Sensitivity test of a source-receptor model(*)

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Summary. — A source-receptor model, derived with a few modifications from the algorithm developed by Stohl in 1996, has been applied for assessing the locations of emission sources of airborne tracers. In this paper, the model sensitivity to the number of receptor points and iterations needed to reconstruct a reliable picture of spatial position of tracer sources has been assessed. This has been done by simulating some sets of schematic air trajectories, and assigning *a priori* both the position of some sources in given cells of a horizontal grid, and the atmospheric concentrations of the tracer associated to each trajectory crossing pre-assigned receptor points. The conditions allowing the model to locate correctly the sources, together with a useful rule for dealing with the grid cells crossed by a limited number of trajectories, have been established.

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1. – Introduction

Seibert *et al.* [1] created in 1994 a new algorithm to estimate the strength and location of sources and sinks of greenhouse gases emitted into the atmosphere; their approach was then completed by Stohl in 1996 [2]. This algorithm, based on a matching of a dynamical model of atmospheric transport and a statistical model for assessing the spatial field patterns of CO_2, represents a promising alternative to the so-called "inversion models" [3, 4] and [5].

The inputs of these models are

a) the concentration measures of a greenhouse gas at each monitorig site (hereafter, receptor point);

b) the backward air trajectories starting at the greenhouse gas receptor point.

(*) The author of this paper has agreed to not receive the proofs for correction.

As a first step, the concentration data are processed in order to remove the annual trend and seasonal variations. Then, the considered geographical region is splitted into mxn cells, and the concentration field is calculated in each cell according to the following relation:

$$\overline{C}_{mn} = \frac{\sum_l \tau_{mnl} \log(c_l)}{\sum_l \tau_{mnl}},$$
(1)

where τ_{mnl} is the residence time in the grid element (m,n) of the l-th trajectory and c_l is the concentration linked to the l-th trajectory. Seibert *et al.* [1] computed the concentration field according to this relation.

Stohl [2] added an iterative process that is composed by the following steps:

1) the trajectory is splitted into points;

2) the mean concentration in the grid cell hit by the i-th point of the l-th trajectory is computed by means of the relation

$$X_{il} = 10^{\overline{C}_{mn}(i)};$$
(2)

3) the average of the mean concentrations over all grid cells hit by the points of the l-th trajectory is calculated as

$$\overline{X}_l = \frac{\sum_{j=1}^{N_l} X_{jl}}{N_l};$$
(3)

4) the redistributed concentrations along the trajectory are evaluated as

$$c_{il} = c_l \frac{X_{il} N_l}{\sum_{j=1}^{N_l} X_{jl}};$$
(4)

5) the process from point 1) to point 4) is recursively repeated for all trajectories;

6) the new concentration fields are computed with the equation

$$\overline{C}_{mn} = \frac{1}{\sum_{l=1}^{M} \sum_{i=1}^{N_l} \tau_{mnli}} \sum_{l=1}^{M} \sum_{i=1}^{N_l} \log(c_{il}) \tau_{mnli};$$
(5)

7) a 9 point smoothing to the gridded values is applied;

8) the process is iterated until the average difference between the concentration field of two successive iterations is below a fixed value.

There have been some applications of this methodology in the literature to real cases: Charron *et al.* [6] applied Seibert's original algorithm to the identification of European area sources of acid pollutants; Stohl [2] applied his method to the detection of European zones responsible for sulfate emission.

