Collaborative Remote Medical Imaging Exploration for Brain Science

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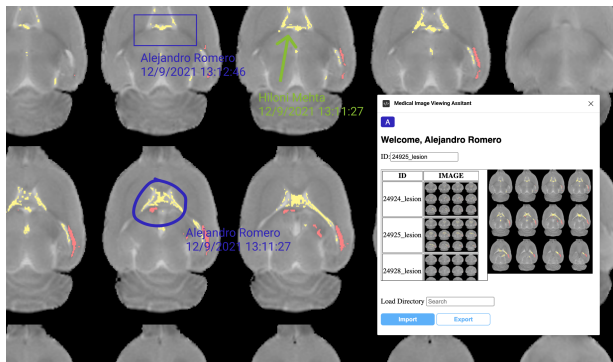Brown University

Figure 1: Demo of Figma plugin for collaborative medical imaging exploration

ABSTRACT

We have developed a novel browser-based tool that allows researchers to remotely and collaboratively explore medical images and annotate them in real time. This paper presents a plugin that extends Figma, a popular collaborative design tool. By evaluating the various features of our plugin in comparison to our collaborators' current workflow, we assess the values of a collaborative annotation workflow in a browser-based environment versus annotation via more rudimentary means such as drawing over a screen-share during a video conferencing meeting.

Keywords: Annotation, collaboration, human-computer interaction, evaluation, medical imaging.

1 INTRODUCTION

A variety of collaborators across different domains and institutions helps reduce the bias associated with performing research in a single setting. However, current tools for viewing and annotating medical images focus on single user experiences and generally do not provide an efficient workflow for collaboratively evaluating data, making observations, and saving findings for future reference.

Our tool benefits scientific research by allowing collaborators from different institutions to quickly and effectively explore data together, regardless of physical location. The software provides researchers the ability to annotate medical imagery, save a comprehensive history of these annotations, and share their explorations with collaborators. By addressing pain points in present workflows, we found greater efficiency when using our software in comparison to current processes; this has been evaluated through user testing, which combined both formative and summative evaluation techniques in the form of observational studies and a qualitative survey.

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2 RELATED WORK

Presently, analysis of medical images is typically conducted locally in a single-user environment. Popular examples of software used in such workflows include 3DSlicer [9] and ImageJ [12]. These and similar tools do not allow for real-time remote image exploration and annotation, and contain graphical user interfaces (GUIs) that assume a certain level of domain expertise, which may dissuade non-expert collaborators from participating in image exploration. We address these issues in our implementation (see Approach). Various software tools have been created to address the gaps in single-user experiences, namely to allow for real-time collaboration and annotation logging. Such software include Mind-Control [5], ePad [10], and Med3D [7]. However, many of these software suites have since become deprecated or simply do not provide smooth user experiences, an issue we address in our tool's implementation. Our approach is further supported through user testing (See Hands-On User Study and Questionnaire).

3 DOMAIN GOALS

Currently, our scientific collaborators utilize screen-sharing annotation features in the Zoom videoconferencing software to perform real-time medical image exploration. They have reported that this workflow is clunky and time-consuming. Our tool improves efficiency during collaborative exploration of medical images via features that result in faster user performance, as we found in our user studies. Our tool has also been designed to assume no set degree of domain-specific knowledge; that is, our tool can be used by both experts and non-experts in the same collaborative environment.

4 APPROACH

Our collaborators' current Zoom workflow relies on a single "driver" to share their screen and complete requests from other meeting attendees. This "driver" then has to export a screen capture of the annotations on-screen, name the file manually, and store it locally for future reference. Due to the pain points highlighted by our collaborators in their current workflow, our tool's main purpose is to allow for robust collaborative image annotation in an environment with a relatively small barrier to entry. Because many similar independent projects have become deprecated, we decided to

build upon Figma, a widespread and routinely maintained collaborative design tool. Via a Figma plugin, users can access our tool online without any local dependencies and view a persistent annotation and version history in a single private environment shared with their collaborators. Each collaborator can view their own instance of the shared environment on their screen, accompanied by their own GUI, such that they need not rely on a single "driver" to manage the scene view (though an option to "view the driver's screen" remains present).

