

Discussion of 'Environment vs. Bacteria' and 'Oxygen Revisited'

Editor's Note: Readers may, or may not, be aware that *GWMR* publishes two types of technical articles: The first undergo the traditional peer-review process, while others are published as submitted by the author(s). Evan Nyer's "Treatment Technology" articles fall into this second category. Thus, Evan has had a forum to express his personal unfiltered technical opinions in a style not available to most contributors to *GWMR*. In my very short tenure as the technical editor of *GWMR*, I have quickly learned that some readers: (a) enjoy Evan's unique style and perspective, but are unaware that these are non-peer-reviewed submissions, or (b) take exception to some of Evan's opinions and wonder why the technical editor allowed the article to be published. Judging by my e-mail traffic, two of Evan's more recent articles raised the ire of some readers—the "geek professor" community (*GWMR*, Winter 2003) was especially vocal.

NGWA staff and I discussed this and decided that it is only fair that readers have an opportunity to respond in print to articles published in *GWMR*. If interested, your responses need to be technically oriented and very brief, and we reserve the right to select ones for publication. To the extent possible, these responses will be published within two issues of being received, if they meet our criteria, and if the space is available. We plan to forward these comments to the article author(s) and give them the option to reply to the response(s) to their article. We also plan to more clearly distinguish peer-reviewed and non-peer-reviewed articles in future *GWMR* issues.

The following are responses to two of Evan's recent articles. Should you wish to respond in the future, e-mail me at paul.c.johnson@asu.edu. Enjoy the debate!

—Paul C. Johnson

Discussion of Environment vs. Bacteria or Let's Play, 'Name that Bacteria'

by Evan K. Nyer, Fred Payne and Suthan Sutherson (2003), *Ground Water Monitoring & Remediation*, v. 23, no. 1, pages 36–45

Discussed by David Major, GeoSyntec Consultants Inc.; Elizabeth Edwards, University of Toronto; Perry McCarty, Stanford University; James Gossett, Cornell University; Edwin Hendrickson, Dupont; Frank Loeffler, Georgia Institute of Technology; Stephen Zinder, Cornell University; David Ellis, Dupont; John Vidumsky, Dupont; Mark Harkness, General Electric; Gary Klecka, Dow Chemical; and Evan Cox, GeoSyntec Constultants Inc.

As academics, industrial representatives, and bioremediation practitioners who have devoted much of our careers to the research and development of effective and peer-reviewed bioremediation technologies for chlorinated solvents, we feel compelled to reply to the article recently published by Nyer et al. (2003). In our collective opinion, Nyer et al. have provided a significant disservice to the remediation industry and the scientific community by presenting selected evidence that represents their personal version/vision of

the technology, while making erroneous statements and ignoring key scientific concepts. This response is an attempt to undo the confusion that has been wrought.

Nyer et al. suggest that the bioremediation field is divided into two groups: One "believes that they can find and name the bacteria responsible for degradation," and the other "believes that the key to degradation in the field is to understand and create the correct environment." We believe that trying to divide the bioremediation profession in

such a way is not useful, and that understanding the characteristics of bacteria responsible for biodegradation is an essential part of determining the correct environment to create for effective bioremediation. Without the insights gained from extensive scientific research on bacteria that reductively dechlorinate chlorinated solvents, the degradation pathways, and the particular nutrient and environmental requirements of the dehalogenating microorganisms, Nyer et al. would not be in the business today of selling their services for chlorinated sol-