We have applied Stohl's algorithm, in particular to look for CO_2 sources and sinks, but we found that there were some open points left, especially concerning the definition of the number of iterations, the criteria to decide about the possible exclusion of cells
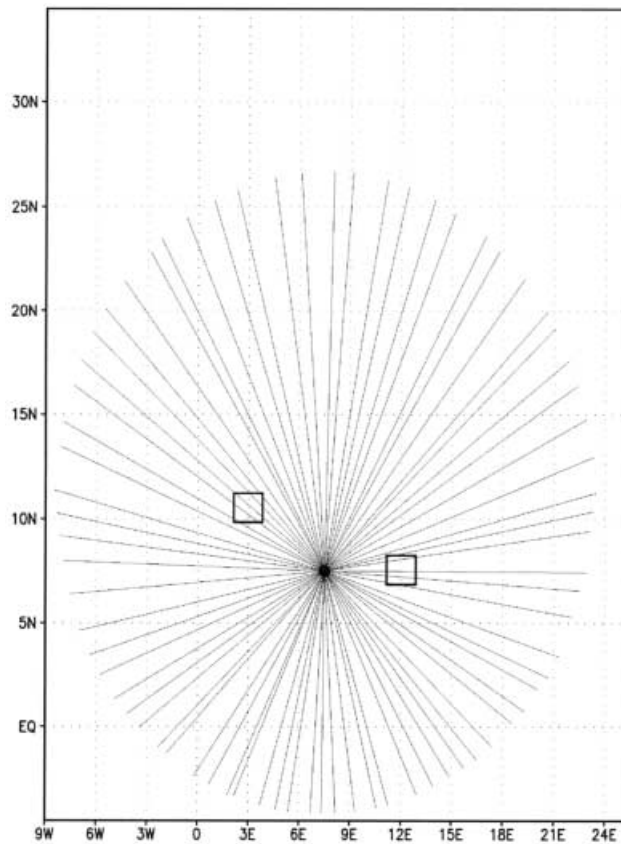
Fig. 1. – The 72 simulated straight artificial air trajectories are shown; the receptor station position is represented by a solid circle, the positions of the two fixed sources are shown by the two open squares.

crossed by a low number of trajectories and the settlement of the range used for the graphical representation of concentration fields. In order to use this model correctly, it has been necessary to make some sensitivity tests, mainly as far as the ability of the model to locate reliably the sources and sinks is concerned.

In conclusion, it was necessary to answer the following questions:

a) Can the pattern of a trajectory set have an influence on the results?

b) How many iterations are necessary to obtain a realistic CO_2 field?

c) How should be treated cells crossed by just a few trajectories?

d) Which is the importance of the monitoring station number?

And, finally, the above-mentioned main question that overshadows the previous three:

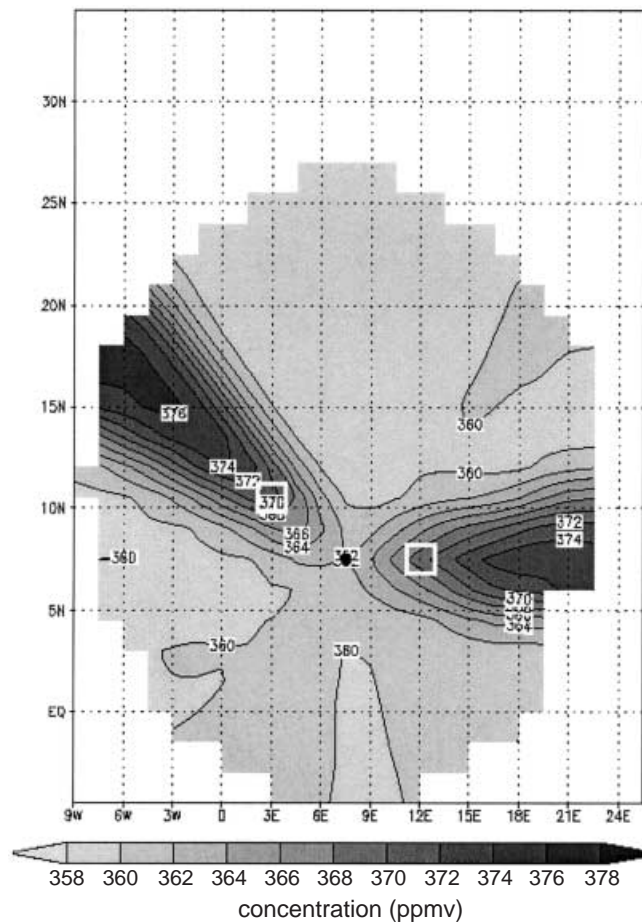e) Is this model suitable to identify sources and sinks?

