - | ? | ✓ | ? | ? | ✓ | - |
| TmaDB [15] | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | - | ✓ | - | 5 | ✓ | - | 1 | ✓ | - | ✓ | ✓ | ✓ |
| Profiler [16] | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | - | ✓ | - | any | ✓ | - | ? | ✓ | ✓ | ✓ | ✓ | - |
| TMABoost [17,18] | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | ✓ | ✓ | ✓ | any | ✓ | - | 7 | ✓ | - | ✓ | - | - |
| TissueChips [19] | - | ✓ | - | ✓ | - | - | - | ✓ | ✓ | ✓ | ✓ | ✓ | 1 | - | - | - | ✓ | - | - | - | - |
| VTM [20] | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | - | ✓ | - | ? | - | - | 2 | ✓ | ✓ | ✓ | - | ✓ |
| Cruella [21] | ✓ | ✓ | - | ✓ | ✓ | - | - | ✓ | - | - | - | - | any | ✓ | - | 1 | ✓ | ✓ | ✓ | ✓ | - |
| Xperanto-TMA [22] | ✓ | ✓ | - | ✓ | - | - | - | ✓ | - | - | ✓ | - | 43 | ✓ | ✓ | >1 | ✓ | ✓ | ✓ | ✓ | - |
| TAMEE [this study] | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | - | any | ✓ | ✓ | >10 | ✓ | ✓ | ✓ | ✓ | ✓ |

1. Berman JJ, Edgerton ME, Friedman BA: **The tissue microarray data exchange specification: a community-based, open source tool for sharing tissue microarray data.** *BMC Med Inform Decis Mak* 2003, **3**:5.
2. Nohle DG, Ayers LW: **The tissue microarray data exchange specification: A document type definition to validate and enhance XML data.** *BMC Med Inform Decis Mak* 2005, **5**:12.
3. Deutsch EW, Ball CA, Bova GS, Brazma A, Bumgarner RE, Campbell D, Causton HC, Christiansen J, Davidson D, Eichner LJ et al.: **Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE).** *OMICS* 2006, **10**:205-208.
4. Bova GS, Parmigiani G, Epstein JI, Wheeler T, Mucci NR, Rubin MA: **Web-based tissue microarray image data analysis: initial validation testing through prostate cancer Gleason grading.** *Hum Pathol* 2001, **32**:417-427.
5. Manley S, Mucci NR, De Marzo AM, Rubin MA: **Relational database structure to manage high-density tissue microarray data and images for pathology studies focusing on clinical outcome: the prostate specialized program of research excellence model.** *Am J Pathol* 2001, **159**:837-843.
6. Coombes KR, Zhang L, Bueso-Ramos C, Brisbay S, Logothetis C, Roth J, Keating MJ, McDonnell TJ: **TAD: a web interface and database for tissue microarrays.** *Appl Bioinformatics* 2002, **1**:155-158.
7. Liu CL, Prapong W, Natkunam Y, Alizadeh A, Montgomery K, Gilks CB, van de RM: **Software tools for high-throughput analysis and archiving of immunohistochemistry staining data obtained with tissue microarrays.** *Am J Pathol* 2002, **161**:1557-1565.
8. Liu CL, Montgomery KD, Natkunam Y, West RB, Nielsen TO, Cheang MC, Turbin DA, Marinelli RJ, van de RM, Higgins JP: **TMA-Combiner, a simple software tool to permit analysis of replicate cores on tissue microarrays.** *Mod Pathol* 2005, **18**:1641-1648.
9. Shaknovich R, Celestine A, Yang L, Cattoretti G: **Novel relational database for tissue microarray analysis.** *Arch Pathol Lab Med* 2003, **127**:492-494.
10. Vrolijk H, Sloos W, Mesker W, Franken P, Fodde R, Morreau H, Tanke H: **Automated acquisition of stained tissue microarrays for high-throughput evaluation of molecular targets.** *J Mol Diagn* 2003, **5**:160-167.
11. Henshall S: **Tissue microarrays.** *J Mammary Gland Biol Neoplasia* 2003, **8**:347-358.
12. De Marzo AM, Morgan JD, Iacobuzio-Donahue C, Razzaque B, Faith DA: **TMAJ: Open Source Software to Manage a Tissue Microarray Database [abstract].** *Arch Pathol Lab Med* 2004, **128**:1094
13. Chen W, Foran DJ, Reiss M: **Unsupervised imaging, registration and archiving of tissue microarrays.** *Proc AMIA Symp* 2002, 136-139.
14. Chen W, Reiss M, Foran DJ: **A prototype for unsupervised analysis of tissue microarrays for cancer research and diagnostics.** *IEEE Trans Inf Technol Biomed* 2004, **8**:89-96.
15. Sharma-Oates A, Quirke P, Westhead DR: **TmaDB: a repository for tissue microarray data.** *BMC Bioinformatics* 2005, **6**:218.
16. Kim R, Demichelis F, Tang J, Riva A, Shen R, Gibbs DF, Mahavishno V, Chinnaiyan AM, Rubin MA: **Internet-based Profiler system as integrative framework to support translational research.** *BMC Bioinformatics* 2005, **6**:304.
17. Dell'Anna R, Demichelis F, Barbareschi M, Sboner A: **An automated procedure to properly handle digital images in large scale tissue microarray experiments.** *Comput Methods Programs Biomed* 2005, **79**:197-208.
18. Demichelis F, Sboner A, Barbareschi M, Dell'Anna R: **TMABoost: an integrated system for comprehensive management of tissue microarray data.** *IEEE Trans Inf Technol Biomed* 2006, **10**:19-27.
19. Rabinovich A, Krajewski S, Krajewska M, Shabaik A, Hewitt SM, Belongie S, Reed JC, Price JH: **Framework for parsing, visualizing and scoring tissue microarray images.** *IEEE Trans Inf Technol Biomed* 2006, **10**:209-219.
20. Conway CM, O'Shea D, O'Brien S, Lawler DK, Dodrill GD, O'Grady A, Barrett H, Gulmann C, O'Driscoll L, Gallagher WM et al.: **The development and validation of the Virtual Tissue Matrix, a software application that facilitates the review of tissue microarrays on line.** *BMC Bioinformatics* 2006, **7**:256.
21. Cowan JD, Rimm DL, Tuck DP: **Cruella: developing a scalable tissue microarray data management system.** *Arch Pathol Lab Med* 2006, **130**:817-822.
22. Lee HW, Park YR, Sim J, Park RW, Kim WH, Kim JH: **The tissue microarray object model: a data model for storage, analysis, and exchange of tissue microarray experimental data.** *Arch Pathol Lab Med* 2006, **130**:1004-1013.