5 ARCHITECTURE AND IMPLEMENTATION

Our tool is built upon Figma's existing annotation framework, adding functionality for quickly and efficiently importing and exporting medical images, assigning users colors in the shared environment that persist across uses, generating labels with timestamps and usernames under corresponding annotations, and directly saving image annotations for future reference. We worked closely with our collaborators to implement these features to be practical and efficient by minimizing overhead and time spent during exploratory tasks.

6 HANDS-ON USER STUDY AND QUESTIONNAIRE

The software was tested using a combination of observational studies and a qualitative survey. Four participants were recruited: two expert collaborators and two non-experts. Participants were asked to complete a variety of tasks in both the Zoom screen-share workflow and the Figma plugin workflow. They were asked to complete tasks independently, then to complete tasks collaboratively with another participant. After the collaborative tasks, participants completed a questionnaire prompting them to provide feedback and rate statements regarding the software on a likert scale.

6.1 Evaluation Criteria

Single user observational studies were evaluated on time taken in seconds to complete each task in the Zoom and Figma workflows, respectively. The collaborative sessions consisted of two participants exploring images together in both the Zoom and Figma workflows. They were given two minutes to collaboratively generate insights together. After the allotted time was over, the number of insights (measured by intentional annotations) generated during that time was recorded. Finally, users were all given a questionnaire to provide feedback as well as their ratings of statements regarding each of the workflows (e.g. "Annotating images was intuitive in Figma"). These statements were each rated on a likert scale (1-5, from "strongly disagree" to "strongly agree").

6.2 Results

Times for all participants in the independent user observational studies were averaged and normalized, demonstrating faster task completion time using the Figma plugin for almost all assigned tasks (Table 1).

	Zoom Workflow (in seconds)	Figma Workflow (in seconds)
Previewing Image	13.5 ± 4.04 26.33 ± 8.02	5.25 ± 1.71 28.25 ± 18.02
Importing Image	39.67 ± 11.37	49.25 ± 33.65
Crop	17 ± 7.70	9 ± 2.64
Zoom	7.5 ± 2.081	4.5 ± 2.081
Annotation	12.25 ± 3.5753	8.1 ± 1.11
Exporting image	51 ± 15.132	12.75 ± 1.5

Table 1: Normally distributed values for time taken (in seconds) to complete tasks in the Zoom and Figma workflows.

The number of insights generated from the 2 minute collaborative sessions were compiled and averaged to 7±1 for both the Zoom and Figma workflows. The questionnaire demonstrated an overall preference for the Figma workflow over Zoom, with users noting that the Figma plugin was more intuitive and enjoyable to use. However, a few unrefined features in our early-stage tool resulted in preference for some of the more familiar tools in Zoom.
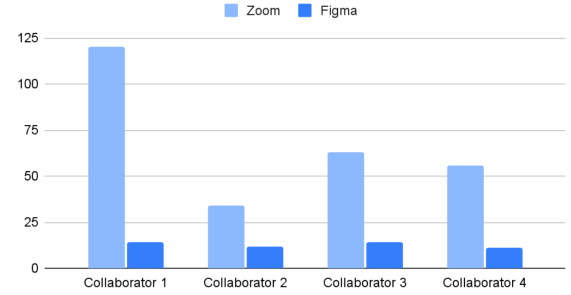

Figure 2: Time taken (in seconds) for users to export an image and its associated annotations in each workflow.

6.3 Discussion

Overall, the results of our user studies demonstrate strong potential for our Figma plugin as a viable tool for collaborative medical imaging exploration and annotation. Across nearly all tasks, users were more efficient when using the Figma plugin than when using the Zoom workflow. To minimize familiarity bias, we acclimated users to the Figma software environment by asking them to complete two blocks of tasks prior to the tasks done in the Zoom workflow. The learning curve in Figma was relatively steep, leveling off after just two blocks of tasks. The third block of tasks consisted of the same tasks completed in Zoom, and were thus the tasks utilized for our data comparison. Our tool's efficiency was most notable in our observations of image exporting (Figure 2).

The number of insights generated in both the Zoom and Figma workflows were the same, suggesting that the significance of our tool lies in the speed with which tasks are completed in the software, not the generation of ideas themselves [11]. Users noted their preference for full control over their own instances of their screen in Figma in comparison to having a single "driver" in Zoom. Users also appreciated the persistent color-coding of user annotations and the timestamps associated with them, allowing for easily keeping track of the annotations made by each user for record-keeping purposes.