Fig. 2. – The concentration field predicted by the first step of the model (Seibert's algorithm) is shown.

2. – Model tests

The model has been submitted to some artificial reference tests with the purpose to answer the above five questions. Different patterns of air trajectories have been simulated, from the simplest case of rectilinear trajectories not intersecting each other with only one receptor point, to the more realistic case of curvilinear trajectories intersecting each other, with two receptor points.

$2^{.}1$. *Test 1*. – A set of 72 simulated straight artificial air trajectories, crossing one *a priori* selected receptor site at different times, has been created. In fig. 1 the receptor station position is represented by a solid circle. All trajectories are composed by 200 points, separated from each other by a time step of 36 minutes; in this way, the length of each trajectory corresponds to 5 days. Air speed was allowed to change continuously with direction, but has been kept constant with time; a minimum speed has been selected for northward trajectories (3 m/s), while a maximum speed has been assigned to southward trajectories (5 m/s) and an intermediate speed to other directions. The trajectories are
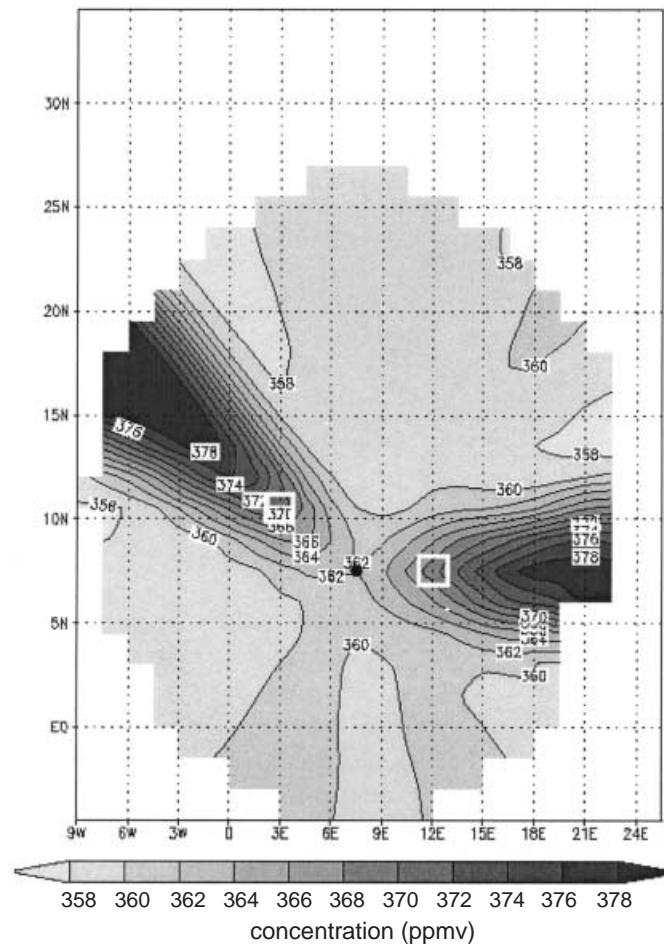
Fig. 3. – The concentration field after the first interation according to Stohl's method is shown.

almost equally distributed in space with a small random margin: in fact, the directions they come from are spaced by angular steps of $(5 \pm 2\alpha)$ degrees, where α is a random number fluctuating from 0 to 1. The whole trajectory set is drawn in fig. 1. The surface geographical domain is composed by a grid of 24 cells in longitude and 27 cells in latitude; the extension of each cell is 1.5×1.5 degrees. Two fixed sources are located in two cells; their positions are marked in the figures by two open squares. Their distances from the receptor station are different. The air trajectories crossing the cells where the sources are located are associated with high values of CO_2 at the receptor site (between 374 and 378 ppmv), while all other trajectories have low values (between 358 and 362 ppmv). The specific value of CO_2 assigned to each trajectory at the receptor station is created by a random number generator algorithm.