Table 1
Isolated Chloroethene-Respiring Bacteria

Isolate	Closest Phylogenetic Affiliation	Dechlorination Steps Performed	Reference
<i>Dehalobacter restrictus</i>	Low G+C Gram positive bacteria	PCE to cDCE	(Holliger et al. 1993)
<i>Dehalospirillum multivorans</i>	Proteobacteria, ϵ subdivision	PCE to cDCE	(Scholz-Muramatsu et al. 1995)
<i>Desulfitobacterium</i> Strain PCE1	<i>Desulfitobacterium</i> Gram positive	PCE to TCE	(Gerritse et al. 1996)
<i>Desulfuromonas chloroethenica</i> Strain MS-1	<i>Geobacter</i> <i>Enterobacteriaceae</i>	PCE to cDCE	(Krumholz et al. 1996)
Strain TEA	Low G+C Gram positive bacteria	PCE to cDCE	(Sharma and McCarty 1996) (Wild et al. 1996)
<i>Desulfitobacterium</i> sp. strain PCE-S	<i>Desulfitobacterium</i> Gram positive	PCE to cDCE	(Miller et al. 1997)
<i>Dehalococcoides ethenogenes</i> Strain 195	Green, nonsulfur bacteria	PCE to ethene	(Maymo-Gatell et al. 1997)
<i>Desulfitobacterium frappieri</i> TCE1	<i>Desulfitobacterium</i> Gram positive	PCE to cDCE	(Gerritse et al. 1999)
<i>Clostridium bifermentans</i> Strain DPH-1	<i>Clostridium</i>	PCE to cDCE	(Chang et al. 2000)
Chlorobenzene-degrading Strain CBDB1	<i>D. ethenogenes</i>	PCE to tDCE	(Adrian et al. 2000)
<i>Desulfitobacterium</i> sp. Strain Y51	<i>Desulfitobacterium</i> Gram positive	PCE to cDCE	(Suyama et al. 2002)
<i>Desulfitobacterium metallireducens</i>	<i>Desulfitobacterium</i> Gram positive	PCE to cDCE	(Finneran et al. 2003)
<i>Desulfuromonas michiganensis</i>	<i>Geobacter</i>	PCE to cDCE	(Sung et al. 2003)

vent bioremediation. Good science is the essential underpinning for engineering advancement.

In the past, we held similar views to those expressed by Nyer et al. regarding some aspects of bioremediation. Specifically, we once believed that many different genera of bacteria had the capabilities to degrade a given compound or contaminant, and that bacteria required to degrade any contaminant were ubiquitous. Which microorganism was involved in the desired biodegradation mechanism was not considered to be important; rather, what was important was the function they carried out and the environmental conditions that they required. This view certainly holds true for aerobic hydrocarbon-degrading bacteria. Hydrocarbon biodegradation can be carried out by a wide variety of different microorganisms, and this activity is generally understood to be ubiquitous. This view is also essentially true for the organisms that convert tetrachloroethene (PCE) and trichloroethene (TCE) to *cis*-1,2-dichloroethene (cDCE). Table 1 provides a listing of

names of many organisms having this capability.

In 1989 and 1991, when the scientific and bioremediation practicing communities demonstrated that PCE and TCE could be completely dechlorinated to ethene (Freedman and Gossett 1989; Major et al. 1991), our expectation was the same—that we would eventually find many different types of organisms that could dechlorinate PCE and TCE to ethene. However, the surprising finding from more than a decade of intense laboratory and field research is that this expectation is not true. To date, only one organism, *Dehalococcoides ethenogenes strain 195*, has been isolated that can dechlorinate cDCE via vinyl chloride (VC) to ethene (Table 1). In strong support of this finding, mixed cultures capable of complete conversion of PCE or TCE to ethene invariably contain organisms closely related to *Dehalococcoides ethenogenes*. Compelling evidence arguing for a critical role for the *Dehalococcoides* species in bioremediation was provided by Hendrickson et

al. (2002), who conducted an extensive survey for the presence of *Dehalococcoides* at multiple contaminated sites. These researchers detected *Dehalococcoides* DNA sequences only at sites where dechlorination proceeded beyond cDCE to VC and ethene, but did not detect *Dehalococcoides* DNA sequences at sites where dechlorination stopped (stalled) at cDCE. More important, at sites where *Dehalococcoides* were not detected and dechlorination stalled at cDCE, the addition of mixed cultures containing *Dehalococcoides* led to complete dechlorination to ethene and the establishment of *Dehalococcoides* organisms in the bioaugmented aquifer (Ellis et al. 2000; Major et al. 2002).