7 CONCLUSION

In this extended abstract, we have presented our work toward more efficient paradigms for a software tool that allows users to collaboratively explore and annotate medical images in a browser-based environment. Moreover, we have generated evidence through user testing that supports many of the feature enhancements employed in our tool. Our results suggest that this tool increases user efficiency when completing common tasks in a collaborative exploration environment, a positive indication that our implementation is a step toward a more holistic methodology for efficient and comprehensive collaborative medical imaging annotation.

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CluMMP: Development and Evaluation of Comparative Visualizations of Galaxy Cluster Mergers

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ABSTRACT

We present and evaluate *CluMMP* (Cluster Merger Matching Program), a comparative visualization tool for matching observed galaxy cluster mergers to corresponding simulations. Due to the complex dynamics and extremely slow evolutions of galaxy cluster mergers, observationally determining the elapsed time of these events is a difficult and uncertain task. This is typically done by matching a merger to a simulation which is similar in morphology and separation to a given observation. Our tool, CluMMP, aims to expedite this matching process by employing a likely-match simulation algorithm and implementing three visualization methods for studying candidate simulations. Our approach performs a one-dimensional nearest neighbors search on precomputed cluster centroid separations, aligns simulation and observation cluster centroids, and displays simulation images in a browser-based UI using three visualizations: "Side-by-side," "Flicker," and "Difference." Our quantitative evaluation of this tool yielded suggests that the "Difference" visualization is the most effective whereas "Flicker" is least effective, although qualitative evidence suggests that the effectiveness of each visualization method varies with the similarity between candidate simulations.

Keywords: Comparative visualization, application, methodology, evaluation.

1 INTRODUCTION

Galaxy cluster mergers are collisions between two gravitationally bound groups of galaxies. Such collisions represent the last stage in the formation of the structure of our universe and thus are important objects in cosmology. One property of interest of a merger is its timescale, i.e., how long the event has been ongoing; however, cluster mergers are slowly evolving events (in the order of 10^9 years) and thus obtaining this information to good approximation from observation alone is difficult.[5] This is typically done by comparing observed mergers with simulations from which we can extract such information[9]; however, current approaches to characterizing timelines of cluster mergers from simulated collisions are largely non-systematic or heuristic.

This extended abstract presents *CluMMP* (Cluster Merger Matching Program), a tool developed to address the demand for an accessible cluster merger observation-simulation matching workflow. The tool seeks to eliminate several degrees of freedom encountered in the matching process by algorithmically producing likely-match candidates, aligning cluster centroids, and providing users three visualization methods; the design and data processing pipeline of the tool is elaborated on in §3. Our tool also expedites the data acquisition process by providing a web-based UI which allows users to load, view, and interact with remote FITS data.

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Figure 1: Clusters 1E2215 and 1E2216 experiencing a merger. Composite X-Ray and optical bands.[1]

In addition to presenting CluMMP, this extended abstract presents and discusses the results of an evaluation of the three visualization methods implemented by CluMMP; see §4. In short, we find quantitative evidence suggesting that a "Flicker" visualization yields the shortest task completion time, and qualitative evidence suggesting that the utility of each visualization varies with similarity between candidate simulations. We discuss these results in §5, and open questions and future directions to take the tool are considered in §6.

2 BACKGROUND AND RELATED WORK

There are no existing parameter space exploration tools for cluster mergers, although there are similar tools for analysis of galaxy mergers.[2] In particular, there are no browser-based tools visualization tools designed to facilitate matching observed astronomical data to simulated data products. Furthermore, little work has been done in applying and evaluating the effectiveness of comparative visualization techniques in the context of simulated versus observed images of hydrodynamic phenomena. State of- the art algorithmic image comparison is not sufficiently generalizable to 2D projections of 3D subjects, and one expects the performance of such approaches to decrease given the chaotic nature of cluster dynamics[8][4].

There are existing discussions of comparative visualization techniques, philosophies, and approaches[5][4] and high-level implementations of comparison-focused pipelines[3][7], but little work has been done on evaluating the relative effectiveness of each of these methods, in particular as applied to a simulation-observation matching procedure.

