SIR2002: its heir SIR2004 and IL MILIONE

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SIR2002 is a well established program for the ab initio crystal structure solution of small-, medium - and macro-molecules ([1]Burla et al. 2003). It does not need prior information but requires atomic resolution for the experimental data. The heir of **SIR2002**, the package **SIR2004**, is under beta-testing. It shows several advantages :

1) the sequential procedure of **SIR2002** (all the trials provided by the tangent procedure are sequentially refined in direct space) is replaced by a faster procedure using early figures of merit just after the tangent step. This eliminates non promising trials and makes the procedure much faster.
2) the phasing process has been powered , and allows to solve protein structures even if data have quasi-atomic resolution (1.4 A) ([2] Burla et al. 2003).

SIR2004 has been implemented into the package **IL MILIONE** , a set of programs designed for global phasing.

It is able :

1) to combine direct methods with SIR-MIR, SIRAS-MIRAS, SAD-MAD techniques (i.e., substructure determination, structure factor phasing, solvent flattening).
2) to solve and refine crystal structures from powder data.

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