Nyer et al. conclude that “there should be no presumption that bioaugmentation is ‘absolutely’ required to achieve complete enhanced reductive dechlorination” and that bioaugmentation “is not required to assure the success of any project.” We agree that bioaugmentation is not required at all sites. There is no useful purpose served

by bioaugmentation at sites where it is clear from the analytical data that reductive dehalogenation to ethene is occurring naturally (many sites fall into this category) and where the presence of dechlorinating *Dehalococcoides* is already documented. For example, complete dechlorination to ethene following biostimulation with lactate was demonstrated at the Bachman Road site, where *Dehalococcoides* populations were already present in the aquifer (He et al. 2003; Lendvay et al. 2003). While dechlorination at this site was accelerated by bioaugmentation with a culture containing *Dehalococcoides*, bioaugmentation was not required to achieve the end result. In contrast, at sites where dechlorination of PCE and TCE is not occurring or stalls at cDCE, then bioaugmentation can help ensure that the necessary microorganisms are present to achieve complete dechlorination to ethene. This can significantly reduce the risk of a long, unfruitful, and costly acclimation period, and can reduce the great uncertainty of bioremediation success through electron donor addition alone.

In the following sections, we will summarize peer-reviewed literature that conveys what is known regarding the *Dehalococcoides* group of organisms, and that illustrates real-world sites where dechlorination to ethene was limited by a lack of required *Dehalococcoides* organisms, and not by “incorrect” environmental conditions. Furthermore, in these peer-reviewed case studies, bioaugmentation of the subject aquifer with natural microbial cultures containing *Dehalococcoides* promoted rapid and complete dechlorination to ethene, underlining the importance of the *Dehalococcoides* organisms in successful reductive dechlorination. It is the collected evidence from these and many other studies that has evolved our view and led to such great interest in the *Dehalococcoides* group of microorganisms. We have learned well enough to be careful not to conclude that no organisms outside of the *Dehalococcoides* group may be capable of reductive dehalogenation of cDCE and VC, but the presence of such organisms, if they exist, has not yet been well documented. In addition to providing information on *Dehalococcoides*, we will demonstrate how the case studies

presented by Nyer et al. are entirely consistent with our position.

What Science Has Told Us About *Dehalococcoides*

Different *Dehalococcoides* organisms have now been identified and have been shown to share a similarity (greater than 97%) in their 16S rRNA gene sequences, suggesting that they may be members of the same genus. The small differences in these gene sequences suggest that there may be different species, or perhaps different strains within the same species of *Dehalococcoides*. Although distinctions between species and strains is not always clear, they must be real as different *Dehalococcoides* members do have different dechlorinating enzymes. For example, as detailed in what follows, some obtain energy from reductive dehalogenation of PCE, TCE, and cDCE while others cannot dehalogenate PCE but obtain energy from dehalogenation of TCE, cDCE, and VC, and one apparently uses chlorobenzenes in preferences to chloroethenes. Overall, we can draw the following conclusions from the peer-reviewed literature:

1. Many microorganisms have been isolated in pure culture that can couple reductive dechlorination of PCE and TCE to metabolism, and obtain energy from the process for cell growth (refer to Table 1). PCE and TCE serve as terminal electron acceptors in the microorganism's metabolism, much as humans use oxygen. These microorganisms are called halo-respiring or dehalorespiring bacteria. Most of these microorganisms use simple substrates as electron donor, such as acetate or hydrogen.
2. In the environment, dechlorinators live as part of an anaerobic microbial community, where fermenting, acetogenic, and other microorganisms provide electron donor (for example, hydrogen), carbon (for example, as acetate), and possibly other nutrients to the dechlorinating organisms.
3. All laboratory mixed cultures that dechlorinate PCE or TCE beyond cDCE to ethene have been found to

contain organisms in the *Dehalococcoides* phylogenetic group (Adamson and Parkin 2000; Cupples et al. 2003; Dennis et al. 2003; Duhamel et al. 2002; Ellis et al. 2000; Fennell et al. 2001; He et al. 2003; Maymo-Gatell et al. 1997; Richardson et al. 2002). The only exception is a recent article by Rossetti et al. (2003) who reported that they did not detect *Dehalococcoides* sequences in a clone library made from a culture that dechlorinates PCE to VC and only traces of ethene. While the absence of *Dehalococcoides* may be a real result, the method used to detect *Dehalococcoides* was not specific. Biases that commonly occur when amplifying mixed population DNA with generic polymerase chain reaction (PCR) primers may have resulted in a false negative result. Time will tell if this result holds true.