The model can provide, as an output, the average concentration values and concentration maps of CO_2 over the integration grid at each iteration; in this way it is possible to monitor the evolution of the field towards its equilibrium pattern. It has been observed that at each consecutive iteration the standard deviation of the average field over the
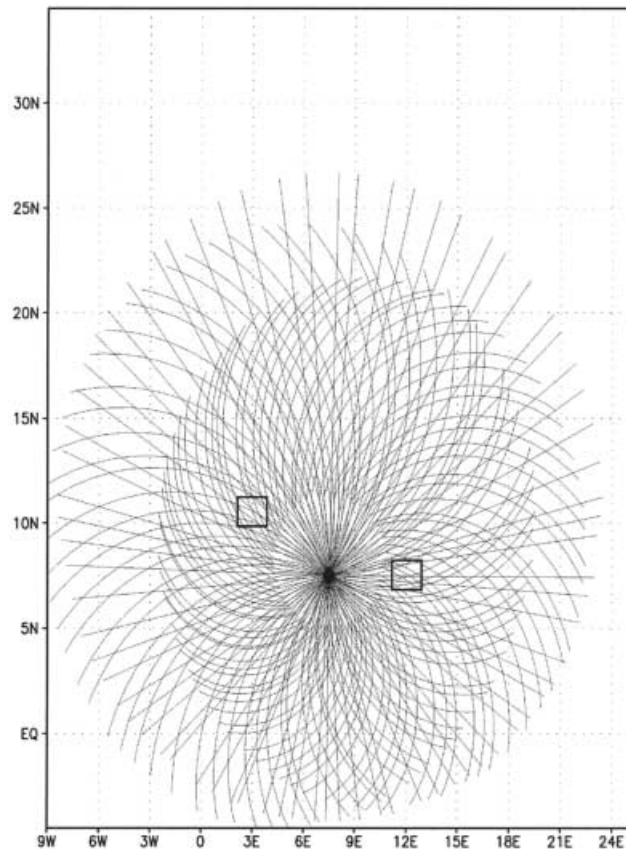
Fig. 4. – The 3 artificial trajectory sets are shown; the receptor station position is represented by a solid circle, the positions of the two fixed sources are shown by the two open squares.

integration grid increased: the concentration field at each cell became less uniform and showed sharper and larger maxima and minima. At each iteration the values for maxima (minima) rose (diminished) until they reached even non-realistic levels (more than 378 ppmv, less than 358). If, however, we fixed the range of the computed concentration pattern to the highest and lowest values recorded at the monitoring station, the non-realistic values were not anymore visible and the maxima did not evolve with any further iterations once the upper limit of the scale was reached.

For this reason, fixing the range also means to fix the number of iterations. Therefore, to find this number is sufficient to fix the range to the minimum and maximum values measured at the receptor site and then to consider only the iteration step after which the concentration field stops evolving. This rule will be used in the following tests.

