Center for Macromolecular Modeling and Bioinformatics

VMD 2011 User Survey Report

Administration and Results

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VMD 2011 SURVEY REPORT

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Executive Summary

The 2011 VMD User Survey was announced to a random portion of 56,575 VMD 1.8.7 and 1.9 users on August 2, 2011 and ran until August 8 of that year. Survey questions examined user satisfaction, the impact of the program on work quality, and user ratings of existing and planned features.

- A total of 934 usable responses were returned for the survey, a sample which provides a confidence level of 95% and a confidence interval of +/-3% (i.e., one is 95% confident that an answer from the sample represents the population value at plus or minus 3%)
- 94% of respondents indicate they use VMD for research
- 47% of users reported that they do biomedically relevant work with NAMD
- 16% of all respondents reported at least partial NIH funding
- Most users, 73%, have more than one VMD user at their site, and 60% use VMD for all or most of their molecular visualization tasks
- 90% of users are satisfied with VMD
- 87% of respondents indicated that VMD is important to their research
- 82% of users indicated that VMD has improved the quality of their work
- When asked to rate planned VMD features, the greatest interest was in improving built-in trajectory analysis capabilities, improving publication rendering features, and in the capability to analyze/visualize simulation trajectories larger than available computer memory.

Overview

VMD (Visual Molecular Dynamics) is a molecular visualization program for displaying, animating, and analyzing large biomolecular systems using 3-D graphics and built-in scripting. More information about the program is available at the VMD home page (www.ks.uiuc.edu/Research/vmd). The VMD 2011 survey is part of an ongoing effort (similar surveys were conducted in 2006, 2003 and 2000) to ensure that VMD is up to date, relevant, and of high quality. VMD users were identified via registration records, and contacted via email with requests that they complete an on-line survey during August 2011 (see appendix for survey questions; the survey form is available here: www.ks.uiuc.edu/Research/vmd/survey/survey2011.html). The following report details the administration and results of the survey.



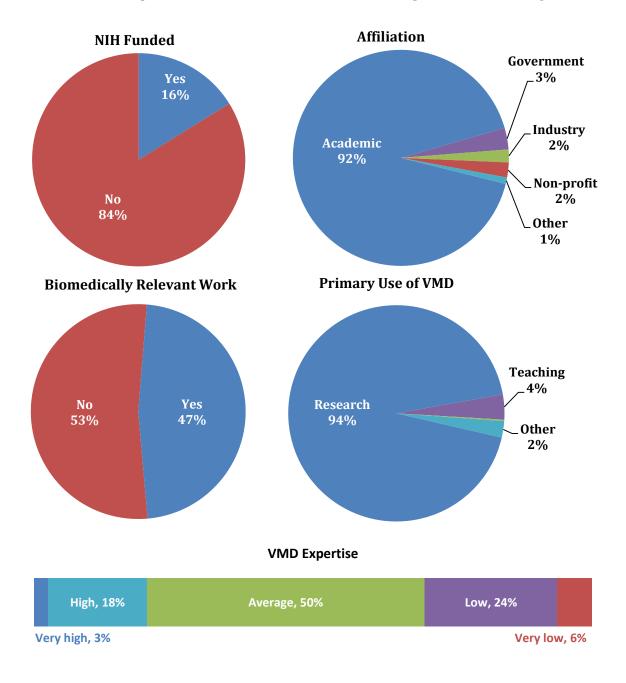
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2011 VMD Survey Results

VMD USER PROFILE

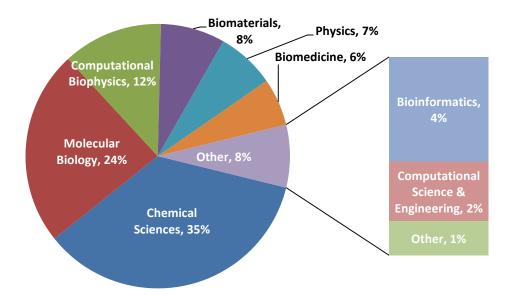
- 92% of users report academic affiliations
- 47% of respondents use VMD for biomedically relevant work
- 94% of respondents use VMD for research; 16% reported NIH funding



Visual Molecular Dynamics

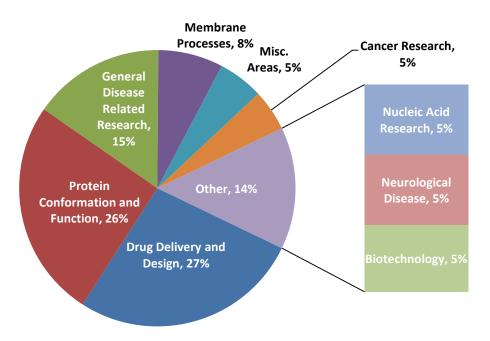
RESEARCH INTEREST / AREA OF STUDY

• Chemical Sciences, Molecular Biology, and Computational Biophysics encompass 71% of the areas of study of VMD users