4. Many *Dehalococcoides* 16S rRNA gene sequences have been analyzed to date. Although they are similar, they are not identical. These sequences fall into three clusters, designated the Cornell (containing *D. ethenogenes* strain 195), Victoria, and Pinellas groups (Hendrickson et al. 2002).
5. Nyer et al. state “*Dehalococcoides* [strain 195] cannot achieve the cDCE to ethene transition except through cometabolic means.” This statement is incorrect. *D. ethenogenes* strain 195 obtains energy from all dechlorination steps except the final step from VC to ethene (Maymo-Gatell et al. 1999; Maymo-Gatell et al. 2001). Because the final step is cometabolic, cultures of strain 195 show an accumulation of VC, and slower conversion of VC to ethene. Several mixed cultures have also shown tendency for accumulation of VC and slower conversion to ethene. For example, a culture described by Dennis et al. (2003) only slowly transformed VC, and the *Dehalococcoides* 16S rRNA sequence from this culture was similar to that of strain 195, falling within the Cornell group.
6. Some mixed cultures show rapid conversion of PCE or TCE to ethene with little accumulation of

intermediates. These cultures show sustained dechlorination of VC to ethene, when supplied with only VC as electron acceptor (Duhamel et al. 2002; He 2003). Such cultures are likely using VC as a metabolic substrate. Recently, through molecular monitoring of *Dehalococcoides* growth kinetics, it has been proven that some *Dehalococcoides* species actually obtain energy from VC dechlorination to ethene (Cupples et al. 2003). The *Dehalococcoides* 16S rRNA gene sequences from these VC dechlorinating cultures fall into the Pinellas or Victoria groups.

7. Not all *Dehalococcoides* strains dechlorinate chloroethenes to ethene. Some, such as CBDB1 (Adrian et al. 2000), dechlorinate chlorobenzenes and polychlorinated dibenzodioxins (Bunge et al. 2003), while more distant relatives dechlorinate PCBs (Wu et al. 2002). Therefore, the presence of *Dehalococcoides* does not necessarily mean that full dechlorination of cDCE to ethene will occur. However, all studies to date have found that the converse is true: If *Dehalococcoides* are absent, then dechlorination past cDCE (to VC and ethene) did not occur.

Evidence from Field and Laboratory Microcosm Studies

The Remediation Technologies Development Forum (RTDF), a collaboration between federal and industrial partners (www.rtdf.org), evaluated accelerated anaerobic bioremediation and natural attenuation of TCE in ground water at Dover Air Force Base (AFB) in Delaware. The RTDF constructed more than 1000 microcosms (Lee et al. 2000) using site soil and ground water amended with various electron donors including volatile fatty acids (acetate, lactate), alcohols, sugars (including molasses), and complex organics. Although TCE was reduced to cDCE regardless of the amendment used, conversion past cDCE to VC and ethene was observed in only a small percentage of microcosms incubated during the course of these studies (up to 500 days), even when methanogenesis was occurring. This shows that *Dehalo-*

coccoides is sparsely distributed at this site because TCE should have been dechlorinated beyond cDCE in a greater percentage of these microcosms. Thus, we can conclude that microorganisms capable of converting cDCE to ethene were either not present, very sparsely distributed, or inactive at this site.

Harkness et al. (1999) demonstrated the need for bioaugmentation using columns filled with soil from the Dover AFB site. TCE was not reduced beyond cDCE in columns that had been fed only electron donors for up to 200 days. This time frame should have been sufficient time to stimulate the growth and activity of any indigenous *Dehalococcoides*. Injection of a small volume of a culture containing *Dehalococcoides* (the Pinellas culture) into one of the columns stimulated complete dechlorination of cDCE to ethene within 20 days in that column. The same effect was later observed in a second column injected with the same culture. VC production was transient in both bioaugmented columns, with rapid conversion to ethene. This supports the conclusion that *Dehalococcoides* microorganisms were not initially present in the aquifer material, but were responsible for complete dechlorination after their addition.

This conclusion was supported by the results of a field bioaugmentation demonstration at the site (Ellis et al. 2000). The pilot treatment area was fed lactate for 269 days, during which time TCE was stoichiometrically dechlorinated to cDCE. VC and ethene were not produced during this interval. Only after the aquifer was amended with the same culture used in the column studies was cDCE completely reduced to ethene (Ellis et al. 2000). This result demonstrates the value of bioaugmentation when evidence clearly indicates the absence of organisms capable of complete conversion of cDCE to ethene. Follow-on analysis using molecular probes (Hendrickson et al. 2002) demonstrated that the *Dehalococcoides* present in the culture used for inoculation was detected only within, and not outside of, the pilot test area, again indicating the need for, and success of, bioaugmentation.

