

## Supplementary table 2 for 'Ten Simple Rules': examples of poorly posed questions, and how to improve them

Example 1: question that can be splitted into multiple questions.

Original Question	Improved Question
<p><b>biopython</b></p> <p>Hello people, I am trying to install biopython on a Ubuntu 11.04 64-bit machine. I followed the documentation on the wiki, but I don't understand whether I should be using the easy_install egg or download from github.</p> <p>Moreover, I need to write a script to parse Fasta files using biopython. Can anyone explain me how to do it?</p> <p>Finally, I would like to know if biopython can also read fastq files.</p>	<p><b>Installing biopython on Ubuntu</b></p> <p>Hello people, I need to install biopython on a Ubuntu 11.04 machine. I followed the documentation on the wiki, but I don't understand whether it is better to use the easy_install egg or to download from github. What do you recommend me?</p>
	<p><b>Parsing Fasta sequences with biopython</b></p> <p>I need to write a script to parse Fasta files using biopython. So far, I wrote the following code (..)</p>
	<p><b>Can biopython read fastq files?</b></p> <p>Hello, does anyone know how can I read fastq files with biopython?</p>

Always ask only one single question for each message.

Asking too many questions is confusing, and people do not know what to answer first. (see rule #2)

Split the question!

If you have more than one question to ask, split it into multiple discussions. (see rule #2)

Example 2: question having a poor subject and missing information.

Avoid titles like 'Help!', 'Urgent!', 'Help needed!'. (see rule #5)

Be concise. You don't need to explain your full background everytime. (see rule #2)

Check if you are providing all the details needed to answer you. Which version of the software are you using? Have you looked at the documentation? (see rule #2)

Original Question	Improved Question
<p><b>Help needed urgently...!!!</b></p> <p>Dear members, My name is Frank from the University of .... For my thesis project, I am working on simulation of certain models of protein myosin. We are interested in predicting a three dimensional structure of this protein in mouse.</p> <p>When I use the grompp_mpi (for position restraint), it gives me an error message as "Fatal error: Invalid line in em.gro for atom 3642:" and the program is aborted. Could you please tell me what could be the possible mistake?? Waiting for your reply... Thanks</p>	<p><b>Gromacs: fatal error when parsing file</b></p> <p>Dear members, I am having problems parsing files with gromacs.</p> <p>This is the command line that I am executing:</p> <pre>\$: grompp_mpi -np 32 -f em_cc.mdp -po det_em2.mdp -c em.gro -p myprot_em.top -o myprot_em.tpr</pre> <p>When I call this command line, it gives me the error: "Fatal error: Invalid line in em.gro for atom 3642:"</p> <p>I searched the manual for this error, but did not find any references. Can you see where the error is?</p> <p>I am running gromacs 4.5.1 on a Linux 64 bit machine and Ubuntu 11.04 as operating system.</p>

If the title is good, people are able to understand what the question is about before reading your message. (see rule #5)

Be sure that you are providing all the details needed to answer you, such as software version, the command you executed, and so on., (see rule #2)

Example 3: question where the user asks for help to solve an assignment

Original Question	Improved Question
<p><b>Double stranded DNA</b></p> <p>Hey guys, here I report one of the exercises I had yesterday in the examination of Organic Chemistry:</p> <p>"How can you determine quickly, whether a particular DNA forms double strands or not by NMR?"</p> <p>Who knows the answer? Thanks!</p>	<p><b>The use of NMR for determining the contacts in a DNA double helix.</b></p> <p>Dear all, I am trying to solve a question from an exam of Organic Chemistry I had yesterday.</p> <p>The problem says: "How can you determine quickly, whether a particular DNA forms double strands or not by NMR?".</p> <p>My reasoning is that in a double-stranded DNA the imino protons are hydrogen-bonded, so exchange with water is slow and the lines are comparably sharp. So, NOE (Nuclear Overhauser Effect ) information could be used to discern double-helix DNA strands by NMR.</p> <p>Can you please tell me if my reasoning is correct?</p>

Other people will not solve assignments or do homework for you. (see rule #6)

Explain how you tried to solve the problem, and ask people to check it. (see rule #6)

Example 4: questions where the user asks other people to write a software.

Other people will not your work for you. (see rule #6)

Original Question	Improved Question
<p><b>Software to parse fasta sequences</b></p> <p>Hello, I need to write a software to parse a fasta sequence. Can you please write it for me?</p>	<p><b>Software to parse fasta sequences</b></p> <p>Hello, I need to write a software to parse a fasta sequence.</p> <p>So far, I wrote the following python code:</p> <pre>filename = 'myseq.fasta' sequence = " for line in open(filename, 'r'):     if not line.startswith('&gt;'):         sequence += line print sequence</pre> <p>How can I improve this code? Do you see any error? Thanks</p>
	<p><b>Collaboration needed – software to parse fasta sequences</b></p> <p>Hello people, my group needs a software to parse fasta sequences.</p> <p>If anyone can help us and write the software for us, we will acknowledge it in the paper we are writing. Here are some more information (...)</p>

Demonstrate that you have tried to solve the problem by yourself (see rule #6)

Alternatively, if you need other people to do something for you, explain how you will acknowledge them (see rule #6)

Example 5: incomplete question.

Original Question	Improved Question
<p><b>Imidazole concentration</b></p> <p>Dear all, what is the imidazole concentration for the washing step?</p>	<p><b>Imidazole concentration in the washing step on a nickel column.</b></p> <p>Dear all, I am experiencing troubles with the purification of my protein from <i>E.coli</i>.</p> <p>I am following the protocol in (references). During the washing step with 50mM imidazole I loose quite a lot of protein. I know that this concentration of imidazole is high, but if I use less I have more contaminants in my elution.</p> <p>What concentration for imidazole do you recommend me? Can you point me to some literature reference on what is the best concentration for imidazole? Thank you very much.</p>

This question is not complete: people will have to ask for more details to understand what the question is about. (see rule #2)

Use an informative title(see rule #6)

Provide all the details needed to understand what are you doing and what is the problem you are facing. (see rule #2)

Example 6: question written in not-concise English

Be concise.  
 Avoid using too many adverbs and adjectives.  
 Also, do not abuse of transitions like 'These days', 'In fact', 'eventually', and others (see rule #7)

Original Question	Improved Question
<p><b>How to calculate the micelle size of a detergent?</b></p> <p>Hello,</p> <p>These days I have been looking for a method that would allow me to calculate how big (in kDa) are the micelles formed by the detergent DDM.</p> <p>In fact, during a dialysis step after my purification, my protein precipitates and I think that maybe it could be due to the pores size of my dialysis bag (10 kDa).</p> <p>...</p>	<p><b>How to calculate the micelle size of a detergent?</b></p> <p>Hello,</p> <p>How can I calculate the size of the micelles formed by the detergent DDM?</p> <p>I am following the protocol available at (...) to purify protein XYZ. However, after purification, during the dialysis step, the protein precipitates.</p> <p>I suspect it is due to the pores size of the dialysis bag I am using (10 kDa).</p> <p>...</p>

Prefer simple present and simple past temps. Avoid conditionals (see rule #7)