Our tool relies on ZuHone et al.'s Galaxy Cluster Merger Catalog (GCMC) for simulation data; in particular, we access data from the yt Hub (`girder.hub.yt`) via the Girder Python API, and acknowledge that the functionality of CluMMP is reliant on the upkeep and extension of these catalogs and tools.[10]
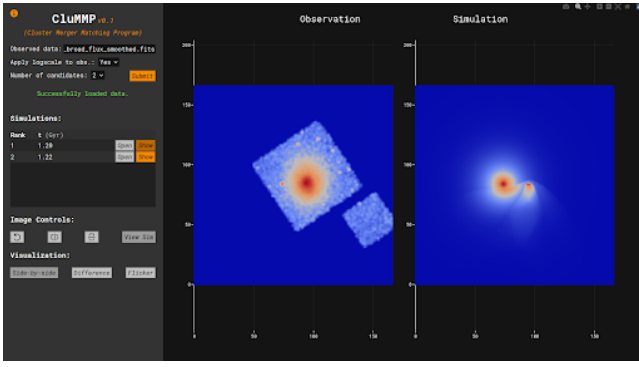
Figure 2: CluMMP with "Side-by-side" visualization.

3 METHODOLOGY

3.1 Data

GCMC simulations were pre-processed in order to obtain cluster X-Ray emissivity centroid separation for usage in the nearest-neighbors candidate suggestion algorithm, and results were stored in a SQL database. Upon receiving a request for n candidates, CluMMP performs a one-dimensional nearest-neighbors search on centroid separation obtained from observation data. CluMMP then uses the Girder Python API (girder.readthedocs.io) to download GCMC data products, applies the alignment procedure to simulation and observation data (see §3.2), generates the "Difference" visualization for each simulation, optionally applies a pixel-value stretch to the observation data, then submits a response to the client with appropriate data. Observation data are obtained through a user-provided path to any FITS file in the Oscar computing cluster, which has been mounted to the CluMMP backend.

3.2 Image Alignment for Comparison

Aiming to eliminate superfluous degrees of freedom which may inhibit the observation-simulation matching worfklow, CluMMP eliminates translational and rotational variation among simulations by aligning all pairs of cluster centroids across observation and simulation data. We define the centroid of a cluster as the peak X-Ray emissivity point in the cluster. This point is estimated by computing the level sets of the surface represented by the image's pixel data, obtaining the highest-value level set containing two disconnected paths, and finding the centroid of each path.[1]

We then determine the largest image in area I_{ref} and use this as reference for alignment and resizing in order to prevent loss of information from downsizing. A "source triangle" $\triangle_{\text{src}}$ is constructed by using the cluster centroids of I_{ref} as base vertices $\mathbf{x}_1$ and $\mathbf{x}_2$ and generating a third vertex $\mathbf{x}_3 = \mathbf{F}(\mathbf{x}_1, \mathbf{x}_2)$ from the base vertices such that the triangle is isosceles. A "destination triangle" $\triangle_{\text{dest}}$ is then computed by positioning two base vertices $\mathbf{x}_1'$ and $\mathbf{x}_2'$ along the horizontal midline of I_{ref} such that their midpoint is the center of I_{ref}, then again finding an apex vertex $\mathbf{x}_3' = \mathbf{F}(\mathbf{x}_1', \mathbf{x}_2')$. Then for every simulation/observation image I_i we perform the affine transformation defined by $\triangle_{\text{src}_i} \to \triangle_{\text{dest}}$, and crop I_i on the scale $6 \cdot |\mathbf{x}_2' - \mathbf{x}_1'|$ at $1:1$ aspect ratio to emphasize local morphology. Users are provided with transform controls to explore the additional degree of freedom of image orientation.

3.3 Visualization Methodologies

We three visualization methods for displaying and comparing a selected simulation against an observation. The "Side-by-side" vi-

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[1] Defined by $(1/N)\overline{\sum_i^N \mathbf{x}_i}$ where N is the number of points in that path and $\mathbf{x}_i = (x_i, y_i)$ are the coordinates of that point.