The need for, and value of, bioaugmentation with *Dehalococcoides* was also demonstrated at Kelly AFB in

Texas. A key aspect of the field test was the inclusion of field control plots, coupled with molecular probes to assess the presence of *Dehalococcoides* prior to and after adding an enrichment culture containing *Dehalococcoides* (Major et al. 2002). Microcosms amended with a culture (referred to as KB-1) containing *Dehalococcoides* converted cDCE to ethene, whereas nonbioaugmented electron donor treatments stalled at cDCE. Two field control plots exhibited conversion of PCE to only cDCE when amended with electron donors. In contrast, the test plot bioaugmented with *Dehalococcoides* completely reduced TCE to ethene. The most conclusive evidence was obtained from molecular techniques, which showed that the "fingerprint" of the *Dehalococcoides* species in the KB-1 culture had spread throughout the bioaugmented test plot, whereas *Dehalococcoides* was not detected in the control plots or outside of the bioaugmented test plot. This study also showed that there were naturally occurring *Dehalococcoides* organisms present at a geographically isolated area of Kelly AFB. Interestingly, these *Dehalococcoides* were located in a waste pit that was very clayey, with little to no ground water movement, and that had received organic waste and chlorinated solvents for decades. This *Dehalococcoides* had a different "fingerprint" than the KB-1 bioaugmentation culture, and this different signature was not detected in the field pilot plot that was bioaugmented. The Kelly AFB results clearly demonstrate that

1. Native *Dehalococcoides* are not uniformly distributed or present throughout the Kelly AFB site.
2. Native *Dehalococcoides*, if present, did not grow or otherwise become active and promote complete dechlorination in the non-bioaugmented electron donor test plot.
3. Bioaugmentation with *Dehalococcoides* was required to further dechlorinate cDCE to ethene.
4. *Dehalococcoides* can migrate through the aquifer.

These results unequivocally demonstrate the benefit of bioaugmentation to establish reductive dechlorination at *Dehalococcoides*-deficient sites.

Review of Case Studies Presented by Nyer et al. (2003)

Nyer et al. present evidence from four field applications as proof that the addition of sugar-water solutions (e.g., diluted molasses) was sufficient to achieve complete dechlorination of PCE/TCE to ethene, and that their technology has worked at “every site.” We have reviewed the four case studies presented, and find that the data do not support Nyer’s conclusions in three of the four cases. Ironically, Nyer et al. explain the need to express concentrations of chloroethenes and ethene in molar units when reporting data (rather than in mass units), but then present their data in mass units with misleading scales.

Case Study #1: In Figure 1 of Nyer et al. (2003), the data for the chloroethenes are presented in μM , while the data for ethene are presented in ng/L . If the concentrations are expressed in the same units, we see that a maximum of 27 μM *c*DCE (2700 $\mu\text{g/L}$) was produced through dechlorination. While this *c*DCE concentration subsequently decreases to zero, a maximum of only 0.002 μM ethene (0.065 $\mu\text{g/L}$) was detected as a single data point (i.e., not sustained ethene production). This amount of ethene represents only 0.007% of the *c*DCE that disappeared. This raises the obvious question of where did the other 99.993% of the *c*DCE go? Furthermore, 65 ng/L of ethene can be generated by other means, such as abiotic reactions with naturally reduced metals, or even fortuitous reactions with the highly reduced co-factors and proteins possessed by many anaerobic microorganisms. In any case, the situation is clear: there was significant conversion of PCE to *c*DCE, but essentially no conversion of *c*DCE to VC or ethene despite repeated additions of high concentrations of electron donor (molasses). The observed concentration decreases of *c*DCE may be attributable to dilution or other degradation processes, but the data do not support *c*DCE mass loss due to dechlorination.

Case Study #2: Although the data in Figure 2 of Nyer et al. (2003) are not presented in molar units, we agree that in this case the conversion to ethene is significant. The data from Figure 2 of

Nyer et al. show that ~ 1.65 mM of *c*DCE (160 mg/L) were produced, with further transformation to ~ 0.64 mM VC (40 mg/L), and 0.5 mM ethene (14 mg/L). In this case, VC and ethene make up a significant portion of the dechlorination products, and therefore significant dechlorination beyond *c*DCE is occurring. This is a site where bioaugmentation is not required and *Dehalococcoides* is most likely present. Nyer et al. should consider collecting ground water samples from this and their other sites for molecular analysis of *Dehalococcoides*. They may find the results enlightening.

