

Effective Communication through Technical Writing

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[illegible]

Index Terms—IEEE, IEEEtran, journal, L^AT_EX, paper, template.

I. INTRODUCTION

THE introduction section is meant to introduce the reader to the problem you are solving in a very quick way. You want to use this section to motivate why the problem you're addressing is important and give any preliminary information that is necessary before the reader moves into the rest of the paper. The introduction should not be more than a page so that the reader is getting to the meat of the paper quickly.

You should state the objectives of your research early on, so that the reader knows whether or not the paper is of value to him or her.

You can use the introduction section to summarize relevant literature, if that does not merit a section of its own. See section II for more information about the purpose of background review.

At the end of the Introduction section, you need to give an outline of the rest of the paper. This will look something like:

Section II provides an overview of relevant research and the current state of the art for addressing this problem. The newly developed methodology is described in detail in Section III. Results of an application of this methodology are given in Section IV. Finally, Section V gives the conclusions of this work and the outlook for future research.

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II. BACKGROUND

It is important to put your work into context, both in terms of the problem you want to solve (which should happen in the Introduction) and how other people have tried to solve this problem before. The Background section is where you would summarize relevant research that other people (or you previously) have done to address this problem.

As you write your Background section, you should highlight how people have addressed your problem in the past and *what the shortcomings of those approaches were*: “Author A developed an ordinary least squares regression for predicting body fat percentage [1]. This method achieved prediction accuracy of 0.5%*bodyfat*; however, this model requires the measurement of blood glucose level, which is an invasive measurement requiring a blood sample.” Basically you are making the case that the previous work was not sufficient in some way and you are filling those gaps. You should not leave it to the reader to identify the holes in the previous research. You should not leave it to the reader to do anything but read - hit him or her over the head with the point you want to make!

The references in your literature survey should primarily be to articles from peer-reviewed journals. You can also cite and summarize conference presentations, although this should not be the bulk of your references. Technical reports and documents (such as NRC NUREGs) are also fair game, but these have not been peer-reviewed. You should **NEVER** cite wikipedia. Wikipedia is a useful resource, but it is not a scholarly reference.

Your background section should include articles published in the journal you are submitting to whenever possible. If you can’t find relevant articles in the journal’s archive, that suggests that your work may be out of the journal’s scope.

The background section should be complete, but should not be the bulk of your article. One to one and a half pages is usually a good limit for the background section. If the background section is substantially shorter than that, you can completely subsume it in the Introduction without giving it a dedicated section.

III. METHODOLOGY

This is where you talk about the methods you are applying to solve your problem. Methodology or Results should be the bulk of your paper. If your paper is more focused on the algorithm development, then methodology will likely be your largest section. If the focus of your paper is on a particular application, then the experiment and results section will be your largest section.

You should have a transition paragraph here (and between all the major sections): “Prior efforts to predict the body fat percentage have relied on intrusive measurements and expert domain knowledge. The proposed approach uses easily

Algorithm 1: PLS Training and Prediction

Training:

```

 $X_1 = X$ 
 $y_1 = y$ 
for  $i = 1$  to  $k$  do
     $\mathbf{u}_i = X_i^T y_i$ 
     $\mathbf{s}_i = X_i \mathbf{u}_i$ 
     $\beta_i = \mathbf{s}_i^T y_i / (\mathbf{s}_i^T \mathbf{s}_i)$ 
     $y_{i+1} = y_i - \beta_i \mathbf{s}_i$ 
     $\mathbf{p}_i = X_i^T \mathbf{s}_i / (\mathbf{s}_i^T \mathbf{s}_i)$ 
     $X_{i+1} = X_i - \mathbf{s}_i \mathbf{p}_i^T$ 
end

```

Prediction:

```

 $x_1 = x$ 
 $y_1 = 0$ 
for  $i = 1$  to  $k$  do
     $\mathbf{s}_i = x_i \mathbf{u}_i$ 
     $y_{i+1} = y_i + \beta_i \mathbf{s}_i$ 
     $x_{i+1} = x_i - \mathbf{s}_i \mathbf{p}_i^T$ 
end
 $\hat{y} = y_{k+1}$ 

```

obtained measurements of body features in an empirical modeling approach that does not require any explicit knowledge of the relationship between measurements and percent body fat.”

Then give a quick and dirty introduction to the methodology that you will expand on in later subsections. “Body fat percentage is predicted by first preprocessing the measurement data to extract only the useful information in each measurement. These preprocessed data are then used to train and optimize a prediction model. Several prediction algorithms are evaluated, including linear regression, principal component regression, and locally weighted regression. The optimal model amongst all selected is chosen based on the accuracy of the predictions on a test data set. Future predictive performance is quantified using a third, independent data set.”