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sualization displays the observed merger next to a selected simulated merger; see Figure 2. The "Difference" visualization displays a heatmap of $|I_{\text{sim}}(\mathbf{x}) - I_{\text{obs}}(\mathbf{x})|$ where $I_{\text{sim(obs)}}(\mathbf{x})$ is the value of the pixel of the simulation (observation) at position $\mathbf{x}$. Lastly, the flicker observation overlays the aligned images and allows the user to toggle between the observation and simulation images.

4 RESULTS

4.1 Web Application

A demo distribution of CluMMP can be accessed at lucasbrito.site/clummp; note that the demo version of the software is a static webpage and has limited functionality.

4.2 Evaluation

The visualizations implemented by CluMMP were evaluated using the standard speed/accuracy metric. In order to perform the evaluation, five simulations with similar cluster separations were selected from the GCMC, and from each a mock observation was generated using GalSim's photon shooting method.[6] A professional astronomer was given the task of, given a mock observation and the five selected simulations, find the simulation from which the observation was generated. Time was measured in seconds taken to confidently deduce a match-simulation, and accuracy was measured as a Boolean representing whether the chosen simulation was correct. The user was instructed to perform this task using four different workflows: using each of the three visualizations in isolation, and using all three. For the latter workflow, time spent using each of the visualizations was measured; results are displayed in Table 1. These workflows were not compared against the existing workflow due to conflation with efficiency obtained from the simulation suggestion algorithm.

In addition, after the completion of the quantitative evaluation, the user was asked to provide an oral evaluation of the tool. The user stated that the tool is "extremely useful" and "really powerful." The user also postulated that as similarity between simulations increases, "Difference" and "Flicker" visualizations would become more effective, but that for dissimilar simulations "Side-by-side" is the most effective. Lastly, the user suggested that a signed difference visualization would display information useful for the matching procedure.

5 DISCUSSION

The evaluation results displayed in Table 1 suggest that all visualizations provide sufficient information to accurately deduce a correct matching simulation, and that the least effective visualization method is "Flicker" whereas the most effective method is "Difference." For the "All" workflow, wherein the user was allowed to freely use all visualizations, the user spent the majority of the time using the "Flicker" visualization; we postulate that these results are due to a steeper learning curve for the "Flicker" visualization given its interactive component.

6 CONCLUSION

This extended abstract presented CluMMP, a browser-based utility for matching observed and simulated galaxy cluster mergers. We in addition presented our evaluion of this tool, which demonstrated qualitatively that the tool is of significant utility to astronomers, and that in particular a "Difference" visualization is most effective in aiding the matching procedure.

Further work on CluMMP entails updating the tool as the GCMC expands, implementing a signed-difference visualization, filtering point sources from the centroid-identification algorithm, and distributing the full version of the application with implemented support for observation data from a user-defined SMB-compliant directory and user-uploaded observation data. Further evaluation work

Table 1: Evaluation results.

Vis	Time (s)	Correct sim.	Time spent using
Side-by-side	49	True	7.8%
Difference	14	True	3.1%
Flicker	66	True	89.1%
All	56	True	100%

entails determining the accuracy of the simulation-suggestion algorithm, performing further user testing with simulation data with varying degrees of similarity, and evaluating a signed difference visualization against the existing "Difference" visualization.

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Collaborative Remote Exploration Of Medical Imaging using Figma

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1 ABSTRACT

We developed a web-based collaborative platform that allows researchers from different fields to view, explore, annotate and discuss MRI data collaboratively. The new developed workflow uses the design tool: Figma for basic features and additional features are supported by plugins developed in Figma.We evaluated certain important features necessary for collaborative exploration of MRI data by getting insights on existing workflow consisting of file managing application and zoom and developed a new workflow using Figma Plugins. We further evaluate both the workflows and provide insights on each workflow based on feedback from user testing.

Keywords: Figma Plugin, Collaboration, Annotation, Evaluation, Exploration.

2 INTRODUCTION

We created a workflow that can help experts explore, annotate, collaborate and record previous discussions on images to make it easier to collaboratively perform research. We studied the current workflow of exploring MRI data where the actions were performed by a single driver using zoom application. Our newly developed workflow supports individual driver where each collaborator could independently view and import the images, annotate collaboratively or independently on their own time and export annotations locally. The main focus of our workflow was to provide support for collaborators to explore images independently or collaboratively at their own time rather then a fixed specific time in a zoom meeting with single driver. We perform both quantitative as well as qualitative evaluation between previous workflow and our newly developed workflow by calculating time for completing exploration tasks by collaborators and their feedback on experiences with each of the workflow. Additionally, we also got insights on learning curve for Figma to get an idea on time take by users to get acquainted to this new design software.