Case Study #3: The data in Figure 3 of Nyer et al. (2003) are presented in both $\mu\text{g/L}$ and in $\mu\text{mol/L}$ (also symbolized as μM). There are two apparent problems with the data. First, there is an error in the unit conversions from mass basis to molar basis for VC. According to Figure 3, VC reaches a maximum of ~ 2500 $\mu\text{g/L}$, which should convert to 40 μM in the bottom panel of the figure. However, in the bottom panel, VC concentrations are all below detection, leaving the reader confused as to which data is correct. In addition, there are no ethene concentrations reported. It is not stated whether ethene was measured and not detected or simply not measured. Nyer et al. conclude from these data that “It is clear to see the complete transformation of TCE within 9 to 12 months.” In reality, it is not possible to see or conclude from the data presented that transformation was complete because the VC concentrations are uncertain, and no ethene concentrations were reported.

Case Study #4: As in Case Study #1, the data are reported in mixed units in Figure 4 of Nyer et al. TCE, *c*DCE, and VC are plotted in $\mu\text{g/L}$ on one axis, while ethene is plotted in ng/L on the opposite axis. Nyer et al. state that the increase in TCE and *c*DCE was a cosolvency and surfactant effect, and that there were “high” levels of ethene. After converting the concentrations of ethene to the same units as the chlorinated ethenes, it is clear to see that the peak concentration of ethene (~ 25 $\mu\text{g/L}$ or 0.4 μM) was $\sim 0.6\%$ of the maximum *c*DCE concentration (6500 $\mu\text{g/L}$ or 67 μM) that “disappeared.” Further dissolution of TCE combined with rapid conversion of VC to ethene, as Nyer et

al. speculate, would create significantly (orders of magnitude) more ethene than what was observed, even if one makes allowance for some dilution. The data presented are far more suggestive of dilution, perhaps related to the repeated sugar-water injections, than dechlorination activity associated with *Dehalococcoides*.

Conclusions

Perhaps the differences in opinion between the science-based community and Nyer et al. are not as large as one would gather, based on reading Nyer’s article. We agree that consortia of microorganisms are involved in complete dechlorination, including the dehalogenation reaction itself, and in creating conditions suitable for growth of dehalorespiring microorganisms. However, available data show that suitable dehalorespiring bacteria are not present at every site and that, where suitable dechlorinators appear absent, addition of cultures containing *Dehalococcoides* organisms can achieve the rate and extent of dechlorination to ethene required for effective bioremediation remedies. There should never be a presumption that bioaugmentation is “absolutely required to achieve complete enhanced reductive dechlorination at any site,” only the presumption that the appropriate *Dehalococcoides* populations need to be present (naturally or through bioaugmentation) for conversion of past *c*DCE to ethene. We can conclude this with confidence based on peer-reviewed results from diverse and extensive laboratory and field research and demonstration programs. We do not believe that the case studies by Nyer et al. contradict our conclusions. In fact, they clearly support them.

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Author's Reply

By *Evan K. Nyer*

I love this stuff. Great ideas thrown back and forth with absolute supporting data. Makes a regulator's head spin. I do feel a little ganged up on; I had only two co-authors and one company, they had a lot more. Also, just once could someone disagree with me without telling me that I am not scientific, used bad judgment, or some similar thing? Couldn't I just be wrong (low probability) or they simply have come to a dif-

ferent conclusion and would like to share why they have come to that conclusion. Can't we just get along?

As far as all of their data, I am sorry, but they still have not convinced me. I do not like the design of their experiments, and I think that other conclusions can be reached from the data that they collected. Someday, maybe we can all design an experiment together that will satisfy everyone.

Until that time, I look forward to two or three years of good arguments on this subject. I hope that all of the opinions are presented in a manner that is equal to the quality of Major et.al's response, sans the scientific jab. However, I will not take this argument to the next level in this forum. I have always tried to use this column as a method to bring new ideas to the reader, not to have a detailed technical presentation. There are many journals and conferences available for that type of detail, and I will try to keep my column as an outpost for simple ideas presented with a little fun.