RESEARCH INTEREST / BIOMEDICALLY RELEVANT WORK

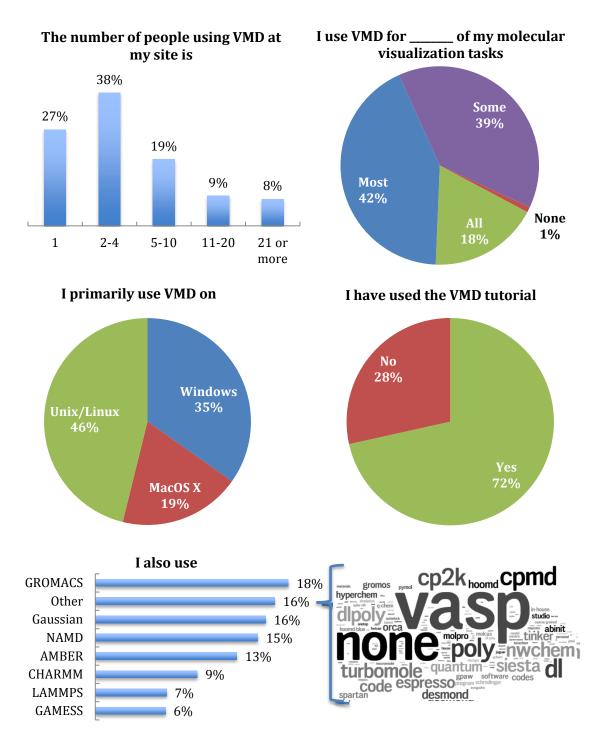
• Drug delivery and Design, Protein Conformation and Function, and General Disease Related Research describe 68% of the biomedically related work of VMD users



Kisual Molecular Dynamics

VMD USAGE PROFILE

- 60% of respondents report using VMD for most or all of their molecular visualization tasks.
- Most respondents have 2-4 VMD users at their site, and a slight majority favors the Unix/Linux platform
- Almost ³/₄ of respondents report using the VMD tutorial

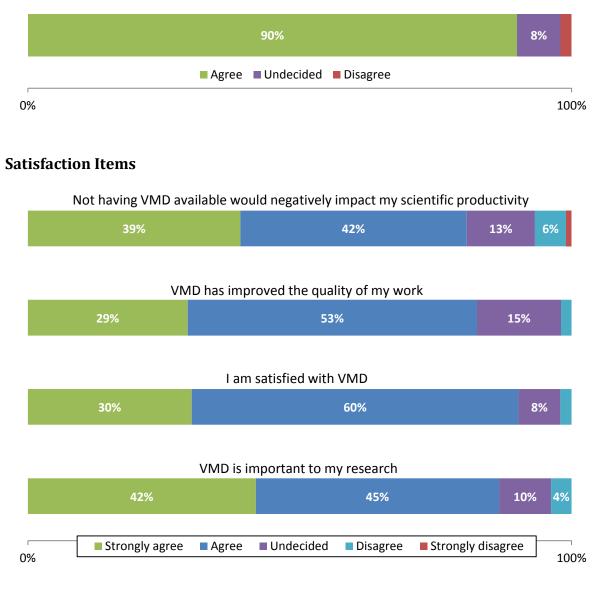


Visual Molecular Dynamics

SATISFACTION RATINGS

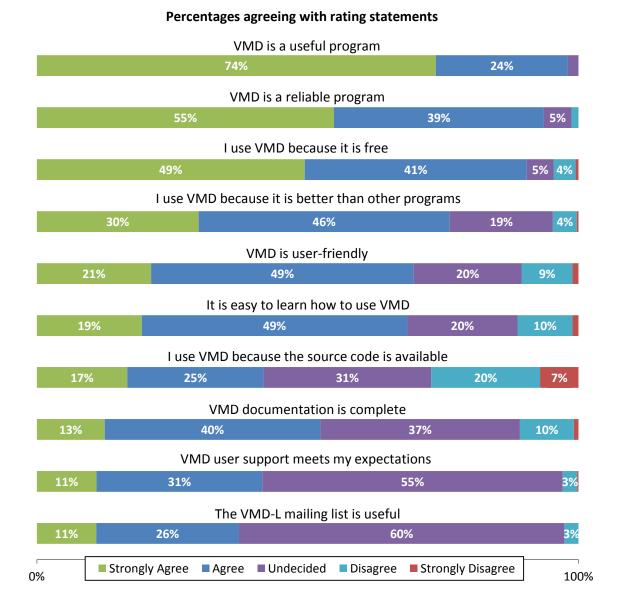
- 90% of users strongly agree or agree that they are satisfied with VMD
- 87% of respondents indicate that VMD is important to their research
- 82% agree that VMD has improved the quality of their work
- 81% of users indicate not having VMD available would hinder their research productivity