Our developed workflow aims to allow experts from different field to collaborate, saves expert's time by allowing independent and synchronous exploration and easy tracking of previous records.

3 RELATED WORK

MindControl: MindControl[2] is an efficient collaborative web-based application with image viewer, editor, link descriptive metrics and annotation toolbox to help experts study data and provide research insights. However, this software isn't supported any longer since it fails to have required bandwidth, has local dependencies and doesn't provide smooth user experience. Our workflow supports in-depth features for annotations and collaboration by providing time stamp with user name for annotation tracking, have bandwidth to support collaboration since it uses Figma software and is improved upon based on user-testing.

From the previous work[2] [1] [4][7], we could see that most of the existing workflow that provides either single user annotation support or lacks all essential features in same workflow. Each of this research provides annotations or collaborations, however not a very strong proposal of a user-efficient workflow for all features: annotations, collaborations, keeping track of previous annotations, etc. Our developed workflow will focus on supporting all important features necessary to make collaboration and research easier.

4 METHODS

Based on the analysis from the previous existing workflow, where collaborators addressed issues with single driver, working on collaboration at a specific time in meeting and keeping track of previous annotations, we decided on a workflow that will address those issues. Since, Figma: a collaborative design work space supports individual instances, infinite workspace to import images, text and hand-drawn annotations, collaborations, etc. efficiently, we decided to use this software to build a new workflow to avoid any local dependencies. Even though Figma has few in-built features, we developed Figma plugin to support additional features such as previewing images, easily importing images from the plugin, assigning different annotation color to each user, adding user and time stamp to each annotation and export image automatically with file name and time for easy record keeping of previous annotations. Since, Figma plugin supports independent instances where each user can explore,import and annotate images using Figma Plugin independently on their own time or collaboratively, it solves the issue of single driver raised in previous workflow. Based on the feedback received from the collaborators from previous workflow, we worked on building on additional features in Figma plugin and provided smooth user experience by improving upon user's feedback.
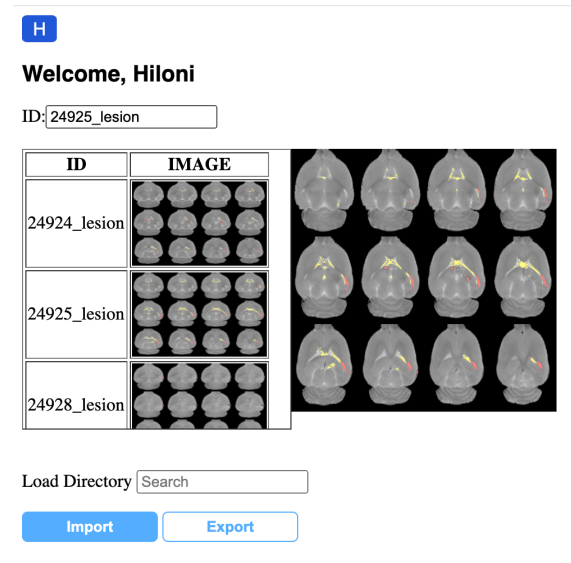

Figure 1: Figma Plugin

Since our collaborator lacked familiarity to Figma, we performed evaluation by giving some tasks to users and studying learning curve of Figma for each user. We evaluated time taken by each user to perform tasks in previous and our developed workflow and got more insights on each of the workflow by survey.

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5 RESULTS

We performed evaluation by giving tasks to be performed to four collaborators. Each user test involved them performing tasks independently and collaboratively in file managing application + zoom workflow and then using Figma Plugin workflow.

