This book comes at an extraordinary time for those of us in the Clinical Front Line. The scale and pace of diagnostics development is ever accelerating, matched only by the rising expectations of our patients and our Governments. There must be more answers, more correct answers, ever faster, ever cheaper.

Until recently molecular diagnostics only achieved real clinical traction in Virology Departments, where culture has all but disappeared. Virologists were the first to develop these techniques for real (and real-time!) clinical benefit, more recently extending from monoplex PCR-based diagnostics for single pathogens to a more syndromic, multiplex diagnostic approach. In addition, our ability to rapidly sequence PCR products has in addition allowed for rapid antiviral resistance analysis for HIV.

Virologists certainly led the charge; and clinical bacteriologists are at last becoming more comfortable with molecular diagnostics, which do not use a rather slow biological PCR-based phenomenon referred to as “colony formation” using solidified essence of Japanese seaweed, sometimes complemented with other dubious natural products such as Horse Blood. Perhaps some die-hards will bemoan the lack of smell in the Bacteriology laboratory of the future.

Joking apart – the development of molecular diagnostics in bacteriology is now beginning to release the potential offered by speed – “same day” bacteriology was hitherto impossible due to the seemingly universal requirement for culture to the point where enough material was available for direct visualization and biochemical profiling. Whilst modern automation without doubt made the bacteriology laboratory’s work more efficient and less “hands on” – the fact that pathogens had to be allowed to grow first remained an absolute barrier to rapid diagnostics. Not so with molecular tests, which are ever faster, currently easily achievable in the same half-day, and perhaps soon within the hour. These tests can furthermore be brought to bear not only on questions of identification, but also antibiotic resistance. The latter remains a very significant contributor to the necessary delay incurred by the need to not only grow the organism, but to then subsequently re-grow it (or not) in the presence of a range of antibiotics. Delay times of 72 hours continue to be accepted – if not acceptable. Similarly, gone are the bad old days where initial forays into microbe detection were constantly marred by issues of cross contamination and false positive results due to PCR product contamination at the front end of the process, although false conclusions can still be made for such reasons of exquisite sensitivity, as illustrated in one of this book’s chapters.

These technologies are now also being brought to bear on myriad other matters of Human Biology as this relates to our Genome, both in health and disease, inherited and acquired. There are parallels here with pathogen diagnostics, where initially monoplex PCR-based systems are being replaced by several other far more advanced search strategies – both in terms of “wet chemistry” but also in silico.

Accordingly, the time is rapidly approaching where the technology will make it simpler and cheaper to openly sequence the tumour or even the whole individual, and then subsequently ask relevant questions of sequence in silico.
Many challenges remain: can, where and why should this technology be applied near to the patient? The much-vaunted and possibly rather ill-defined “Point of Care Testing” paradigm is nowhere near being resolved – due not so much to the power of the technology to deliver in such a format, but more because such instruments have to contribute to delivering a clinical solution, rather than merely a test result. Knowing that a sequence of interest, either human or pathogen, is, or is not there – is pointless if you cannot bring this to bear on an improved clinical outcome.

Similarly, how to reduce the vast amount of data which the more recent Next Generation technologies yield for Human Genomes into a framework of “normality”? This last question can only be answered when our data layers are sufficiently populated with Human sequence information in order to intelligently interpret any particular sequence variant. This will take time, although thankfully it appears that Cloud Based computing can stay one step ahead of the vast computational needs of such problems.

I suspect that the rapidly emerging field of Human transcriptomics will also very heavily rely on such high dimensional computing power.

In conclusion, what only a few years ago remained the property of very few, very well funded academic centres, with publications rather than patient benefit as output, is set to step into the clinical arena – providing not just test results, but solutions for far more complex problems.

And yet – we remain several years away from seeing the every day application of such powerful technologies truly embedded for patient benefit.

Nevertheless, molecular diagnostics have arrived and are here to stay. I’m not sure where “here” is, or will end up. But I do look forward to watching the “here” emerge and take its place at the centre of the New Medicine.

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