Percentage agreement with the statement "I am satisfied with VMD"



RATINGS OF SUPPORT, DOCUMENTATION AND OVERALL USABILITY

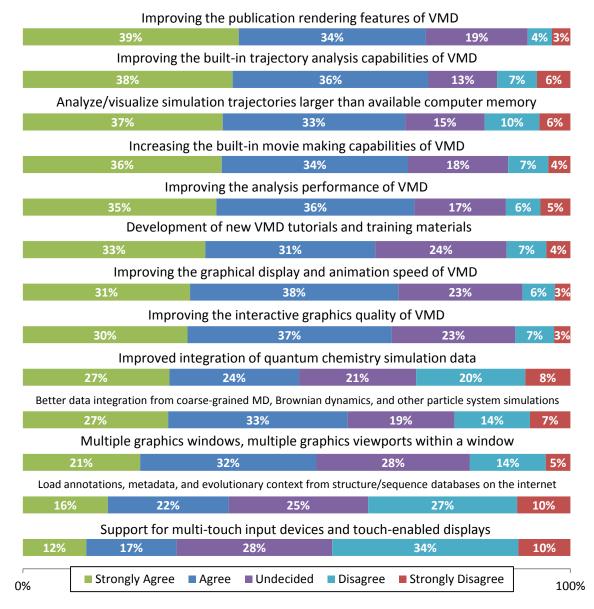
- Primary reasons for using VMD are that it is useful, reliable and free.
- 75% of respondents feel that VMD is better than other programs.
- 70% of respondents indicate that VMD is user-friendly, and 68% agree that it is easy to learn how to use VMD





FUTURE VMD DEVELOPMENT

- Improving the built-in trajectory analysis capabilities of VMD is a priority for 74% of survey respondents
- 73% of users agree that improving the publication rendering features of VMD is a priority
- 70% of respondents would like to see VMD analyze/visualize simulation trajectories larger than available computer memory (out-of-core processing)

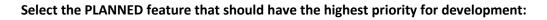


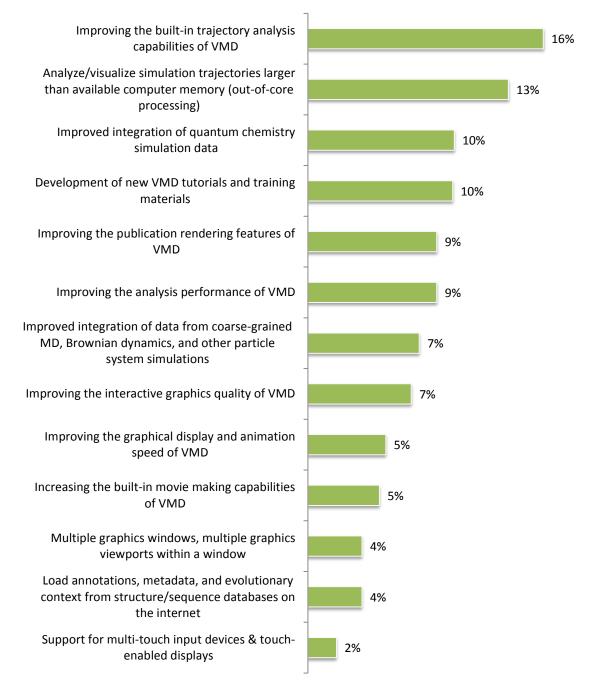
Rate the importance of the following PLANNED features to your work



FUTURE VMD DEVELOPMENT, continued

 When asked to rank the importance of planned features, users selected improving VMD's trajectory analysis capabilities, adding analysis/visualization capabilities beyond available computer memory, and improved integration of quantum chemistry simulation data as priorities







Survey Methodology

Following are details about the administration of the survey, including survey method, target population, survey schedule and response rates, sample validity, and questions used on the survey.

SURVEY METHOD

Population members received an e-mail solicitation asking them to complete an online survey, with the link to the survey containing information about the user. Participants were asked to complete all items on the survey form and submit their responses; upon submission, participants were to complete any items they had skipped, with an option to submit without doing so. After submission, users were thanked for their participation.

TARGET POPULATION AND RANDOM SAMPLE

Users of VMD 1.8.7 (released August, 2009) and VMD 1.9 (released March, 2011), as identified via registration records, constituted the target population of the survey.

SURVEY SCHEDULE AND RESPONSE RATE

The initial solicitation email was sent to 24,000 randomly selected users (including 16,000 who only downloaded a single version of VMD) of the 56,575 on 2 August 2011. The survey was not sent out to all 56,575 users, as it was estimated that using 24,000 would generate the needed sample. The survey was concluded 8 August 2011, by which time 934 usable responses had been received, corresponding to a 3.9% response rate.