A. What goes into Methodology?

The Methodology section and subsections should describe the **algorithms** and **analyses** you are doing. They should not describe the implementation in code (unless that is explicitly the purpose of the paper). The reader wants to know what the analysis is doing, not how you coded the analysis into MATLAB. Pseudocode can be very helpful here, but be careful to put pseudocode into natural language as much as possible, not programming language. For instance, the PLS algorithm can be given in pseudocode, like that shown in Algorithm 1.

You should use this section to discuss how important decisions in your approach are made. For instance, if it is important to standardize your data, don’t just state that - describe why it is important (and also explain what standardization is with an equation). “If data are not mean-centered prior to performing principal component analysis, the first principal component will connect the origin to the mean of the data. Data may need to be fully standardized (equation 1) to ensure that all variables are equally important in the analysis.”

$$x_s = \frac{x - \bar{x}}{\sigma_x}, \quad (1)$$

where x is the original measured data, \bar{x} is the mean of the training data, and σ_x is the standard deviation of the training data.

This is where you explain how decisions are made in general. In the results section, you can talk about the specific decisions made for your application.

B. Step 1

The methodology will probably have subsections to help the reader walk through the full methodology. If you can break it up into meaningful steps, this will help a lot with organizing your process and with the reader's comprehension.

Whenever is appropriate, you should highlight the steps that address some of the gaps that you identified in Section II. Again - don't assume the reader will draw the conclusions you want him or her to draw; tell the reader what he or she should be taking away from your discussion.

C. Step 2

Here's where you describe the next part of your methodology.

1) *Step 2a*: Maybe there is an option for Step 2 of the methodology

2) *Step 2b*: More methodology

There should be a transition statement here indicating that your methodology is fully developed and you're moving on to look at the application of this methodology to a specific problem.

IV. RESULTS

Again, have a transition statement or paragraph to help the reader move from methodology to application: "The proposed methodology was applied to prediction of body fat percentage based on straightforward, non-intrusive measurements of body composition. Measurements collected from 217 men and women age 18 to 43 were used to evaluate the efficacy of the methodology."

You should always consider how to best present your results. You have basically three options: block of text, table, or figure. Generally speaking, you will use a combination of these three things. Any time you put a table or a figure in your paper, it must be called out and explained in the text. Additionally, the table or figure must have a *descriptive caption*. "Plot of results" is not a descriptive caption. "Model predictions show the effect of measurement error on prediction uncertainty" is getting better.

Tables are good for quickly comparing and contrasting a few numbers or features. Table I summarizes the results of several models for predicting acceleration time. The results of five empirical models suggest that a nonlinear model is most appropriate for this prediction problem. Be sure that you use an appropriate number of significant figures in your table. Just because MATLAB gave you the digit doesn't mean it's significant!

Plots and figures are useful for showing relationships across a range of conditions. If the accuracy of your model varies with the value of a particular input, then a plot of that input versus accuracy can be very powerful. Plots should always have labeled axes. If more than one data series is on a plot, then

TABLE I
PERFORMANCE OF EMPIRICAL MODELS FOR ACCELERATION TIME PREDICTION

Model Type	RMSE (s)	Uncertainty (s)
Linear Regression	1.73	0.32
Nonlinear Regression	1.43	0.25
Principal Component Regression	1.72	0.15
Partial Least Squares Regression	1.73	0.52
Nonlinear PLS	1.44	0.50

there needs to be a legend. Think about how the plot will print in black and white - will the data series still be distinguishable? If not, you may need to use markers or some other method to distinguish them. Figure 1 gives the results of the dynamic heat balance model prediction of primary flow rate during normal operational transients [2]. The uncertainty in the prediction is indicated by the shaded region. These results show very strong agreement between the model prediction and the measured flow rate.

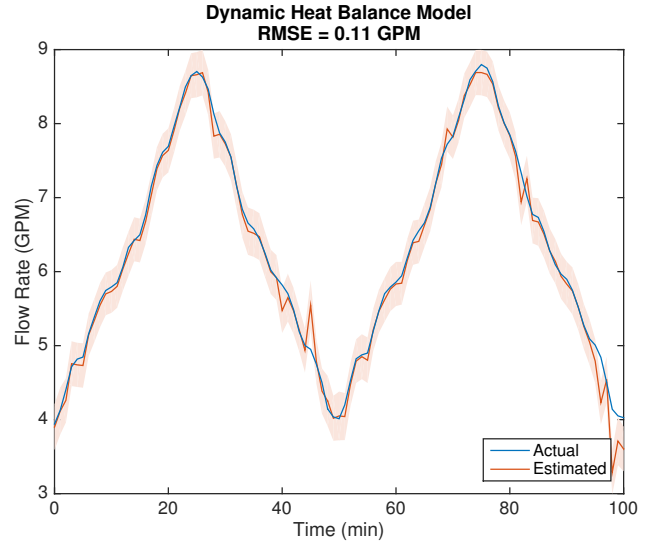


Fig. 1. Dynamic heat balance model predictions. This approach gave RMSE of 0.11 GPM across all tested ramps, with an average 95% prediction variance band of ± 0.30 GPM. [2]

The results section should present the results AND discuss what they mean. If possible, compare your results to prior work so that you can put what you've done into the broader context. If there are any obvious shortcomings of your methodology or application, acknowledge those. For instance, did you use simulated data? If so, how did you ensure that the data are realistic?