Some more quantitative results are shown in figs. 2 and 3: in these graphics the extremes of the concentration range are fixed to 358 and 378 ppmv, respectively, corresponding to the above-mentioned minimum and maximum values recorded at the receptor site. Figure 2 shows the concentration field predicted by the first step of the model (eq. (1), Seibert's algorithm), while fig. 3 shows the field pattern after the first iteration according to Stohl's method (eq. (5)). In both cases it can be noted that the
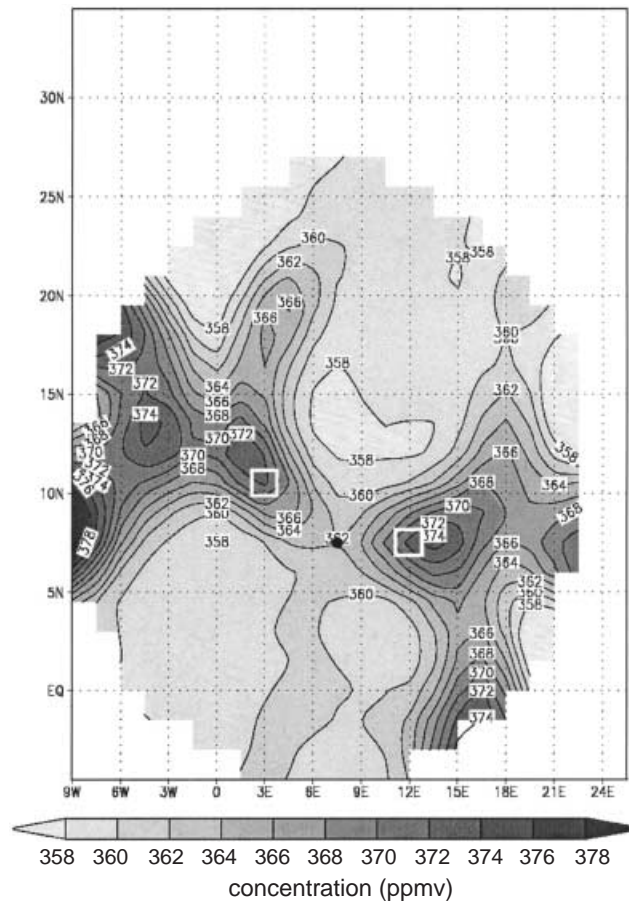
Fig. 5. – The concentration field after the third interation of the model is shown.

source locations do not correspond to the regions of computed maxima, which are close to the boundaries of the domain. The first guess (Seibert's model, fig. 2) underestimates also the maximum value, which is reached instead with the first iteration (Stohl's model, fig. 3). The computation stops after the first iteration, because the value of 378 ppmv is reached and also because the subsequential iterations do not modify substantially the calculated field.

With the first test using only straight trajectories it is not possible to determine correctly the locations of the sources, especially with Seibert's first guess. On the basis of these preliminary considerations, it has been decided to adopt, in the following tests, only Stohl's model, which uses an iterative method.

2˙2. *Test 2*. – In order to consider a more realistic situation, including also trajectories crossing each other, 3 new artificial trajectory sets have been created (fig. 4). The first one is composed by 72 straight trajectories (it is the same set of the previous test), the second one is made by 72 anticyclonic trajectories (they bend by 5 degrees every 12 points), the third one is made by 72 trajectories whose first 40 points lie on straight lines and the subsequent ones lie on curved lines (they bend by 7 degrees every 12 points).
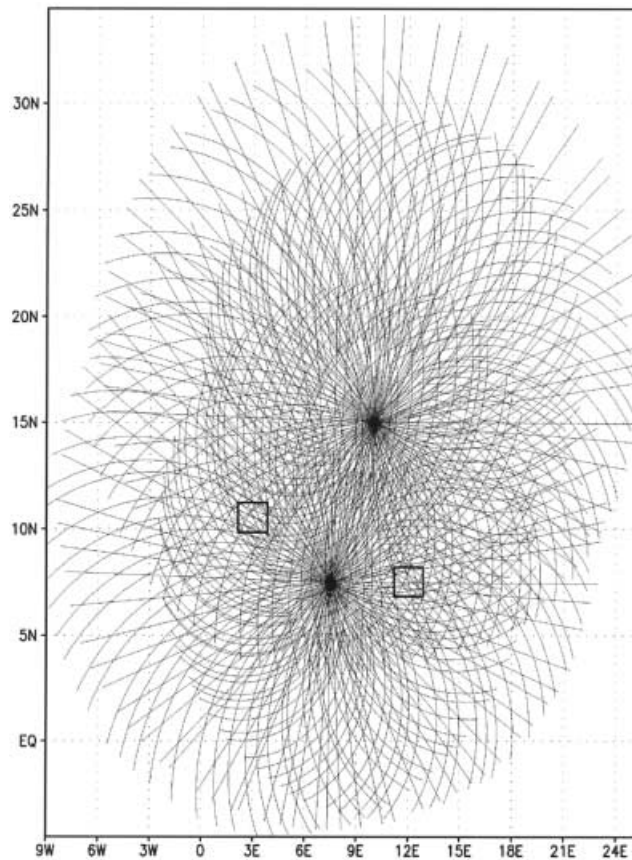
Fig. 6. – The 6 artificial trajectory sets are shown; the receptor station positions are represented by two solid circle, the positions of the two fixed sources are shown by the two open squares.