DATA EDITING

After review, 25 responses were removed from the dataset due to incomplete submissions, or comments made in the survey itself indicating the respondent had downloaded but not used VMD.

CONFIDENCE IN SURVEY SAMPLE SIZE

Data editing reduced the sample size to 934 usable records. Consultation of a sample size calculator (www.surveysystem.com/sscalc.htm) indicates for a population of 56,575, the sample provides a 95% confidence level, with a +/-3.18% confidence interval. The confidence level indicates how certain one can be that the true percentage of the population would pick an answer as represented by the sample, while the confidence interval reflects a margin of error. For example, 72% of respondents in the survey sample indicated they had used the VMD tutorial. One can be 95% confident that the true percentage of the population lies between 68.82% and 75.18.



Survey Questions

Following below are questions used on the survey, in the order they appeared, and with a description of the scale or response options presented for each item.

1. E-mail address: Response in text box

2. Affiliation: Response Options: Academic, Government, Industry, Non-profit, Other

3. Area of study Response in text box

4. The work I do with VMD is funded (at least partially) by NIH: Response Options: Yes, No

5. The work I do with VMD is biomedically relevant: Response Options: No, Yes - briefly describe relevance (response in text box)

6. My level of expertise in using VMD is: Scale Options: Very high, High, Average, Low, Very low

7. I use VMD for _____ of my molecular visualization tasks: Scale Options: All, Most, Some, None

8. I primarily use VMD on: Response Options: Windows, MacOS X, Unix/Linux

9. I use VMD primarily for: Response Options: Research, Teaching, Business, Other

10. The number of people using VMD at my site is: Response Options: 1, 2-4, 5-10, 11-20, 21 or more

11. Indicate your level of agreement with the statements below:
VMD is a useful program
VMD is a reliable program
It is easy to learn how to use VMD
VMD is user friendly
VMD documentation is complete
The VMD-L mailing list is useful
VMD user support meets my expectations
I use VMD because it is free
I use VMD because it is better than other programs
I use VMD because the source code is available
Scale Options: Strongly Agree, Agree, Undecided, Disagree, Strongly Disagree



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12. Rate the importance of these PLANNED features to your work:

Load annotations, metadata, and evolutionary context from structure/sequence databases on the internet

Analyze/visualize simulation trajectories larger than available computer memory (out-of-core processing)

Improving the built-in trajectory analysis capabilities of VMD

Improving the analysis performance of VMD

Improved integration of quantum chemistry simulation data

Improved integration of data from coarse-grained MD, Brownian dynamics, and other particle system simulations

Improving the interactive graphics quality of VMD

Improving the publication rendering features of VMD

Improving the graphical display and animation speed of VMD

Increasing the built-in movie making capabilities of VMD

Multiple graphics windows, multiple graphics viewports within a window

Support for multi-touch input devices and touch-enabled displays

Development of new VMD tutorials and training materials

Scale Options: Very Important, Important, Somewhat Important, Unimportant, Undecided

13. Select the PLANNED feature that should have the highest priority for development: Load annotations, metadata, and evolutionary context from structure/sequence databases on the internet

Analyze/visualize simulation trajectories larger than available computer memory (out-of-core processing)

Improving the built-in trajectory analysis capabilities of VMD

Improving the analysis performance of VMD

Improved integration of quantum chemistry simulation data

Improved integration of data from coarse-grained MD, Brownian dynamics, and other particle system simulations

Improving the interactive graphics quality of VMD

Improving the publication rendering features of VMD

Improving the graphical display and animation speed of VMD

Increasing the built-in movie making capabilities of VMD

Multiple graphics windows, multiple graphics viewports within a window

Support for multi-touch input devices and touch-enabled displays

Development of new VMD tutorials and training materials

Response Options: participants selected one item from the above list as their top priority

14. I am a user of (check all that apply):

Response Options: AMBER, CHARMM, GROMACS, LAMMPS, NAMD, GAMESS, Gaussian, Other

15. I have used the VMD tutorial: Response Options: Yes, No

16. VMD is important to my research: Scale Options: Strongly Agree, Agree, Undecided, Disagree, Strongly Disagree

17. I am satisfied with VMD: Scale Options: Strongly Agree, Agree, Undecided, Disagree, Strongly Disagree

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18. VMD has improved the quality of my work: Scale Options: Strongly Agree, Agree, Undecided, Disagree, Strongly Disagree

19. Not having VMD available (e.g., in case of discontinued funding of VMD development) would negatively impact my scientific productivity:

Scale Options: Strongly Agree, Agree, Undecided, Disagree, Strongly Disagree