V. CONCLUSIONS

The conclusions should summarize conclusions of the full paper: what was the problem you solved? how did you solve it? what were the results? There should not be any statement in the conclusions that is not fully supported by the evidence in the preceding paper.

APPENDIX MATLAB CODE

For the purpose of your final project report, you need to include your MATLAB code in an appendix. It should be commented and clean. Remove any lines of code that are not necessary. Provide comments so that we can easily follow your code with a simple read-through.

```

1  %% Continuous GA %%
2
3  Nvar = 2; % Chromosome length = 2 % 2 variable to be optimized
4  Npop = 16; % Population = 8 %
5  Nkeep = 2; % N_keep = 2 %
6  MR = 0.2; % Mutation rate = 0.2 %
7  Ngen = 25; % Number of generations = 25 %
8
9  Ngenes = Nvar*Npop; % total number of genes in the population %
10 Nmutate = floor(MR*Npop*Nvar); % number of things to mutate %
11
12 % Generate random initial population %
13 pop = rand(Npop,Nvar)*10; % uniform random numbers between 0 and 10
14
15 n = 0; % initial generation
16
17 f = figure;
18 w = waitbar(0,['Iteration ' num2str(n) ' out of ' num2str(Ngen)]);
19
20 while n<Ngen % could use a for loop, but here we can easily add additional stopping
    criteria %
21
22     waitbar(n/Ngen,w,['Iteration ' num2str(n) ' out of ' num2str(Ngen)]); % include
        waitbar because sometimes this is slow
23
24     % enforce constraints -10 <= x <= 10 %
25     if any(any(pop<0) | any(pop>10))
26         % if any values are outside the bounds, generate a new random
27         % solution
28         [indx indy] = find(pop>10 | pop<0);
29         pop(unique(indx),:) = rand(numel(unique(indx)),2)*10;
30     end
31
32     % evaluate fitness %
33     fitness = fun2(pop);
34
35     bestVal = min(fitness);
36     bestSolution = pop(fitness == bestVal,:);
37
38     % plot current population - just for visualization %
39     hold off
40     figure(f);
41     surf(x1,x2,z,'facealpha',0.7)
42     shading interp
43     hold on;
44     plot3(pop(:,1),pop(:,2),fitness,'ko','markersize',15.0)
45     plot3(bestSolution(1),bestSolution(2),bestVal,'rx','markersize',15.0);
46     xlabel('x_1')
47     ylabel('x_2')
48     view(2)
49     drawnow
50

```

```

51     %% Reproduction (cloning and mating) %%
52     [cost,ind] = sort(fitness,'ascend');
53     newPop(1:Nkeep,:) = pop(ind(1:Nkeep),:); % keep top performers %
54
55     % select mates (weighted random) %
56     wts = exp(-fitness/2)/sum(exp(-fitness/2)); % selected this weighting scheme
        rather randomly myself ...
57     wts2 = cumsum(wts);
58
59     for ii = 1:(Npop-Nkeep)/2
60         % select parents from all chromosomes%
61         ma = find(rand<wts2,1);
62         pa = find(rand<wts2,1);
63         while ma==pa % make sure the parents aren't the same chromosome %
64             pa = find(rand<wts2,1);
65         end
66
67         % perform blending cross-over to get two new kids %
68         beta = rand; % random integer 1 - Nvar %
69         newPop(3+(ii-1)*2,:) = beta*pop(ma,:)+(1-beta)*pop(pa,:);
70         newPop(4+(ii-1)*2,:) = (1-beta)*pop(ma,:)+beta*pop(pa,:);
71     end
72
73     %% Mutation %%
74     ind = randi(Ngenes-Nvar,Nmutate,1); % first (best) chromosome does not mutate %
75     newerPop = newPop(2:end,:);
76     newerPop(ind) = rand(size(ind))*10; % replace identified genes with new random
        numbers
77     newPop(2:end,:) = newerPop;
78
79     pop = newPop;
80
81     n = n+1;
82 end
83
84 close(w) % get rid of waitbar %
85
86 [bestSolution bestVal]

```