The whole ensemble of trajectories considered for this test is the superposition of the three sets just mentioned.

Figure 5 shows the third iteration of the model; in this picture two maxima nearer the sources appears. The maximum concentrations are between 372 and 376 ppmv. There are also 5 other maxima totally unrelated to the sources. Four of them are open maxima located in the shadow upwind of the sources and are still close to the domain boundaries, like in test 1. In the following subsections these maxima will be called "border maxima". The effect is the same of that observed in fig. 3: the cells crossed only by trajectories that will cross a source, become maxima. It looks as, with this model, upwind cells are somehow influenced by downwind sources. Of course, these maxima should obviously be excluded from the discussion of results: they are due to the particular pattern of trajectory set and are difficult to individuate and erase. In order to try to delete them, the number of receptor sites has been increased.

2˙3. *Test 3*. – A second receptor station has been now introduced; its position is marked in figs. 6 and 7 by a second solid circle. Trajectories involved in this test are drawn in fig. 6. Figure 7 shows the simulation (fifth iteration). In this case the model
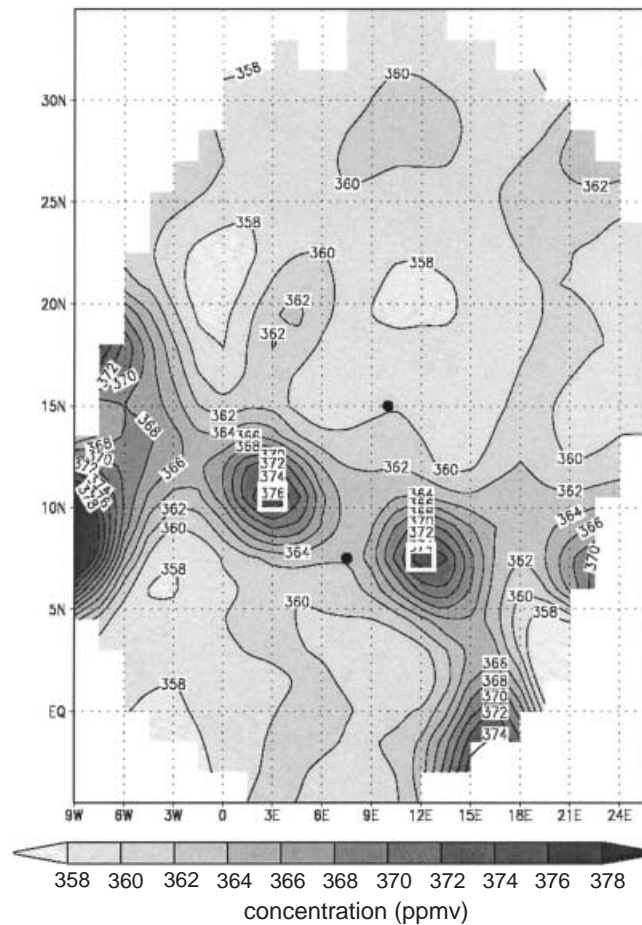
Fig. 7. – The concentration field after the fifth interation of the model is shown.

is able to identify the sources correctly, whereas the border maxima must be neglected again.

2˙4. *Test 4.* – At last, a real set of trajectories has been considered, to whom two sources of artificial strength have been assigned like in the previous tests. The backward trajectories start from the monitoring site located at Plateau Rosa (45.93 N, 7.70 E, 3480 m) and are computed by the model TRAIETN [7] using the ECMWF wind fields. The 1459 trajectories used in this test have been computed every 6 hours for the whole year 1997.