Since, most of our collaborators were familiar to zoom and weren't acquainted with Figma workflow, we decided to get insights on learning curve of figma by giving some annotation tasks shown in 2.
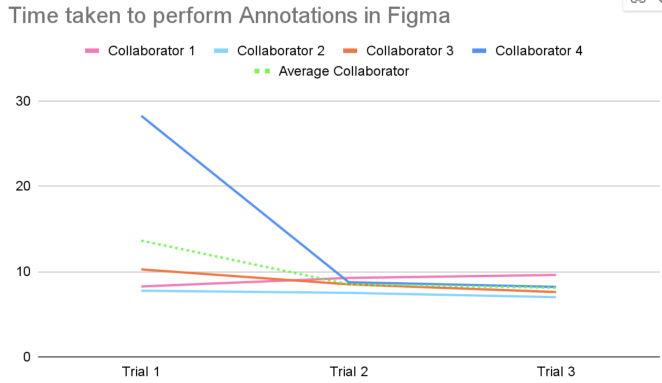

Figure 2: Learning curve for Figma, each trial consisted of 5 annotation tasks

Quantitative Insights: We recorded time taken by each user to perform given tasks to get insight on each workflow. The average time taken(in seconds) with standard deviation, for each of the tasks and workflow is mentioned in the Table 1.

Tasks	Previous Work-flow Average Time taken(seconds)	Developed Work-flow Average Time taken(seconds)
Preview Image By Name	13.5 ± 4.04	5.25 ± 1.71
Preview Image By Thumbnail	26.33 ± 8.02	28.25 ± 18.02
Importing Image	39.67 ± 11.37	49.25 ± 33.65
Zoom	7.5 ± 2.08	4.5 ± 2.08
Crop	17 ± 7.70	9 ± 2.64
Annotate	12.25 ± 3.58	8.1 ± 1.11
Export Image	51 ± 15.132	12.75 ± 1.5

Table 1: Time taken to perform tasks- Previous Workflow vs Developed Workflow

Qualitative Insights: At the end of user testing, each user provided insights about their experience with each of the workflow by filling in their responses in the questionnaire. The Table 2 shows the summary of the insights received from users for each of the workflow.

Tasks	Feedback on previous workflow	feedback on developed workflow
Preview and Import	Familiarity with file managing application system helped. Limited space and arrangement of images were harder on fixed zoom screen share.	Figma provides unlimited space to arrange multiple images. Lot of scrolling to search image and preview of images were small in Figma Plugin.
Annotation	When image is moved correlation between image and annotations isn't maintained	Liked viewing user and time stamp on annotations
Collaboration	Didn't prefer one driver, harder to keep track on user of each annotation	Preferred having independent instances and viewing other person's cursor.
Export Image	Hard to keep track of folder and name image every time	Liked the inbuilt export file name

Table 2: Feedback provided for: Previous vs Developed Workflow

6 DISCUSSION

From the feedback received by collaborators, it could be inferred that Figma proved to be a good platform for supporting annotation and collaboration. The feedback shows the user's preference of having independent instances instead of a single driver. Additionally, the feedback suggested positive responses for color-coded annotations, user and time stamp for each annotation as well as easy import and export of images. In most of the tasks performed by users, the new developed workflow(Figma) provided much faster results compared to previous Zoom workflow.

The time taken to preview and find image by thumbnail were performed faster in previous workflow rather than Figma. The reason behind this could be that the users are familiar with the computer file system so were able to explore faster. For importing image, we noticed that few collaborators could import images faster in Figma compared to previous workflow and vice versa. Figma provides two options to import image- drag and drop which took lesser time than zoom, place image from menu which took more time. Apart from this, Figma provides infinite space allowing users to import multiple images and place each image side by side. The tasks performed for annotation, exporting images were performed much faster in Figma workflow compared to previous workflow. The export of image and annotations were done much faster since the user just needs to select the annotation and images and it will automatically fetch name of image and timestamp making it easy for user to automatically save it with new name for keeping track of annotations.

7 CONCLUSIONS

Based on the evaluation results, Figma: the collaborative design tool proved to be a good platform for experts to explore, annotate and collaborate. Even though most users aren't acquainted with Figma, the learning curve shows positive response for encouraging the use of such design softwares for collaboration. From the quantitative insights received, the tasks in Figma were performed quicker than previous Zoom workflow. Based on the user feedback, the new workflow could solve the existing issues in previous workflow, improve the speed for completing tasks and provided better support for annotation, collaboration and keeping track of annotations.Figma eventhough being a design software showed promising results for collaboratively exploring scientific imaging.

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