The third iteration (fig. 8) is already able to identify the two sources correctly, but it also shows some relative maxima, not corresponding to any sources (and then not to be considered). This test shows how, with a real set of trajectories and one receptor station, the model identifies correctly the two sources, but it has the drawback of showing other sources too. On the basis of previous tests, it is very likely that if two receptor sites had been available, the model would have enabled us to obtain satisfactory results.
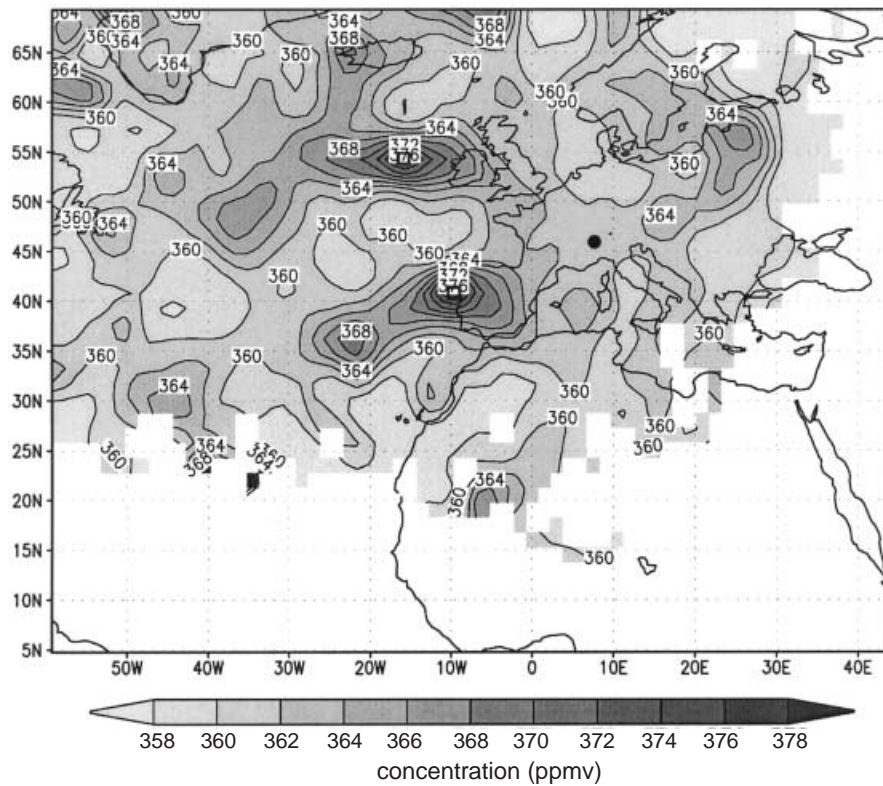
Fig. 8. – The concentration field after the fifth interation of the model is shown, in this case a real set of trajectories has been considered.

3. – Conclusions

The five tests executed have answered the five questions put in the Introduction.

a) The pattern of trajectory set can influence the result. If the trajectories are grouped into beams and do not cross each other, then the result is liable to errors; if, on the contrary, the trajectories follow different paths to arrive at the receptor site and they also cross each other, then the source areas can be located with enough accuracy.

b) Stohl [2] stops the iterative procedure when the average difference between the concentration fields of two successive iterations is below a predeterminated value. The problem then goes back to how identify this value. However, a suggestion coming from this study is to fix the range of the computed concentration pattern to the maximum and minimum values measured at the monitoring site and to iterate the algorithm until, even if the values of maxima (minima) keep on increasing (decreesing), this variation is not yet visible on graphics because it goes out of the upper (lower) limit of the considered range.

c) Stohl [2] deletes cells crossed by a limited number of trajectories. From the tests effected, it seems sufficient to delete the border maxima.

d) The number of receptor stations is important not only because it increases the

trajectory number and consequently improves the statistical treatment, but also because the trajectory sets arriving at different stations are more likely to cross each other, smoothing down in such a way maxima not corresponding to sources.

e) At least two stations are needed for a reliable identification of sources.

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